

Access DB# 86298

SEARCH REQUEST FORM

Scientific and Technical Information Center

M.A. WALICKA

CRF 09/218,702
09/218702

Requester's Full Name: 09/273, 957 Examiner #: 78201 Date: Feb. 6.03
 Art Unit: 1652 Phone Number 30 5-7270 Serial Number: 09/223, 957
 Mail Box and Bldg/Room Location: 10D06 Results Format Preferred (circle): PAPER DISK E-MAIL
10D01

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Phenol oxidizing enzymes

Inventors (please provide full names): WANG et al.

Earliest Priority Filing Date: 12/22/98

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Point of Contact:

Thomas G. Larson, Ph.D.
703-308-7309
GM1, Rm. 6 B 01

Thank you in advance
Please rush.

Wälcke

ABSSD print, 9/21/12
2/11/12
2/12/12

REC-6
(516)

C. Chan
Rush

Point of Contact:
Thomas G. Larson, Ph.D.
703-308-7309
CM1, Rm. 6 B 01

STAFF USE ONLY

Searcher: Larson

Searcher Phone #:

Searcher Location: _____

Date Searcher Picked Up: 2/11

Date Completed: 2/13

Searcher Prep & Review Time: 15

Clerical Prep Time:

Online Time: 16

Type of Search

NA Sequence (#) 2

AA Sequence (#) 1.

Structure (#)

Bibliographic _____

Litigation _____

Fulltext

Patent Family

Other _____

Vendors and cost where applicable

STN

Dialog

Questel/Orbit

Dr. Link _____

Lexis/Nexis

Sequence Systems **ABSS04**

WWW/Internet

Other (specify) _____

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 17:10:31 ; Search time 4505.67 Seconds

(without alignments) 11568.344 Million cell updates/sec

Title: US-09-218-702-1

Perfect score: 1791
Sequence: 1 gtcaataatgcgcgttcaacgc.....atcttgagatcgagagagtaa 1791

Scoring table: IDENTITY_MUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3: gb_in: *
4: gb_om: *
5: gb_ov: *
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9: gb_pr: *
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32: em_hlg_other: *
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1791	100.0	1791	6	AR211556	AR211556 Sequence
2	1778	99.3	7259	6	AX384798	AX384798 Sequence
3	1474	82.3	3677	6	AR211554	AR211554 Sequence
4	685.8	38.3	2126	8	AM0271104	AJ271104 Acromioniu
5	573.2	32.0	1942	8	MYRBOR	D12579 M. verrucar
6	573.2	32.0	1959	6	E05283	E05283 Biliirubin O
7	503.4	28.1	2905	6	AR211555	AR211555 Sequence
8	502.8	28.1	2063	6	AR211557	AR211557 Sequence
9	460.4	25.7	1958	6	AR122996	AR122996 Sequence
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ALIGNMENTS

RESULT 1
AR211556
LOCUS AR211556 1791 bp
DEFINITION Sequence 5 from patent US 6399329.
ACCESSION AR211556
VERSION AR211556.1 GI:21514909
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1791)
AUTHORS Wang, H. and Bodie, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 5 04-JUN-2002;
FEATURES Location/Qualifiers

Source 1. 1791
/organism="unknown"
BASE COUNT 380 a 551 c 451 g 409 t
ORIGIN
Query Match 100.0% Score 1791; DB 6; Length 1791;
Best Local Similarity 100.0% Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
AX384798 7259 bp DNA linear PAT 19-MAR-2002
LOCUS AX384798
DEFINITION Sequence 3 from Patent WO0196543.
ACCESSION AX384798
VERSION AX384798.1 GI:19577933
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
unclassified.
REFERENCE
1
AUTHORS Hood, E., Howard, J.A., Bailey, M., van Gestel, F.J., Ward, M., Wang, H.
TITLE Method of increasing recovery of heterologous active enzymes
JOURNAL Patent: WO 0196543-A 3 20-DEC-2001;

FEATURES
source
1. 7259
/organism="unidentified"
/db_xref="taxon:32644"
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BASE COUNT 1928 a 1745 c 1583 g 1997 t 6 others
ORIGIN

Query Match 99.3%: Score 1778; DB 6; Length 7259;
Best Local Similarity 99.9%: Pred. No. 0;
Matches 1790: Conservative 0; Mismatches 0; Indels 2; Gaps 1;

1 GTCATATATCTGTTCAAGTCATGGCAACTGGCAGACGCTCCGGGCTCGTCTGGAGTC 60
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61 CTCGGCATCCCGATGGACACCGGACGACCCCATTTGAGGCTGTGATCCCGAAGTGAAG 120
5261 CTCGGCATCCCGATGGACACCGGACGACCCCATTTGAGGCTGTGATCCCGAAGTGAAG 5320
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181 CCATACAACTGCTTTACAGAAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATG 240
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6941 AGCGGTACAACCGCTTCGATGAGATCTCTGAGAGATCTTGAATCGAGAGATA 6992

RESULT 3
AR211554
LOCUS AR211554 3677 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6399329.
ACCESSION AR211554
VERSION AR211554.1 GI:21514906
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3677)
AUTHORS Wang, H. and Bodie, E. A.

TITLE	Phenol oxidizing enzymes									
JOURNAL	Patent: US 6399329-A 1 04 -JUN-2002;									
FEATURES	Location/Qualifiers									
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ORIGIN										
Query Match	82.3%;	Score 1474;	DB 6;	Length 3677;						
Best Local Similarity	87.0%;	Pred. No. 3.1e-311;								
Matches 1791;	Conservative	0;	Mismatches	0;	Indels	267;	Gaps	5;		
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Db	1098	CTGGCATCCCGATGGAGCAACGGGACGCCACCCCATTTGAGGCGTTGATCCCAAGGAAG	1157							
OY	121	ACTGAGGCTTCGCGAGCATCCCTCCCTTGGTCGAGCAGGAGGATGAGACACTGGGAGTACCT	180							
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OY	199	-----AGGAATGCCCTGCAATTCACCTGCATCAGACAGCCCAAGAT-----	239							
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OY	240	-----GATCATTTACCAACCTGTGCAC	260							
Db	1338	TTTCTACGAGCAACTCGGGCCCCCGACTATATGATTTCTAGATCATTTACCAACCTGTGCAC	1397							
OY	261	CGGCAAGGACATTTGGTACTATGAGATGAGATCAACGCCATTTTCAGCAAAAG-----	311							
Db	1398	CGGCAAGGACATTTGGTACTATGAGATGAGATCAACGCCATTTTCAGCAAAAGGATGTTT	1457							
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OY	584	-----AAGCTGCTAGAAATGGCTACTTTGGTCAGGCTGCGCCCTACATT	627							
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QY	1294	AAGCCGAGCTCGGACCGCTTGAAGGTCTGGAGACTGAGAACTCCCTGTGAGAGCTGAGAC	1353
Db	2598	AAGCCGAGCTCGGACCGCTTGAAGGTCTGGAGACTGAGAACTCCCTGTGAGAGCTGAGAC	2657
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LOCUS	AMU271104	2126 bp	linear
DEFINITION	Acromonium murorum mRNA for polyphenol oxidase (ppoa gene).		
ACCESSION	AJ271104		
VERSION	AJ271104.1	GI:6996277	
KEYWORDS	oxidase; ppoa gene.		
SOURCE	Acromonium murorum		
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Hypocreaceae; mitosporic Hypocreaceae; Acromonium.		
REFERENCE	1 (bases 1 to 2126)		
AUTHORS	Gouka, R.J., van der Heiden, M., Swarthoff, T., and Verrips, C.T.		
TITLE	Cloning of a phenol oxidase gene from Acromonium murorum and its expression in <i>Aspergillus awamori</i>		
JOURNAL	Appl. Environ. Microbiol.	67 (6),	2610-2616 (2001)
MEDLINE	21268855		
PUBMED	11375170		
REFERENCE	2 (bases 1 to 2126)		
AUTHORS	Gouka, R.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-JAN-2000)		
	Gouka R.J., Biotechnology, Unilever Research Vlaardingen, Olivier van Noortlaan 120, 3133 AR Vlaardingen, NETHERLANDS		
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[illegible]

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RESULT 5
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LOCUS MYROR 1942 bp mRNA linear PLN 01-FEB-2000
DEFINITION M. verrucaria mRNA for bilirubin oxidase, complete cds.
VERSION D12579
DI2579.1 GI:456711
KEYWORDS bilirubin oxidase.
SOURCE Myrothecium verrucaria (strain:MT-1) cDNA to mRNA.
ORANISM Myrothecium verrucaria
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.
REFERENCE 1 (bases 1 to 1942)
AUTHORS Kojikawa, S., Ando, K., Kaji, H., Inoue, T., Murao, S., Takeuchi, K. and Samejima, T.
TITLE Molecular cloning of the gene for bilirubin oxidase from Myrothecium verrucaria and its expression in yeast
J. Biol. Chem. 268 (25), 18801-18809 (1993)
MEDLINE 93366794
REFERENCE 2 (bases 1 to 1942)
AUTHORS Ando, K.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1992) Keiichi Ando, Amano Pharmaceutical Co., Ltd., Tsukuba Research Laboratories; 22 Miyukioka, Tsukuba, Ibaragi 305, Japan (Tel:0298-56-5026, Fax:0298-56-5012)
COMMENT On Feb 26, 1994 this sequence version replaced gi:436235.
Submitted (07-JUL-1992) to DDBJ by: Keiichi Ando
Tsukuba Research Laboratories
Amano Pharmaceutical Co., Ltd.

22 Miyukioka
Tsukuba
Ibaragi 305
Japan
Phone: 0298-56-5026
Fax: 0298-56-5012.
Location/Qualifiers
1. 1942
FEATURES
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Query Match 32.0%; Score 573.2; DB 8; Length 1942;
Best Local Similarity 62.1%; Pred. No. 1.2e-114;
Matches 972; Conservative 0; Mismatches 581; Indels 12; Gaps 4;
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E05283
ACCESSION
E05283.1 GI:2173473
VERSION
JP 1993199882-A/1.
KEYWORDS
Myrothecium verucaria.
SOURCE
Myrothecium verucaria.
ORGANISM
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.
REFERENCE
1 (bases 1 to 1959)
Ando, K., Koike, S. and Samejima, T.
PRODUCTION OF BILIRUBIN OXIDASE
Patent: JP 1993199882-A 1 10-AUG-1993;
AMANO PHARMACEUT CO LTD
COMMENT
OS Myrothecium verucaria
PN JP 1993199882-A/1
PD 10-AUG-1993
PE 24-JAN-1992 JP 1992034126
PI ANDO KEIICHI, KOIKE S, SATOSH, SAMEJIMA TATSUYA PC
C12N1/53, C12N1/19, C12N9/06, (C12N1/53, C12R1:645); CC
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CC topology: Linear;
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Best Local Similarity 62.1%; Pred. No. 1.2e-114;
Matches 972; Conservative 0; Mismatches 581; Indels 12; Gaps 4;
QY 206 CCTGCAATTCACCTGTCACGACGACCAAGATGATTCATTCACCAACCTGTCACGCA 265
DB 220 CACTGCCAATTCCTCTGTTAAGCAGCCCGCTGCTGACTATACCAATTCCTGTAATGAC 279
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RESULT 7
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LOCUS AR211555
DEFINITION Sequence 3 from patent US 6399329.
ACCESSION AR211555
VERSION AR211555.1 GI:21514907
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2905)
AUTHORS Wang, H., and Bodle, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 3 04 -JUN-2002;
FEATURES
source 1..2905
BASE COUNT 714 a 792 c 664 g 734 t 1 others
ORIGIN

Query Match 28.1%; Score 503.4; DB 6; Length 2905;
Matches 998; Conservative 0; Mismatches 511; Indels 138; Gaps 5;

Oy 245 TTACCAACCTCTACACCGGCAAGACATTTGGTACTATGAGATCGAGATCAAGCCATTTC 304
Db 423 TCACGATCTCTTCACAAACAGAGATATGTTACTAGAGATTTGTCATCAACCTTCA 482
Oy 305 AGCAAGATTTTACCCACCTTGGCCCTGCCACTCTGTGCTGCTACGATGCAATGAGCC 364
Db 483 CCACAGAGTCTATCAAGCCCGCCGCTGCTTGTAGTACGATGACGCAATCTCC 542
Oy 365 CTGGCTACTTTCATGATGTTCCAGAGCAAGACAGCTAGTTAGGTTTCATCAACATG 424
Db 543 CAGGTCTTACATCATATGTCGCGAGAGACAGAGAGCTGTTTACGGTTTATTAACCAAG 602
Oy 425 CCACCGTGAAGACTCGGTGTCATCTGCAAGGCTCCCATCGCGTCCCTTTCGATGTT 484
Db 603 GTGATCGGAAAGCTCATCATCTGCAAGGCTCCCGTCCCGCTTTGACGAT 662
Oy 485 GGGCTGAAGATGTACCTTCCCTGGCGAGTACA----- 518
Db 663 GGGCTGATGATGATGATCAAGAGGGGAATCAAGGTACGATGCTGTGATCTACGC 722
Oy 519 -----GGATTTACTTTCACACTA 539
Db 723 ATCAGGAAGCTCTATCATACTTAACAGACTTTCTTCTCAGACTTACTACCCGAAACA 782
Oy 540 CCAATCCGCCCGCTTGTGTGTACCATGACCAACCTTCA----- 580
Db 783 CCAAGCTGCAATTTTGTGTACCAAGATCATGCTATGATGTTGAAGCTTTAACG 842
Oy 581 -----TGAAGACTGCTGAATG 598
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Oy 599 CCTATTTGTGTAGGCTGGCGCTACATTAACAGAGAGGCTGAGATGCTCGGCT 658
Db 903 CCTATTTGGGGAACCGCGGCTTCTGATTCAGACAGCCGGCTGAGATGCTCGGCG 962
Oy 659 TTCTAGTGGCTATGGAGATTGATATCCCTGATCTCGAGGCAAGTACTATTAAG 718
Db 969 TTCTTCAAGTTACGAAATATGACATTTCCGCTGTCTCAAGTACTCAACG 1022
Oy 719 CCGATGATCCCTGCTTCAGACGAGGTGAGACCAAGACCTGTGGGAGATGTCATCC 778

Db 1023 CCGATGAACTCTTAAGACCACTGTGGAGAGAACAAAGATGTTGGGGCGACATCATCC 1082
Qy 779 ATGTACGGAGAGACATGGCTTTCCTTAAGCTCCAGGCCCGGCAAGTACCGTTCCGAT 838
Db 1083 ATGTACAGGAGTACCGCTGGCTTCTTAAGTGTAGGACCTGAAAGTATGCTTCGAT 1142
Qy 839 TCCCTAAGCTCCCTGTCCTGCTGGCTCCTGCTACCTGCTCAGAGACCACTCTCCCA 898
Db 1143 TCCCTAAGCGGCTTTCCTTAAGAACTTGGCCCTTACTTCTGCTCAAGCAAGAACACTG 1202
Qy 899 AGCTGAAATTCCTTTCAGATGATTCCTGATGCTGCTCTTCAAGCCCGCTTC 958
Db 1203 CCAGTACGCTCTTTCAGCTGATTCCTGATGCAAGGGCTACTCACACCGCGTTTC 1262
Qy 959 AGACCTTACCTTACCTGCTGCTGCTGGAGCGTTAGAGATCATTTATGACTTCACA 1018
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Qy 1019 ACTTGTGCGGAGAGACTTGTGACCTGGCCAGCTTGTGAGACCAAGATGTCGGGAGC 1078
Db 1323 CCTATGCCCGCAAACTGTGATGCTGCGCACTTGGCAAAAGGCAATGATTCGGTACC 1382
Qy 1079 AGATGAGTACGCTGCTGCTGCTGAGGTGATGCGCTGCTGCTGCTGCTGCTGCTG 1138
Db 1383 AGGAGACTACGCAAACTGACAAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1442
Qy 1139 AGGACAAAGCAAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1198
Db 1443 TCGATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1499
Qy 1199 GCGCCGCGCAGACACTTCAAGTTTGAAGCAGCAAGCAAGCAAGCAAGCAAGCAAG 1258
Db 1500 CCGACATAGACATCATCTTCCCTTTCATCTGATCAGCAAGCGGAGGCGCATCAAGCA 1559
Qy 1239 TTGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1318
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Db 1620 TTGGGAACCTTGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1679
Qy 1379 ACTTCAAGTCTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1432
Db 1680 ACTTCAAGTCTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1739
Qy 1433 CTGCTGCTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1492
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Qy 1612 --GACTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1669
Db 1920 CTGATTTCCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1979
Qy 1670 TCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1729
Db 1980 TCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2039
Qy 1730 CCGAGCAGGAGCCTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1756
Db 2040 CGCTGAGAGAGCCTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2066

RESULT 8
AR211557

LOCUS AR211557 2063 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6399329.
ACCESSION AR211557
VERSION AR211557.1 GI:21514910
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2063)
AUTHORS Wang, H. and Bodie, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 6 04-JUN-2002;
FEATURES
source 1. 2063
BASE COUNT 501 a 604 c 510 g 448 t
ORIGIN
Query Match 28.1%; Score 502.8; DB 6; Length 2063;
Best Local Similarity 60.4%; Pred. No. 2.8e-99;
Matches 1000; Conservative 0; Mismatches 522; Indels 134; Gaps 5;
Qy 244 ATTACCAACCTGTACCGCGAAGCAATTTGTACTATGATGATGATGATGATGATGATGAT 303
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Qy 364 CCGTGCCTACTTTCATTAATGTTCCAGAGACAGAGACTGTAGTTAGTTCAACAAT 423
Db 430 CCAAGCCCTACATCATCTGCTGCGAGAGACAGAACCGCTTGTACGATTTCTAAACCA 489
Qy 424 GCCACCTGAGAACTCGGCTCATCTGCAGCGCTCCCATCGCGCTTTCGATGCT 483
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Qy 484 TGGCTGAAGATGTACCTTCCCTGGCGAGTCAA----- 518
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Qy 519 -----GATTACTACTTTCACCACTACC 541
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Db 670 AGGCTGCCAGATTTCTGTGTACACGATCATGTGATGATGATGATGATGATGATGATG 729
Qy 580 -----ATGAAGCTGTGGAATGCT 601
Db 730 AATCATGGAGGCAAAAGGAAAGATCGGGCTGACACTTATGACAGCTGGGAAATGCTT 789
Qy 602 ACTTGTGAGGCTGGCGCTTACATTAATCAACGAGGCTGAGATGCTGCGGCTTC 661
Db 790 ATTTTGAAGAGCTGGCGCTTACATGATACAGACCAAGCTAAGAGCGCTTGGCTTC 849
Qy 662 CTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 721
Db 850 CTTCGGGTTACGGAATAATACGATATCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTG 909
Qy 722 ATGTATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
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Qy 782 TCAAGCAGGAGCCTTTCCTTAAGCTCCAGCCCGCAAGTACGCTTTCGATTC 841
Db 970 TCAAGGCTAGCCCTGCGCTTCTTCAAGCTTGAAGCTTGAAGTATGCTTCAATTC 1029
Qy 842 TCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901
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OY	902	TCGAAATTCCTTTCCAAAGTCAATTGCCCTCGATGCTGGTCTCCTTCAAGCCCCCGTTCAGA	961
Db	1090	CTTAGACTTCTTTCCAGGTGCATTTGGCTCTGAATGCAGGGGCTACTCACGCACCGTGCAA	1149
OY	966	CCTTAACCTCACTTGGTGTGTGGCGAGCGTTAGAGATCTAATTAATGTGACTTCACCACACT	1021
Db	1150	CCTCAGATATTTTACGTGGCAGCAGAGAGCGCTACGAGATTTTATTCGACTTTGGCCCTT	1209
OY	1022	TTTGCGCCAGACTCTTGACCTGGCCCAACGTTGCTGAGACAACAGATGTGGCGCAGG	1081
Db	1210	ATGCAGCGCCAGCGATAGATTGTTCCTAACCTTTGCAAGAGCCCAATGGGTCGGCACCGATG	1269
OY	1082	ATGAGTAGCGTCGCACCTCGCGAGGATGCGGCTTGCTGTCAGCTCTGGCACTGTTGAGG	1141
Db	1270	ACGATTATGCAACACTGACAGAGTGTATGCGTTCCATCTACGACGCCAAGAGATGCTGTG	1329
OY	1142	ACAACAGCCAGGTGCCCTCCACTCTCCGTAAGTGTTCTTCCCTCCCTCAAGAGAAAGCC	1201
Db	1330	ATAATCGGTGGTACCCCGCAGCATATCTCAGATCCAGTTCCGCGCGACA-- -AAACCG	1386
OY	1202	CCGCCGACAGACACTTTCAAGTTTGAACGAGCAGCAACGGAACACTACTGATCCAACGATGTTG	1261
Db	1387	GCATGACCCACACTTCGCTTCATCTGCAACCAACGCAAGTGGGCATCAACGGCATCG	1446
OY	1262	GCTTTGCCGATGTCAATGAGCGCTGTCCTTGCCCAAGCCCGAGTGGCACCTGTTGAGGTCT	1321
Db	1447	GCTTTGCAAGAGCTCCAGAACCGTATCTGTGGCAAGGTACCGGGCGGCACCTGTGCGACTAT	1506
OY	1322	GGGAGCTCGAAGACTCTCTGTGGAGCGCTGAGCCACCCCGTGCCATTCACCTTTGTTACT	1381
Db	1507	GGGAACCTCGAGAACAGCTCTCCGGCGGCTGTCTCCACCCCCTTCACGCTCACTGTGCTGACT	1566
OY	1382	TCAAAATCCCTCAAGGGAACCTGGTG-----GTGCTGGCCAGGTCATGCCCTACGAGTCTG	1435
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OY	1436	CTGGTCTTAAAGATGTCTGTGGTGGGCGAGGGGTGAGAACCTCGAACATCGAGGCCACT	1495
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OY	1496	ACCAACCCCGAGACTGGAGCTTACATGTGGCACTGTGCACAACTCAATTCACAGAGATACG	1555
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OY	1556	ACATGATGGCTTATTTCAACGTCAACCGCCATGAGAGAGAAAGGATATTTCTCA---GGAAG	1612
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Db	1867	CGGCGCGAATCGGGGTATCTTCTCAAGAAAGATTCATCAAGGCTAGAGGCTAGAGTGAACGAGTTGGCG	1926
OY	1733	AGCAGAGCCGTACAAACCGCTCGATGAGATCTGG	1768
Db	1927	TGGAACAGCCGCTACAGCGAACTGAGCGCAAGGTCAAGG	1962

RESULT 9			
LOCUS	AR122996	1958 bp	DNA
DEFINITION	Sequence 1 from patent US 6168936.		linear
ACCESSION	AR122996		
VERSION	AR122996.1	GI:14107962	
KEYWORDS			
SOURCE	unknown.		
ORGANISM	unknown.		
	Unclassified.		

AUTHORS	Mang, H.
TITLE	Phenol oxidizing enzymes
JOURNAL	Patent: US 6168936-A 1 02-JAN-2001;
FEATURES	Location/Qualifiers 1. .1958
source	/organism="unknown"
BASE COUNT	394 a 593 c 490 g 481 t
ORIGIN	
Query Match	25.7%; Score 460.4; DB 6; Length 1958;
Best Local Similarity	59.3%; Pred. No. 56-90;
Matches 996; Conservative	0; Mismatches 521; Indels 163; Gaps
QY	241 ATCATTTACCAACCTGTACCCGCGCAGAGACATTTGGTACTATGAGATGACAGTCAAGCA 300
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QY	301 TTTTACGCAAGATTTTATCCCACTTGCCGCGCTGCACATCTGTCGGATGACATGGATG 360
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QY	421 A-----ATGCCACCGTGGAGAACTGGTGCATCTGACAGGCTCCCACTGGGTGCCCT 474
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QY	535 AACTACCAATCCGCCGCTCTGTGTGATCAATGACCAACGCTTTCATGAGACTGCTGAG 594
DB	557 AACAGGAGCGCTGCCCATGCTTTGGTATCAAGACCAATGACCATGTCATACCGCCGAG 616
QY	595 AATGCTACTTGGTGTGAGCGGTGGCGGCTCAATTATCAAGAGAGAGCGTGGAGATGCTGC 654
DB	617 AACGCTACTAGGGCTACAGCGGTGTCTATCATATCATCAGAGACCGCGGTGAGATCCCTG 676
QY	655 GGTCTCTCTAGTGGCTATGCGAGATTCGATATCCCTGATCCTGACGGCCAACTACTAT 714
DB	677 AACCTCCCAACGGCTACGGGAGATTTGATATCCCTTGTTCTGATGCCAAGGATAC 736
QY	715 AACGCCATGTATCCGTCGCTTGACCGAGGATGAGACCAAGACTGTGGGGAGATGTC 774
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QY	775 ATTCATGT----- 782
DB	797 ATTCAATGTTGTAAGTTAGCCCAATGAGATGCTTCAAGATCTTGAAGATATGCAATGATA 856
QY	783 -----CAAGGACAGCATGGCCCTTCTCTTAAG 811
DB	857 AATTGTGATGCTCTAACACAGTGTATCAACAGAAAGGTCAGCGCTTGACCTATGCTCAAG 916
QY	812 TCACAGCCCCGAAGTACCGCTTTCCGATTTCTCAAGCGTGCCTGTGCTGGTGGCTC 871
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QY	932 ATGCTGATCTCTTCAAGCCCGCTTCAGACCTCTAACCTTACTCTTGTGTTGCCAGC 991
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QY	992 GTTACGAGATATTATTGACTTACCAACAATTTTCTGTGGCCAGACTCTTGACCTGCGCAACG 1051
DB	1097 GCTGGAGGTTGTTAGCATCTTCCACACTTCCCTGGCCAGTCCATGATATTCGCCAAC 1156

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QY 1169 GTGACGCTCTTTCC-----TCCTCAAGAAGAGCCCGCGCAAGC 1213
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QY 1641 GGGCGGCTTCTTCAACCGCAAGCATTCATGCTGCGGCGTGAACCTTCCGCCCA 1700
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QY 1701 GTTCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1760
1874 TGCATCACTGACCGCATTCAGAGAGATGCTTCAACCCCTACGCCAGGCTGATGA 1933

RESULT 10
AX101096 1958 bp DNA linear PAT 10-APR-2001
LOCUS AX101096
DEFINITION Sequence 1 from Patent WO0121809.
ACCESSION AX101096
VERSION AX101096.1 GI:13619951
KEYWORDS
SOURCE Stachybotrys chartarum.
ORGANISM Stachybotrys chartarum.
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.
REFERENCE 1 (bases 1 to 1958)
AUTHORS Wang, H.
TITLES Stachybotrys phenol oxidizing enzyme
JOURNAL Patent: WO 0121809-A 1 29-MAR-2001;
GENECOR INTERNATIONAL, INC. (US)
FEATURES
Source Location/Qualifiers
1..1958
/organism="Stachybotrys chartarum"
/db_xref="taxon:74722"

BASE COUNT 394 a 593 c 490 g 481 t

ORIGIN
Query Match 25.7%: Score 460.4; DB 6; Length 1958;
Best Local Similarity 59.3%: Pred. No. 5e-90;
Matches 996; Conservative 0; Mismatches 521; Indels 163; Gaps 6;
QY 241 ATGATTACCAACCTTCAACCGGCAAGACATTTGTTAGTATGATGATCAAGCA 300
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 257 ACCGTCCCAACCCCAACACTGAGAGACATTTTACTACAGATGAGATAGGCC 316
QY 301 TTTCAGCAAGATTTTACCCACCTTGGCCCTGCACTCTGCTGCTGCTGCTGCTGCTG 360
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 317 TTCTCCACCACTTCAATCTGATCTGAGAGCCGCAACATGTTGATGATGATG 376
QY 361 AGCCGCTGCTCTTCAATGTTCCAGAGACACAGACTGATGTTAGTTATCAAC 420
377 TCCCAAGAGCTTCAATCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436
QY 421 A-----ATGCCACGCTGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 474
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 437 AGGAGAGAGACACCTTCCCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
QY 475 TTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 534
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Db 497 TTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 556
QY 535 AACTTACCAATCCCGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 594
557 AACGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 616
QY 595 AATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 654
617 AACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676
QY 655 GGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 714
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QY 715 AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774
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QY 775 ATTCATGT----- 782
1111 1111
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783 -----CAAGGAGAGCCATGCGCTTCTTCAAG 811
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 857 AATTGTGATGCTTCAACAGTGTATCAAGAGAGGTCAGCCCTTATGCTCAAG 916
QY 812 TCGAGCCCGCAAGTACCGTTTCCGATTCCTCAAGCGCTGCTGCTGCTGCTGCTG 871
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Db 917 TCGAGCCCGCAAGTACCGTTTCCGATTCCTCAAGCGCTGCTGCTGCTGCTGCTG 976
QY 872 TCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 931
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QY 932 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 991
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QY 992 GTTCAGAGATCATTTATGACTTCAACACTTGTGCTGCTGCTGCTGCTGCTGCTG 1051
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Db	1277	GAGATGTTCTCTTTTCCCGAGGGCGGCAACTGGGACCCCGCAAAACCCCACTAGACGAGA	1336	
QY	1214	ACTTCAGATTTGAACGACAGCAACGACACACTACCTATCAACGATGTGGCTTTGGCGATG	1273	
Db	1337	CTTTCACCTTGGCGCGCTGCTATATGACAGATGACATATCAACGAGATTACCTTCTCGATG	1396	
QY	1274	TCAATGAGCGTGTCTGGCCAAAGCCCGAGCTGGCACCCTTGAGGTCTGGGAGCTCGAGA	1333	
Db	1397	TGGAAGAACGTCGTGCTCCGCAATGTGCCCGCGACACATGTTGAGATCTGGCGACTTGGAGA	1456	
QY	1334	ACTGCTTGGAGAGCTGGAGGCCACCCCGTCCACATTCACCTTGTATCTTCAAGATCTCA	1393	
Db	1457	ACAACCTCCAAACGCTTGGAGCTACCTGTTTCATTCACCTGTTGATCTCCGAGCTCTT	1516	
QY	1394	AGCGAAGCTGTGGTGTGGGCGAGCTCATGCCCTACGATCTGTGCTTAAAGATGTGCG	1453	
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QY	1454	TCTGTGTGGGCAAGGGGTGAGACCTTGACCAATGAGGCCCACTACCAACCTGAGC----	1508	
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QY	1509	-----TGGAGCTTACAT	1520	
Db	1634	TTCCTGCGCTTTTACTTAAGTGGTTTCACTCATGCTTAACATCTTACAAGTGGTGTCTACAT	1693	
QY	1521	GTGGCACTGTCAACAACCTCATTTACAGAGAGTAAACGACATGATGCTGTATTCAACGTCAC	1580	
Db	1694	GTTCGACTGCCCAACCTGTATCTCAGAGGACACACATGATGGCTGTTCATATGTAC	1753	
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Sequence 1 from Patent WO0121748.				
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VERSION				
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KEYWORDS				
SOURCE				
ORGANISM				
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Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.				
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1 (bases 1 to 1958)				
AUTHORS				
Convents D.U., Doornink M.U., de Vries C.H. and Wang H.				
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AUTHORS	1		
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JOURNAL	Topozada, A., de Vries, C. H. and Wang, H.		
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ORIGIN			
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Best Local Similarity	59.3%;	Pred. No. 5e-90;	
Matches 996;	Conservative 0;	Mismatches 521;	Indels 163; Gaps 6;
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OY	361	AGCCCTGGCTCCATCTTTTCANGTGTTCCCAAGGGAAGACAGACTGTGTAGTTCATCTCAAC	420
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Db	1097	GCTGGGAGTGTGTATGCACTTCTCCACACTCTGCTGGCGACGTCATCATATCCGCAAC	1156
OY	1052	TTGTCGAGAACCAAGATGTGGGCGAGAGAGATGATGACCTGCGACTGCGAGGTGATGC	1111
Db	1157	TTTCTGTGCTGAGCGTCTGTGTGTGAGCTGTAGTGTATACACTGACAAAGGTCAATGC	1216
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Db	1277	GAGATGTTCTCTTTTCCCGGAGGGCGGCACTGGGACCCCGCAAAACCCCACTGATGACGAG	1336
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LOCUS Sequence 3 from Patent WO0121809.
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ACCESSION AX101098.1 GI:13619952
VERSION AX101098.1
KEYWORDS
SOURCE Stachybotrys chartarum.
ORGANISM Stachybotrys chartarum.
REFERENCE 1 (bases 1 to 2095)
AUTHORS Wang, H.
TITLE Stachybotrys phenol oxidizing enzyme
JOURNAL Patent: WO 0121809-A 3 29-MAR-2001.
GENECOR INTERNATIONAL, INC. (US)
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source location/Qualifiers
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VERSION				

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Db	981	TGCAGCCGGCAGAGTACCGTCTCCGGTCTCTCAACGCTCCGCTCCACGCTTTTTCGCTC	1040
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Db	1041	TGTATCTGTCTACCTCTGAGGATTCAGAGACCAAGACTTCCCTTCACAGGTCAATGGCTGTG	1100
OY	932	ATGTGCTGTCTCTTCAAGCCCCCGTTACAGACCTTAACCTTAACCTGTCTGTGGCGAGC	991
Db	1101	ACGGTGGTCTGTCTTGAGGGCCCTGTGGACACTGTACACTGTACACTCTATGAGCGCAGAC	1160
OY	992	GTTACGAGATCATATTATTGACTTCTACCAACTTTTGCTGGCCAGACTGTGACTGTGGCAAG	1051
Db	1161	GCTGGAGGTTGTATGTACACTTCTCCACCTGTGCGTGGCAGTCCATGTGATATCCGCAAC	1220
OY	1052	TTGTGTAGACCACGATGTGTGGGAGAGGATGTAGTACGCTGTGCACTCTCGAGGTGATGC	1111
Db	1221	TTTCTGTGTGTGACGAGCTGTGGGTGTGAGCTGTAGTTTATTAACACTGTACAAGGTCAATGC	1280
OY	1112	GCTTCTGTCTACGCTCTGGGCACTGTTGAG--GACAAACAGCCAGGTCCCTCTTCACTCTCC	1168
Db	1281	GATTCGTGTGTGATGAGAGTCTCTTAGTGTGGCGGCACACTCTAGAGTGGCTGTGCACACTCC	1340
OY	1169	GTCAGTTCCTTTCC-----TCTTCACAAGAGAGCCCCCGCCGACAAAC	1213
Db	1341	GAGATGTTCCTTTCCCGGAGGGGCAACGTGGAGCCCCCAACCCCACTGATGTAGCAGA	1400
OY	1214	ACTTCAGTTTGAAAGCGAGCAAGGAGCACTACTGATTCAGCATGTGTGGCTTTGGCGGATG	1273
Db	1401	CTTTTACCTTGTGGCCGTGTAAATGAGACAGTGCACATTCACAGGAGTTCCTTCTGTGATVG	1460
OY	1274	TCAATGAGCGGTCTCTGGCCCAAGCCCGAGCTGGGCACTGTAGGCTGTGGAGGCTCGAGA	1333
Db	1461	TCGAGAACCGCTCTCTCCGCAATGTGTGCCCGGCACACTTGTAGATCTGTGGCACTTTGAGA	1520
OY	1334	ACTCTCTTGAGCGCTGGAGCCACCCTCGTCACATTCACCTTGTGTCAATCAATCTCA	1393
Db	1521	ACAACCTCCAACGGTTTGGACATCCACTGTTTACATTCACCTCGTTTACCTCCAGATCTTTT	1580
OY	1394	AGCGAACTGGTGTGTGTGGGCGCAGGTCAATGCGCTACAGTCTGTGTCTTAAGATGTGCG	1453
Db	1581	CTCTGTCCACTGCCCCGG---AGTGGAGCTTATATAGGCTCTGTGTCAAGGATGTTTG	1637
OY	1454	TCTGTGTTGGGAGGAGGAGAACCCCTGACACTGAGCGCCCACTACCAACCTGAGAC-----	1508
Db	1638	TCTGTGTGGCTCTGTGTGAGGTGTCTATGTTAGGCGCCACTAGCCTCTTTCCCGTAAAG	1697
OY	1509	-----TGAGCTTACAT	1520
Db	1698	TTTCTGCGCTTTTACCTAACAAGTGTTTTCACTCATGATTAACATCTACAAAGTGGTGTACAT	1757
OY	1521	GTTGGCACTGTACAACTCATTTACAGAGATTAACGATAGATGGCTGTATTCANAGTCAAC	1580
Db	1758	GTTGTACACTGCCACAACTGTATTCACAGAGGACCGACATAGATGGCTGTTCATAGTAC	1817
OY	1581	CGCCATGAGAGAGAGGATATCTTTCAGAGGACTTTCGAGAGACCCATATGAACCCCAATGTG	1640
Db	1818	TGTTTCTGGGTACTATGTGCTACAACTACACCGAGTTTCAATTAAGCCCATGTGAACCTCTCTG	1877
OY	1641	GCAGCGCGTTCCTTACAACGCAAGCAAGCTTCAATGCTGTGCGCTGGAGAAATTCCTCCGCGCA	1700

Db 1878 GAGGCCCCGCTTCCTCCTCGAGAGTTGAGAAATGGCTCGGATGACTTCAGCGAGCT 1937
QY 1701 GTCCATCACTGCCCGAGTGCAGAGCTGGCCGAGAGAGCGGTACACCGCCTCGATGA 1760
Db 1938 TGGCATCACTGACCGCATTCAGAGATGGCTACCTCAACCCCTACGCCCGAGGCTGATGA 1997

Search completed: February 13, 2003, 01:07:13
Job time : 4537.67 secs

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 17:04:56 : Search time 351.125 Seconds
(without alignments)
11486.872 Million cell updates/sec

Title: US-09-218-702-1

Perfect score: 1791

Sequence: 1 gtcacatgcctcttcacgtc.....atcttggaatcgagagagtaa 1791

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1791	100.0	1791	20	AAZ27601
2	1791	100.0	1791	21	AAA50019
3	1791	100.0	1791	21	AAA51314
4	1791	100.0	1791	24	AAAL47584
5	1790	99.9	7248	24	ABA92911
6	1786.2	99.7	1791	20	AAZ25727
7	1474	82.3	3676	20	AAZ25728
8	1474	82.3	3677	20	AAZ27602
9	1474	82.3	3677	21	AAA50018

10	1474	82.3	3677	21	AAA51313	Stachybotrys chart
11	1474	82.3	3677	24	AAAL47582	S chartarum phenol
12	1470	82.1	2067	20	AAZ25735	Stachybotrys chart
13	1470	82.1	2067	20	AAZ27609	Stachybotrys pheno
14	685.8	38.3	2110	21	AAZ61243	DNA encoding a phe
15	573.2	33.0	1959	14	AAO47790	Bilirubin oxidase
16	503.4	28.1	2905	21	AAA50020	Bipolaris spicifer
17	503.4	28.1	2905	21	AAA51315	Bipolaris spicifer
18	503.4	28.1	2905	24	AAAL47583	B spicifera phenol
19	502.8	28.1	2063	21	AAA50021	Curvularia pallasc
20	502.8	28.1	2063	21	AAA51316	Curvularia pallasc
21	502.8	28.1	2063	21	AAAL47585	C pallascens pheno
22	460.4	25.7	1958	22	AAAF30028	Stachybotrys chart
23	460.4	25.7	1958	24	ABK50918	DNA encoding pheno
24	460.4	25.7	1958	24	ABK50918	DNA encoding pheno
25	460.4	25.7	2095	22	AAAF82586	Stachybotrys chart
26	460.4	25.7	2095	22	AAAF30029	Stachybotrys chart
27	460.4	25.7	2095	24	ABK50919	DNA encoding pheno
28	460.4	25.7	2095	24	ABK53882	Stachybotrys chart
29	458.8	25.6	1958	22	AAAF82585	Stachybotrys chart
30	188.6	10.5	858	21	AAA50022	Amerosporium atrum
31	188.6	10.5	858	21	AAA51317	Amerosporium atrum
32	188.6	10.5	858	24	AAAL47586	A atrum phenol oxi
33	86.4	4.8	109519	22	AAAS08693	Micromonospora DNA
34	79.8	4.5	1533	22	AAH66018	C glutamicum codin
35	79.8	4.5	1614	22	AAAF71220	Corynebacterium gl
36	79.8	4.5	349980	22	AAH68527	C glutamicum codin
37	59.4	3.3	3446	23	ABU50557	Micromonospora car
38	45.8	2.6	4338	12	AAO11826	Encodes N-terminal
39	45.8	2.6	4649	10	AAAN90659	Sequence encoding
40	45.8	2.6	5721	11	AAO06613	Adenyl cyclase gen
41	45.8	2.6	6381	10	AAAN91167	Sequence encoding
42	45.8	2.6	6442	24	ABK50870	Botryella pertuss
43	44.6	2.4	1470	24	ABK74913	Bacillus lichenifo
44	43.4	2.5	32502	23	AAAS59412	Propionibacterium
45	43	2.4	426	20	AAV89078	EST clone CB15. H

ALIGNMENTS

RESULT 1	
AAZ27601	
ID	AAZ27601 standard; DNA; 1791 BP.
AC	AAZ27601:
XX	
DT	16-DEC-1999 (first entry)
DE	Stachybotrys phenol oxidase coding sequence.
XX	
KW	Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
KW	fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
XX	
OS	Stachybotrys chartarum.
XX	
PN	W09949020-A2.
XX	
PD	30-SEP-1999.
XX	
PF	23-MAR-1999; 99WO-US06327.
XX	
PR	24-MAR-1998; 98US-0046969.
PR	22-DEC-1998; 98US-0218702.
PR	22-MAR-1999; 99US-0273957.
XX	
PA	(GENEV) GENENCOR INT INC.
PI	Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;
DR	WPI; 1999-591088/50.
DR	P-PSDB; AAY39992.
XX	

PT Novel enzyme for modifying coloured compounds used to prevent
PT dye-transfer -

XX Claim 21; Fig 5; 64pp; English.

PS
XX
CC This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
CC of the invention. The invention is used to modify a coloured compound and
CC prevent dye transfer during fabric washing, or for stain bleaching or
CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC and food industries.

XX
SQ Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other:

Query Match 100.0%; Score 1791; DB 20; Length 1791;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCATATGCTGTTCAGTCATGCGACATGCGACAGCTCCGGGCTCCTGTCTGAGTC 60
DB 1 GTCATATGCTGTTCAGTCATGCGACATGCGACAGCTCCGGGCTCCTGTCTGAGTC 60
QY 61 CTCGGCATCCCGATGGACACCGGACCGACCCCATTTAGAGCTGTTGATCCGAAGTGA 120
DB 61 CTCGGCATCCCGATGGACACCGGACCGACCCCATTTAGAGCTGTTGATCCGAAGTGA 120
QY 121 ACTGAGGCTTCTGCTGACTCCCTCTTGTCTGACAGAGCGGATGACGACTGGAGTCACT 180
DB 121 ACTGAGGCTTCTGCTGACTCCCTCTTGTCTGACAGAGCGGATGACGACTGGAGTCACT 180
QY 181 CCATACACATCTGCTTTACAGGAATGCCCTGCCAATTCACCTGTCAAGACGCCAAGATG 240
DB 181 CCATACACATCTGCTTTACAGGAATGCCCTGCCAATTCACCTGTCAAGACGCCAAGATG 240
QY 241 ATCATATACCAACCCGTGTACCGGCAAGAGCATTTGGTACTATGATGATGATCAAGCA 300
DB 241 ATCATATACCAACCCGTGTGTACCGGCAAGAGCATTTGGTACTATGATGATGATCAAGCA 300
QY 301 TTTCAGCAAAAGATTTTACCACACCTTGGCGCCTGTGCACATCTCGTGGCTACGATGGCATG 360
DB 301 TTTCAGCAAAAGATTTTACCACACCTTGGCGCCTGTGCACATCTCGTGGCTACGATGGCATG 360
QY 361 ACCCGTGGCTCACTTTCAATGTGCCNAGAGACAGACACTGTAGTTAGTTCAATCAG 420
DB 361 ACCCGTGGCTCACTTTCAATGTGCCNAGAGACAGACACTGTAGTTAGTTCAATCAG 420
QY 421 AATGCCACCGTGGAGAACTCGGTCCATCTGCAGGCTGCCATCGGCTGCCCTTTCGAT 480
DB 421 AATGCCACCGTGGAGAACTCGGTCCATCTGCAGGCTGCCATCGGCTGCCCTTTCGAT 480
QY 481 GGTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTACTTCCCACTAC 540
DB 481 GGTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTACTTCCCACTAC 540
QY 541 CAATCGGCCGCGCTCTGTGTACCATGACCAAGCGTTTATGAAGCTCTGAGATGGC 600
DB 541 CAATCGGCCGCGCTCTGTGTGTACCATGACCAAGCGTTTATGAAGCTCTGAGATGGC 600
QY 601 TACTTTGCTCAGGCTGGCGCTACATTATCAAGAGAGAGGCTGAGAGTCTCGGTCTT 660
DB 601 TACTTTGCTCAGGCTGGCGCTACATTATCAAGAGAGAGGCTGAGAGTCTCGGTCTT 660
QY 661 CCTAGTGGCTATGGCGAGTTGATATCCTGTGATCTGACGGCCAAGTACTATAAGCC 720
DB 661 CCTAGTGGCTATGGCGAGTTGATATCCTGTGATCTGACGGCCAAGTACTATAAGCC 720
QY 721 GATGGTACCTCGCTTGCACCGAGGTTGAGAGACAGAGACTGTGGGAAATGTCAATCAT 780
DB 721 GATGGTACCTCGCTTGCACCGAGGTTGAGAGACAGAGACTGTGGGAAATGTCAATCAT 780
QY 781 GTCACAGGACAGCATGGCTTTCTTAAGTGTACAGCCCGGCAAGTACGTTTCGATTTC 840
DB 781 GTCACAGGACAGCATGGCTTTCTTAAGTGTACAGCCCGGCAAGTACGTTTCGATTTC 840

QY 841 CTCACAGCTGCCGTGTCTGCTGTGGCTCTCTACCTCTGTCAGAGACAGCTCTCCCAAC 900
DB 841 CTCACAGCTGCCGTGTCTGCTGTGGCTCTCTACCTCTGTCAGAGACAGCTCTCCCAAC 900
QY 901 GTCAGAAATTCCTTCCCAATCAATGCTGTGATGCTGCTCTTCAAGCCCGCTTCAG 960
DB 901 GTCAGAAATTCCTTCCCAATCAATGCTGTGATGCTGCTCTTCAAGCCCGCTTCAG 960
QY 961 ACCCTTAACCTTACCTTCTGCTTGGCGAGCTTACGAGATCATTTAGCTTCAACCAAC 1020
DB 961 ACCCTTAACCTTACCTTCTGCTTGGCGAGCTTACGAGATCATTTAGCTTCAACCAAC 1020
QY 1021 TTTGCTGGCAGACTTGTGACCTGCGCAAGCTTGTCTGAGACCAAGAGATGCGGACGAG 1080
DB 1021 TTTGCTGGCAGACTTGTGACCTGCGCAAGCTTGTGTGAGACCAAGAGATGCGGACGAG 1080
QY 1081 GATGAGTACGCTGTGACCTGTGAGGATGAGCGCTTGTGTGAGCTGTGGACTGTGAG 1140
DB 1081 GATGAGTACGCTGTGACCTGTGAGGATGAGCGCTTGTGTGAGCTGTGGACTGTGAG 1140
QY 1141 GACACAGCCAGGTCCCTCCACTCTCCGTGACGTTCTTCCCTCCCTCACAAGAGAGGC 1200
DB 1141 GACACAGCCAGGTCCCTCCACTCTCCGTGAGCTTCCCTCCCTCACAAGAGAGGC 1200
QY 1201 CCCGCCGACAGCACTTCAAGTTTGAAGCAGCAACGACACTACCTGATCAACGATGTT 1260
DB 1201 CCCGCCGACAGCACTTCAAGTTTGAAGCAGCAACGACACTACCTGATCAACGATGTT 1260
QY 1261 GGGCTTTGGGATGCAATGAGGCTGTGCTGGCCAGGCCGAGCTGTGGCCCGCTTGAAGTTC 1320
DB 1261 GGGCTTTGGGATGCAATGAGGCTGTGCTGGCCAGGCCGAGCTGTGGCCCGCTTGAAGTTC 1320
QY 1321 TGGGAGCTCGAGAACTCTCTGTGAGGCTGTGAGCCACCCCGTCACTTACCTTTGTGAC 1380
DB 1321 TGGGAGCTCGAGAACTCTCTGTGAGGCTGTGAGCCACCCCGTCACTTACCTTTGTGAC 1380
QY 1381 TTCAAGATCTTCAAGCGAAGCTGTGTGCTGTGGCCAGGCTATGCCCTACGAGTCTGTGAT 1440
DB 1381 TTCAAGATCTTCAAGCGAAGCTGTGTGCTGTGGCCAGGCTATGCCCTACGAGTCTGTGAT 1440
QY 1441 CTTAAGGATGCTGTGCTGTGGGAGGAGGAGTGTGAGACCTGACATGAGGCGCACTACCA 1500
DB 1441 CTTAAGGATGCTGTGCTGTGGGAGGAGGAGTGTGAGACCTGACATGAGGCGCACTACCA 1500
QY 1501 CCCGTGACTGAGACTTACATGTGGCACTGTCAACACCTCATTACAGAGGATTAACGACATG 1560
DB 1501 CCCGTGACTGAGACTTACATGTGGCACTGTCAACACCTCATTACAGAGGATTAACGACATG 1560
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DB 1561 ATGGCTGTATTCAAGCTCACCGCATGGAGAGAGAGGATATCTTACAGAGGACTTCCGAG 1620
QY 1621 GACCCCATGAACCCCAAGAGGCGCGCGCTTCTTACCAACCGCAAGCACTTCCATGCTGCC 1680
DB 1621 GACCCCATGAACCCCAAGAGGCGCGCGCTTCTTACCAACCGCAAGCACTTCCATGCTGCC 1680
QY 1681 GCTGGAACCTTCCGCGCAGTTCATCACTGTGCCGAGTGCAGAGAGCTGGCCGAGAGGAG 1740
DB 1681 GCTGGAACCTTCCGCGCAGTTCATCACTGTGCCGAGTGCAGAGAGCTGGCCGAGAGGAG 1740
QY 1741 CCGTACAAACCGCTCGATGAGATCTGTGAGAGATCTTGAATGAGAGATTA 1791
DB 1741 CCGTACAAACCGCTCGATGAGATCTGTGAGAGATCTTGAATGAGAGATTA 1791

RESULT 2

AAA50019 standard; DNA; 1791 BP.

AAA50019;

10-OCT-2000 (first entry)

DE Stachybotrys chartarum phenol oxidising enzyme cDNA.
XX Phenol oxidising enzyme; detergent; bleaching; ss.
XX Stachybotrys chartarum.
OS
FH Key Location/Qualifiers
FT CDS 7..1791
FT /tag= a
PN WO200039306-A2.
XX
XX 06-JUL-2000.
XX
XX 20-DEC-1999; 99WO-EPI0287.
XX
XX 23-DEC-1998; 98US-0220871.
XX 23-JUN-1999; 99US-0338723.
XX
XX (UNITL) UNILEVER NV.
XX (UNITL) UNILEVER PLC.
XX (HIND-) HINDUSTAN LEVER LTD.
XX
XX Bodie EA, Van Der Velden S, De Vries CH, Wang H;
XX WPI: 2000-514528/46.
XX P-PSDB: AAY95537.
XX
XX Detergent composition comprising novel phenol oxidising enzyme obtained
XX from fungus or bacteria, useful for pulp and paper bleaching, bleaching
XX color of stains on fabric and for anti-dye redeposition
XX
XX Disclosure: Fig 5A-B; 45pp; English.
XX
XX The present sequence is that of the Stachybotrys chartarum MUC1 38898
XX cDNA encoding a phenol oxidising enzyme (see AAY95537). The invention
XX relates to detergent compositions comprising novel phenol oxidising
XX enzymes that are encoded by nucleic acids capable of hybridising to
XX the S. chartarum phenol oxidising enzyme gene (see AA50018), provided
XX the enzymes are capable of modifying the colour associated with dyes
XX or coloured compounds, and are produced from a bacterium, yeast or
XX fungus (see AAY9538-40). The phenol oxidising enzymes can be used
XX for pulp and paper bleaching, for bleaching the colour of stains on
XX fabric and for anti-dye transfer in detergent and textile
XX applications. They may also be capable of modifying the colour in
XX the absence or presence of an enhancer. Expression vectors and host
XX cells comprising a nucleic acid encoding a phenol oxidising enzyme,
XX methods for producing the phenol oxidising enzyme, and methods for
XX constructing expression hosts are provided.
XX
XX Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other:
SQ
Query Match 100.0%; Score 1791; DB 21; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 ATCATTTACCAACCGCTGTACCGGCAAGACATTTGGTACTATGAGATCGAGATCAAGCCA 300
QY 301 TTTTCAGCAAGAGATTATACCCACACCTTGGCCCTGCCACTCTGTGGCTACAGATGGCATG 360
Db 301 TTTTCAGCAAGAGATTATACCCACACCTTGGCCCTGCCACTCTGTGGCTACAGATGGCATG 360
QY 361 AGCCCTGGTCTACTTCAATGTTCACAGAGAACGAGACTGTAGTTGATTCAATCAAC 420
Db 361 AGCCCTGGTCTACTTCAATGTTCACAGAGAACGAGACTGTAGTTGATTCAATCAAC 420
QY 421 AATGCCACCGGTGAGAACTCGGTCTCATGACAGGCTCCCAATCGGTCGCCCTTTGAT 480
Db 421 AATGCCACCGGTGAGAACTCGGTCTCATGACAGGCTCCCAATCGGTCGCCCTTTGAT 480
QY 481 GGTGGGCTGAAGANTGTGACCTTCCCTGGCAGATACAGAGATTACTTTCACCAATAC 540
Db 481 GGTGGGCTGAAGANTGTGACCTTCCCTGGCAGATACAGAGATTACTTTCACCAATAC 540
QY 541 CAATCGCGCGGCTCTGTGATACCATGACACACGCTTTCATGAAGCTGTGAGAAATGCC 600
Db 541 CAATCGCGCGGCTCTGTGATACCATGACACACGCTTTCATGAAGCTGTGAGAAATGCC 600
QY 601 TACTTTGTACAGGCTGGCCCTACATTTATCAACGACGAGCTGAGGATGCTCGGCTTT 660
Db 601 TACTTTGTACAGGCTGGCCCTACATTTATCAACGACGAGCTGAGGATGCTCGGCTTT 660
QY 661 CCTAGTGGCTATGCGGAGTTTGATATCCCTGTGATCTGACGCGCAAGTACTATTAAGCC 720
Db 661 CCTAGTGGCTATGCGGAGTTTGATATCCCTGTGATCTGACGCGCAAGTACTATTAAGCC 720
QY 721 GATGGTACCTCGCTTCGACCGAGGCTGAGACACGAGACTGTGGGAGATGATCATCAT 780
Db 721 GATGGTACCTCGCTTCGACCGAGGCTGAGACACGAGACTGTGGGAGATGATCATCAT 780
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Db 781 GTCAACGACAGCATAGGCTTTCTTAAAGTTCACGACCGCCGAAGTACGTTTCCGATTC 840
QY 841 CTCACGCTGCGGTCTGTGCTGTGGCTCTCTACCTGTGTGACGACAGCTCTCCCAAC 900
Db 841 CTCACGCTGCGGTCTGTGCTGTGGCTCTCTACCTGTGTGACGACAGCTCTCCCAAC 900
QY 901 GTCAAGATTCCTTTCCAAATCATGTGCTGTGATGTGCTCTTCAACCCCGCTTCAG 960
Db 901 GTCAAGATTCCTTTCCAAATCATGTGCTGTGATGTGCTCTTCAACCCCGCTTCAG 960
QY 961 ACCTCTAACCTCTACCTTGTGCTGTGGCAGCGTTACGAGATCATTTACTTCAACCAAC 1020
Db 961 ACCTCTAACCTCTACCTTGTGCTGTGGCAGCGTTACGAGATCATTTACTTCAACCAAC 1020
QY 1021 TTTTGTGCGCAGACTCTGTACCTCGGCAACGTTGCTGTAGACCAACGATGTGGCGCAG 1080
Db 1021 TTTTGTGCGCAGACTCTGTACCTCGGCAACGTTGCTGTAGACCAACGATGTGGCGCAG 1080
QY 1081 GATGAGTACGCTGCGACTCTGAGAGATGATGCGCTGTGTGACGCTGTGAG 1140
Db 1081 GATGAGTACGCTGCGACTCTGAGAGATGATGCGCTGTGTGACGCTGTGAG 1140
QY 1141 GACACAGGCGAGTCCCTCTCACTCTCGGTGAGCTTCTTCCCTCTCTCAACAAGAGAGC 1200
Db 1141 GACACAGGCGAGTCCCTCTCACTCTCGGTGAGCTTCTTCCCTCTCTCAACAAGAGAGC 1200
QY 1201 CCGCGCGACAGCACTTCAAGTTTGAACGACGACGACACTACCTGATCAACGATGTT 1260
Db 1201 CCGCGCGACAGCACTTCAAGTTTGAACGACGACGACACTACCTGATCAACGATGTT 1260
QY 1261 GGGTTGGCGATGTCAATGAGGCTGCTGGCAAGCCGAGACTGGGCAACGCTTGAAGTTC 1320
Db 1261 GGGTTGGCGATGTCAATGAGGCTGCTGGCAAGCCGAGACTGGGCAACGCTTGAAGTTC 1320
QY 1321 TGGGAGCTCGAGAACTCTCTGTGAGGCTGAGACCAACCCGCTCAATTCACCTTGTGAC 1380
Db 1321 TGGGAGCTCGAGAACTCTCTGTGAGGCTGAGACCAACCCGCTCAATTCACCTTGTGAC 1380

Db	1321	TG6AGCTCGAGAACTCCTCTGTGAGGCTGGAGCCACCCCGTCCACATTCCTCTGTTCAC	1380
Qy	1381	TTCAAGATCCTCAAGCCGAACTGGTGGTCTGTGCGCCAGGTCATGCCCTACGAGTCTGTGCT	1440
Db	1381	TTCAAGATCCTCAAGCCGAACTGGTGGTCTGTGCGCCAGGTCATGCCCTACGAGTCTGTGCT	1440
Qy	1441	CTTAAGATGTCGCTGTGGTGGGCGAGGGGTGAGACCCCTACCATGAGAGCCCACTACCAA	1500
Db	1441	CTTAAGATGTCGCTGTGGTGGGCGAGGGGTGAGACCCCTACCATGAGAGCCCACTACCAA	1500
Qy	1501	CCCTGAGACTGGAGGTTACATGATGTGGACACTGTCCAAACCTTACACGAGGATTAACGACATG	1560
Db	1501	CCCTGAGACTGGAGGTTACATGATGTGGACACTGTCCAAACCTTACACGAGGATTAACGACATG	1560
Qy	1561	ATGCGCTGATTTCAACGTCACCCGCCATGAGAGAGAGGATATCTTCAGAGGACTTGCAG	1620
Db	1561	ATGCGCTGATTTCAACGTCACCCGCCATGAGAGAGAGGATATCTTCAGAGGACTTGCAG	1620
Qy	1621	GACCCCATGAAACCCCAAGTGGGCGCGCTTCCTTACACCGCAACGACTTCATCTCTGCG	1680
Db	1621	GACCCCATGAAACCCCAAGTGGGCGCGCTTCCTTACACCGCAACGACTTCATCTCTGCG	1680
Qy	1681	GCTGGAAACTTCTCCGCGGAGTCCATCACTGCCCAGTCCAGAGACTGGCCGAGCGAGAG	1740
Db	1681	GCTGGAAACTTCTCCGCGGAGTCCATCACTGCCCAGTCCAGAGACTGGCCGAGCGAGAG	1740
Qy	1741	CCGTACCAACGCGCTCGATGAGATCTTGGAGAGATCTTTGGAATGGAGAGTAA	1791
Db	1741	CCGTACCAACGCGCTCGATGAGATCTTGGAGAGATCTTTGGAATGGAGAGTAA	1791

RESULT 3	
AAAS1314	
ID	AAAS1314 standard; DNA; 1791 BP.
XX	
AC	AAAS1314;
XX	
DT	09-OCT-2000 (first entry)
XX	
DE	Stachybotrys chartarum phenol oxidizing enzyme cDNA.
XX	
KW	Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
RW	pulp; paper bleaching; ss.
XX	
OS	Stachybotrys chartarum.
XX	
PH	Key
FT	Location/Qualifiers
FT	7..1791
FT	/*tag= a
FT	/product= Phenol_oxidizing_Enzyme
XX	
PN	WO200037654-A2.
XX	
PD	29-JUN-2000.
XX	
PF	20-DEC-1999; 99WO-US31009.
XX	
PR	23-DEC-1998; 98US-0220871.
PR	23-JUN-1999; 99US-0338723.
XX	
PA	(GENV) GENENCOR INT INC.
XX	
PL	Wang H, Bodie EA;
XX	
DR	WPI: 2000-452191/39.
DR	P-PSDB: AAY96761.
XX	
PT	New phenol oxidizing enzyme for modifying colors associated with dyes
PT	or colored compounds, is obtained from fungus and is encoded by a
PT	nucleic acid comprising a specific nucleotide sequence
XX	
PS	Disclosure; Fig 5A-B; 45pp; English.
XX	

This CDNA encodes stachyoltyrosyl charrarum phenol oxidizing enzyme. Phenol oxidizing enzymes encoded by nucleic acid sequences which hybridize to this DNA are claimed, as long as the enzyme is capable of modifying the colour associated with dyes or coloured compounds. The enzymes are useful in detergent compositions and for modifying colors associated with dyes or colored compounds which occur in stains in a sample. The enzymes are also useful for pulp and paper bleaching, anti-dye transfer in detergent and other textile applications.

Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

Query Match	100.0%	Score 1791	DB 21	Length 1791
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1791; Conservative	0	Mismatches	0	Gaps 0;

QY	1	GTAAATATAGCTGTTCACATCATGCGCACTGGCACACGCTTCGCGGCTCTCTGTCTGGAGTC	60
Db	1	GTCAATATAGCTGTTCACATCATGCGCACTGGCACACGCTTCGCGGCTCTCTGTCTGGAGTC	60
QY	61	CTCGGCATCCCGATGGAGACACGGCAGCCACCCTAATTGAGGCTGTATTCCCGAAGTGAAG	120
Db	61	CTCGGCATCCCGATGGAGACACGGCAGCCACCCTAATTGAGGCTGTATTCCCGAAGTGAAG	120
QY	121	ACTGAGGCTTCGCGTACGCTCCCTCTCTCTGTCGACAGAGCGATGACGACTGGAGTCACT	180
Db	121	ACTGAGGCTTCGCGTACGCTCCCTCTCTCTGTCGACAGAGCGATGACGACTGGAGTCACT	180
QY	181	CCATCAACACTTGCTTTACAGAGATAGCCCTGGCAATTTCACCTGTCAAGCAGCCCAAGATG	240
Db	181	CCATCAACACTTGCTTTACAGAGATAGCCCTGGCAATTTCACCTGTCAAGCAGCCCAAGATG	240
QY	241	ATCATTTACCAACCCCTGTACCGCGCAAGGACATTTGTACTGTGAGATCGAGATCAAGCCA	3000
Db	241	ATCATTTACCAACCCCTGTACCGCGCAAGGACATTTGTACTGTGAGATCGAGATCAAGCCA	3000
QY	301	TTTTGACAAAGGATTTTACCCACCTTTGGCCCTGCACATCTGCTGCGCTACGATGGCATG	3600
Db	301	TTTTGACAAAGGATTTTACCCACCTTTGGCCCTGCACATCTGCTGCGCTACGATGGCATG	3600
QY	361	AGCCCTGTCTACTTTCAATATGTTCCAGAGAGAACAGAGACTGTATGATAGTTCATCAAC	4200
Db	361	AGCCCTGTCTACTTTCAATATGTTCCAGAGAGAACAGAGACTGTATGATAGTTCATCAAC	4200
QY	421	AATGGCACCGTGTGAACAACTCGGTCCATGTGACAGGCTCCCATGGCTGCCCTTTTGAT	4800
Db	421	AATGGCACCGTGTGAACAACTCGGTCCATGTGACAGGCTCCCATGGCTGCCCTTTTGAT	4800
QY	481	GGTTGGGCTGAAGATGTACCTTCCCTGGCGAGTACAAGATTTACTACTTTCGCCACTAC	5400
Db	481	GGTTGGGCTGAAGATGTACCTTCCCTGGCGAGTACAAGATTTACTACTTTCGCCACTAC	5400
QY	541	CAATCCGCCGCCCTTCTGTGTGATACCATACCAACGCTTTCATGAAGACTGCTGAGATAGCC	6000
Db	541	CAATCCGCCGCCCTTCTGTGTGATACCATACCAACGCTTTCATGAAGACTGCTGAGATAGCC	6000
QY	601	TACTTTGGCAGGGCTGGGCGCTACACTTTCACAGCAGCGAGGCTGAGATGGCTCGGGCTT	6600
Db	601	TACTTTGGCAGGGCTGGGCGCTACACTTTCACAGCAGCGAGGCTGAGATGGCTCGGGCTT	6600
QY	661	CCTAGTGGCTATGGGAGTTCGATATCCCTTGATTCGACGAGCGCAAGTACTATTAACGCC	7200
Db	661	CCTAGTGGCTATGGGAGTTCGATATCCCTTGATTCGACGAGCGCAAGTACTATTAACGCC	7200
QY	721	GATGTTACCTTCGCTTTCGACGAGGCTGAGACCAAGCAAGCACTGTGTGGAGATGTATCAT	7800
Db	721	GATGTTACCTTCGCTTTCGACGAGGCTGAGACCAAGCAAGCACTGTGTGGAGATGTATCAT	7800
QY	781	GTCAACGGCAGCAACCTGAGCGCTTCTCTTAAGCTCAAGCCCGGCAAGTACCGTTTCCGATTC	8400
Db	781	GTCAACGGCAGCAACCTGAGCGCTTCTCTTAAGCTCAAGCCCGGCAAGTACCGTTTCCGATTC	8400
QY	841	CTCAACGCTGCGCTTCTCTGCTGTGGCTCTTCACTGCTCAAGACAGCTCTCCCAAC	9000

QY	421	AATGCCACGCTGGAGAACTCGGTGCATCTGCAAGGCTCCCACTCCGCTGCCCTTTCGAT	480
Db	421	AATGCCACCGGGAGAACTCGGTGCATCTGCAAGGCTCCCACTCCGCTGCCCTTTCGAT	480
QY	481	GGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTACTTCCAACTAC	540
Db	481	GGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTACTTCCAACTAC	540
QY	541	CAATCCGCGCGCTTCTGTGTGTACCATGACACGCTTTCATGAAGACTCTGAGAACTCC	600
Db	541	CAATCCGCGCGCTTCTGTGTGTACCATGACACGCTTTCATGAAGACTCTGAGAACTCC	600
QY	601	TACTTTGGTCAGGCTGGCGCTCAATTATCAACGAGAGGCTGAGAGTCTCTGGCTTT	660
Db	601	TACTTTGGTCAGGCTGGCGCTCAATTATCAACGAGAGGCTGAGAGTCTCTGGCTTT	660
QY	661	CCTAGTGGCTATGGCGAGTTCGATATTCCTCTGTATCCTACAGCGCAAGTACTATTAAGCC	720
Db	661	CCTAGTGGCTATGGCGAGTTCGATATTCCTCTGTATCCTACAGCGCAAGTACTATTAAGCC	720
QY	721	GATGTGTACCTGGCTGTGACCCAGAGGCTGAGAGACCAAGACTGTGGGAGATGTCAATCAT	780
Db	721	GATGTGTACCTGGCTGTGACCCAGAGGCTGAGAGACCAAGACTGTGGGAGATGTCAATCAT	780
QY	781	GTCACAGGACAGCATAGGCTTTCCTTTAACAGTCCACCCCGCAAGTACCGTTTCGATTC	840
Db	781	GTCACAGGACAGCATAGGCTTTCCTTTAACAGTCCACCCCGCAAGTACCGTTTCGATTC	840
QY	841	CTCAACGCTCGCTGTCTGTCTGTGGCTCTCTACTCTGTGAGACCAAGCTCTCCCAAC	900
Db	841	CTCAACGCTCGCTGTCTGTCTGTGGCTCTCTACTCTGTGAGACCAAGCTCTCCCAAC	900
QY	901	GTCAGAAATTCCTTCCCAAGCATTTGGCTCGTGAATGCTGCTCTTCAAGCCCCCGTTAG	960
Db	901	GTCAGAAATTCCTTCCCAAGCATTTGGCTCGTGAATGCTGCTCTTCAAGCCCCCGTTAG	960
QY	961	ACCTCTAACTCTACTTCTGCTGTGGCCGAGCGTTACGAGATCATTTAGCTTCCCAAC	1020
Db	961	ACCTCTAACTCTACTTCTGCTGTGGCCGAGCGTTACGAGATCATTTAGCTTCCCAAC	1020
QY	1021	TTTTCTGGCCAGACTCTTGACCTCGGCGCAACGTTGGTGAAGCAAGATGTCCGGCAGAG	1080
Db	1021	TTTTCTGGCCAGACTCTTGACCTCGGCGCAACGTTGGTGAAGCAAGATGTCCGGCAGAG	1080
QY	1081	GATGAGTACGCTGCACCTCTCGAGGTATGCGCTTGTGTGAGCTGTGGCACTCTTGAG	1140
Db	1081	GATGAGTACGCTGCACCTCTCGAGGTATGCGCTTGTGTGAGCTGTGGCACTCTTGAG	1140
QY	1141	GACAAAGCCAGGTCCTCTCACTCTCGGATCTCGGATGCTTTCCTCTCCACAAAGAAAGC	1200
Db	1141	GACAAAGCCAGGTCCTCTCACTCTCGGATCTCGGATGCTTTCCTCTCCACAAAGAAAGC	1200
QY	1201	CCCCGCACAAGCACTTCAGTTTGAAGGAGCAAGGACATCACTTATCAACAAGATT	1260
Db	1201	CCCCGCACAAGCACTTCAGTTTGAAGGAGCAAGGACATCACTTATCAACAAGATT	1260
QY	1261	GGCTTTCCCATGTGCATGTAGGCTGTCTTGCCCAACCCGAGCTCGGCAACCGTTGAGGTC	1320
Db	1261	GGCTTTCCCATGTGCATGTAGGCTGTCTTGCCCAACCCGAGCTCGGCAACCGTTGAGGTC	1320
QY	1321	TGGGAGCTCGAAGAACTCTTGAGAGGCTGGAGCCACCCGCTCCAAATTCACCTTTGTATC	1380
Db	1321	TGGGAGCTCGAAGAACTCTTGAGAGGCTGGAGCCACCCGCTCCAAATTCACCTTTGTATC	1380
QY	1381	TTTCAAGATTCCTCAAGCGAACTGGTGTGCTGGGCGAGGCTATGCTCTACGAGTCTCTGT	1440
Db	1381	TTTCAAGATTCCTCAAGCGAACTGGTGTGCTGGGCGAGGCTATGCTCTACGAGTCTCTGT	1440
QY	1441	CTTAAAGATGTCTGTGTGTGGCGAGGGGTGAGACCTTGACCATCGAGGCCCATCTACCA	1500
Db	1441	CTTAAAGATGTCTGTGTGTGGCGAGGGGTGAGACCTTGACCATCGAGGCCCATCTACCA	1500

Qy	1501	CCGGAGCTGGAGCTTACATGTGGACCTGCAACACCTATTCACGAGGATTAACACATG	1560
Db	1501	CCCTGGACTGGAGCTTACATGTGGACCTGCAACACCTATTCAGAGGATTAACACATG	1560
Qy	1561	ATGCGCTGATTTCAACGTCACCGGCATGAGAGAAAGGATCTTTCAGAGGACTTTCAG	1620
Db	1561	ATGCGCTGATTTCAACGTCACCGGCATGAGAGAAAGGATCTTTCAGAGGACTTTCAG	1620
Qy	1621	GACCCCATGAACCCCAAGTGGCGCGCGCTTCTTACACCGCAACGACTTCCATGCTGCG	1680
Db	1621	GACCCCATGAACCCCAAGTGGCGCGCGCTTCTTACACCGCAACGACTTCCATGCTGCG	1680
Qy	1681	GCTGGAACCTTTCGCGCGAGTCCATCACTGCGCCGAGTGCAGAGACTGCGCGAGCAGAG	1740
Db	1681	GCTGGAACCTTTCGCGCGAGTCCATCACTGCGCCGAGTGCAGAGACTGCGCGAGCAGAG	1740
Qy	1741	CCGTACACCGCGCTCGATGAGATCTTGAGAGATCTTTCGATTCGAGAGTA	1791
Db	1741	CCGTACACCGCGCTCGATGAGATCTTGAGAGATCTTTCGATTCGAGAGTA	1791

RESULT 5
ABA92911
ID ABA92911 standard; DNA; 7248 BP.

AC	ABA92911;
XX	
DT	09-APR-2002 (first entry)

DE *Stachybotrys chartarum* laccase gene

KM Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;
KM copper; metal cofactor; gene; plant; ds.

OS Stachybotrys chartarum

PN W0200196543-A2.

PD 20-DEC-2001.

14-JUN-2001; 2001WO-US19174.

15-JUN-2000; 2000US-211732P.

PA (PROD-) PRODIGENE INC.

(JELM) GENENCON INC.
XX
FA

PI HODD E, HOWARD JA, WOODARD S:

XX
XX
WPB: 2002-090304 /13

Improving recovery of
XX
DE

transitional metal complex

PT it to cofactor -

PS Example 5; Fig 16A-E;

CC The present invention

CC metal cofactor for act

to the metal cofactor.

preferably for improving

active organophosphate

comprises adding bicar

CC fungal stachybotrys ch
CC blue conner oxidases a

CC the oxidation and reduction

The present invention describes a method for improving the recovery of an active enzyme from a plant where the enzyme requires a transitional metal cofactor for activity. The method comprises introducing into the plant nucleotide sequences encoding the enzyme and exposing the enzyme to the metal cofactor. The method is useful for improving recovery of active enzyme which requires a transitional metal cofactor for activity, preferably for improving recovery of active laccase which requires copper for activity. The method can be used for improving recovery of active organophosphate hydrolase (OPH, E.C. 3.1.8.1) which requires zinc, nickel, cobalt or manganese for activity, where the method further comprises adding bicarbonate ion salt. The present sequence encodes the fungal *Stachybotrys chartarum* laccase enzyme. Laccases are also called blue copper oxidases and use copper to accept and donate electrons in the oxidation and reduction of substrates.

XX Sequence 7248 BP; 1928 A; 1744 C; 1579 G; 1997 T; 0 other:
SQ
Query Match 99.9%; Score 1790; DB 24; Length 7248;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1790; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAATATGCTGTTCAGTATGCAACTGGACAGACCTCCGGGCTCCTGTCTGGAGTC 60
DB 5192 GTCAATATGCTGTTCAGTATGCAACTGGACAGACCTCCGGGCTCCTGTCTGGAGTC 5251
QY 61 CTCGGATATCCGATGAGACACCGGACACCCCATTTAGAGCTTTTATCCCAAGTGAAG 120
DB 5252 CTCGGATATCCGATGAGACACCGGACACCCCATTTAGAGCTTTTATCCCAAGTGAAG 5311
QY 121 ACTGAGGCTTTCGCTGACACCTCCTTGGTGCAGACGGGATGAGACTGGGAGTACCT 180
DB 5312 ACTGAGGCTTTCGCTGACACCTCCTTGGTGCAGACGGGATGAGACTGGGAGTACCT 5371
QY 181 CCATACAACTTGTCTTACAGGAATGCCATTCACCTGTCTCAAGACGCCCAAGATG 240
DB 5372 CCATACAACTTGTCTTACAGGAATGCCATTCACCTGTCTCAAGACGCCCAAGATG 5431
QY 241 ATCATTTACCAACCCCTGTACCGGCAAGACATTTGCTACTATGAGATCGAGATCAAGCA 300
DB 5432 ATCATTTACCAACCCCTGTACCGGCAAGACATTTGCTACTATGAGATCGAGATCAAGCA 5491
QY 301 TTTTACCAAGATTTTACCCACCTTGGCCCTGGCAGCTGTGGGATACGATGGCGATG 360
DB 5492 TTTTACCAAGATTTTACCCACCTTGGCCCTGGCAGCTGTGGGATACGATGGCGATG 5551
QY 361 ACCCCTGTCTCTATTTCAATGTTCACAGAGAACAGACTGTATGATGTTTCAATCAAC 420
DB 5552 ACCCCTGTCTCTATTTCAATGTTCACAGAGAACAGACTGTATGATGTTTCAATCAAC 5611
QY 421 AATGCCACCGTGGAGAACCTGGTCCATCTGCACAGGCTCCCATCGGTCGCCCTTTGCAT 480
DB 5612 AATGCCACCGTGGAGAACCTGGTCCATCTGCACAGGCTCCCATCGGTCGCCCTTTGCAT 5671
QY 481 GGTGGGCTGAAGATGTGACCTTCCCTGGCGATGACAAAGATTTACTTCCCAACTAC 540
DB 5672 GGTGGGCTGAAGATGTGACCTTCCCTGGCGATGACAAAGATTTACTTCCCAACTAC 5731
QY 541 CAATCCGCGCGCTTCTGTGTACCATGACCAAGCTTTTATGAAAGACTCTGAGAAATGCC 600
DB 5732 CAATCCGCGCGCTTCTGTGTACCATGACCAAGCTTTTATGAAAGACTCTGAGAAATGCC 5791
QY 601 TACTTTGGTCAAGCTGGCGCTTACATTTAACAAGACGAGAGCTGAGATCTCTCGGCTTT 660
DB 5792 TACTTTGGTCAAGCTGGCGCTTACATTTAACAAGACGAGAGCTGAGATCTCTCGGCTTT 5851
QY 661 CCTAGTGGCTATGGGAGTTCGATATCCCTGATGCTGACGGCCAAAGTAAATAAGGCG 720
DB 5852 CCTAGTGGCTATGGGAGTTCGATATCCCTGATGCTGACGGCCAAAGTAAATAAGGCG 5911
QY 721 GATGTATCCCTCGTTTGCAGCAGAGGTGAGACCAAGACCTGTGGGAGATGTCAATCAT 780
DB 5912 GATGTATCCCTCGTTTGCAGCAGAGGTGAGACCAAGACCTGTGGGAGATGTCAATCAT 5971
QY 781 GTCAACGAGACCATGAGCTTTCTTAAAGTTCAGACCCCGCAAGTACCGTTTCGATTC 840
DB 5972 GTCAACGAGACCATGAGCTTTCTTAAAGTTCAGACCCCGCAAGTACCGTTTCGATTC 6031
QY 841 CTCAACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 6032 CTCAACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6091
QY 901 GTCAAGATTCCTTTCAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 6092 GTCAAGATTCCTTTCAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6151
QY 961 ACCTCTAACCTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 1021 ACCTCTAACCTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

DB 6152 ACCTCTAACCTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6211
QY 1021 TTTTGGTGGCAGACCTTGTGACCTGGCAACGTTTGTGAGACCAAGCATGTGGCGACGAG 1080
DB 6212 TTTTGGTGGCAGACCTTGTGACCTGGCAACGTTTGTGAGACCAAGCATGTGGCGACGAG 6271
QY 1081 GATGATGAGCTTCGACCTTCGAGGTGATGCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 6272 GATGATGAGCTTCGACCTTCGAGGTGATGCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTG 6331
QY 1141 GACACAGCCAGGTCCCTTCACCTCTCGGTGACGTTTCTTTCCCTCTCTACAAAGAGGC 1200
DB 6332 GACACAGCCAGGTCCCTTCACCTCTCGGTGACGTTTCTTTCCCTCTCTACAAAGAGGC 6391
QY 1201 CCGCGGACAAAGACCTTCAAGTTTGAACGACAGAAAGGACACTGATGATCAAGATGTT 1260
DB 6392 CCGCGGACAAAGACCTTCAAGTTTGAACGACAGAAAGGACACTGATGATCAAGATGTT 6451
QY 1261 GGCCTTTCGCGATGTCAATGAGCGTGTCTTGGCCAAAGCCGAGCTGGCAACCGTTGAGTTC 1320
DB 6452 GGCCTTTCGCGATGTCAATGAGCGTGTCTTGGCCAAAGCCGAGCTGGCAACCGTTGAGTTC 6511
QY 1321 TGGGACCTGAGACACTCTCTGTGAGGCTGAGACACCCGCTCCACATTCACCTGTTGAC 1380
DB 6512 TGGGACCTGAGACACTCTCTGTGAGGCTGAGACACCCGCTCCACATTCACCTGTTGAC 6571
QY 1381 TTCAAGATTCCTCAAGGACCTGCTGTGCTGGCCAGGCTATCCCTACAGAGTCTGTGCT 1440
DB 6572 TTCAAGATTCCTCAAGGACCTGCTGTGCTGGCCAGGCTATCCCTACAGAGTCTGTGCT 6631
QY 1441 CTTAAGATGTGCTGTGTTGGGACAGGCTGAGACCCCTGACCATGAGGCCCCACTACCA 1500
DB 6632 CTTAAGATGTGCTGTGTTGGGACAGGCTGAGACCCCTGACCATGAGGCCCCACTACCA 6691
QY 1501 CCTGTGACTGAGACTTACATGTGTGACCTGTCAACACCTTACACGAGATTAACGACATG 1560
DB 6692 CCTGTGACTGAGACTTACATGTGTGACCTGTCAACACCTTACACGAGATTAACGACATG 6751
QY 1561 ATGGCTGTATTAAGTCAACGCGCATGAGAGAGGATATCTTCAGAGAGACTTCCAG 1620
DB 6752 ATGGCTGTATTAAGTCAACGCGCATGAGAGAGGATATCTTCAGAGAGACTTCCAG 6811
QY 1621 GACCCCATGAACCCCAAGTGGCGCGCGCTTCTTCAACCCGCAAGACTTCCATGCTGCG 1680
DB 6812 GACCCCATGAACCCCAAGTGGCGCGCGCTTCTTCAACCCGCAAGACTTCCATGCTGCG 6871
QY 1681 GCTGGAACCTTCTCCGCGAGTTCATGCTGCCGAGTGCAGAGAGCTGGCGAGCAGAG 1740
DB 6872 GCTGGAACCTTCTCCGCGAGTTCATGCTGCCGAGTGCAGAGAGCTGGCGAGCAGAG 6931
QY 1741 CGGTACAAACCGGCTGATGAGATCCGAGAGATCTTGGAAATGAGAGATG 1790
DB 6932 CGGTACAAACCGGCTGATGAGATCCGAGAGATCTTGGAAATGAGAGATG 6981

RESULT 6
AA25727
ID AA25727 standard; cDNA; 1791 BP.
XX AA25727;
XX
XX 05-JAN-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidising enzyme encoding cDNA.
XX
XX Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
KW detergent; anti-dye transfer; stain removal; bleaching; ss.
XX
XX Stachybotrys chartarum.
OS
XX W09949010-A2.
PN
XX
PD 30-SEP-1999.

QY 1681 GCTGGAACTTCTCCGCCGAGTCCATCATTCCCGAGTGCAGAGAGCTGGCCGAGCAGAG 1740
| | | | |
Db 1681 GCTGGAACTTCTCCGCCGAGTCCATCATTCCCGAGTGCAGAGAGCTGGCCGAGCAGAG 1740
QY 1741 CCGTACAAACGCGCTCGATGATCCTGAGAGATCTTGGATCCGAGGAGTAA 1791
| | | | |
Db 1741 CCGTACAAACGCGCTCGATGATCCTGAGAGATCTTGGATCCGAGGAGTAA 1791

RESULT 7
AA25728
ID AA25728 standard; DNA; 3676 BP.
XX
AC AA25728;
XX
DT 05-JAN-2000 (first entry)
XX

DE Stachybotrys chartarum phenol oxidising enzyme genomic DNA.
XX
KW Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
XX detergent; anti-dye transfer; stain removal; bleaching; ds.
XX
OS Stachybotrys chartarum.
XX

PN WO949010-A2.
XX
PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-EP02042.
XX
PR 24-MAR-1998; 98US-0046969.
XX
PR 22-DEC-1998; 98US-0218702.
XX

PA (UNIL) UNILEVER NV.
XX (UNIL) UNILEVER PLC.
XX
PI Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;
PI Wang C;
XX
XX
DR WPI: 1999-601211/51.
XX
DR P-PSDB: AAY45222.
XX

PT Detergent composition containing phenol oxidase from Stachybotrys, used
XX to bleach stains and prevent dye transfer -
XX
XX

PS Example 14; Fig 6; 56pp; English.
XX

CC The present invention describes a detergent composition containing a
CC purified phenol oxidising enzyme derived from Stachybotrys. The present
CC sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The
CC enzyme can be used to modify the colour of dyes and other coloured
CC compounds (e.g. for use in pulp and paper bleaching also for removing
CC stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
CC transfer during fabric washing.
XX
XX

SQ Sequence 3676 BP; 822 A; 1056 C; 849 G; 948 T; 1 other:
XX

Query Match 82.3%; Score 1474; DB 20; Length 3676;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

QY 1 GTCATATGCTGTTCAAGTCATGGAACAGTGGAGACGCTCCGGGCTCGTGTGAGATC 60
| | | | |
Db 1038 GTCATATGCTGTTCAAGTCATGGAACAGTGGAGACGCTCCGGGCTCGTGTGAGATC 1097
QY 61 CTCGGCATCCGATGGACACCGGACGACCAACCCATTGAGCGTGTGATCCGAAGTGAAG 120
| | | | |
Db 1098 CTCGGCATCCGATGGACACCGGACGACCAACCCATTGAGCGTGTGATCCGAAGTGAAG 1157
QY 121 ACTGAGGCTGTGCTGAGTCCCTGCTTGTGAGGAGGAGATGACACTGGGAGTACCT 180
| | | | |
Db 1158 ACTGAGGCTGTGCTGAGTCCCTGCTTGTGAGGAGGAGATGACACTGGGAGTACCT 1217

QY 181 CCATACAACTTGGCTTTAC----- 198
| | | | |
Db 1218 CCATACAACTTGGCTTTACAGTGAGACACCTGTCACACTGTTTCCCTGATTAAC 1277
QY 199 -----AGGATGCGCTGCCAATTCCACTGTCAAGACGCCAAGAT----- 239
| | | | |
Db 1278 TCTTATAGGAATGCCCTGCCAATTCCACTGTCAAGACGCCAAGATGATGTCCTTGGAT 1337
QY 240 -----GATCATTAACCAACCTGTGAC 260
| | | | |
Db 1338 TTTCTACGAAGCAACTCGGCCCGGACTAATGTATTCTAGAGATCTTACCAACCTGTGAC 1397
QY 261 CGGCAAGGACATTTGGTACTATGATCGAGATCAAGCCATTTCAGCAAG----- 311
| | | | |
Db 1398 CGGCAAGGACATTTGGTACTATGATCGAGATCAAGCCATTTCAGCAAGGATGAGTTT 1457
QY 312 -----GATTTACCCCACTT 326
| | | | |
Db 1458 GCTCAGAAACCTTGTGTAAATATCATTTGTACTGACCTTTCAGATTTACCCCACTT 1517
QY 327 GCGCCCTGCGACTCTGTGCGTACGATGCGATGAGCCCTGCTGCTTCAATGTTC 386
| | | | |
Db 1518 GCGCCCTGCGACTCTGTGCGTACGATGCGATGAGCCCTGCTGCTTCAATGTTC 1577
QY 387 CAGAGCAACAGACTGTAGTTAGTTTCAATCAACATGCCACGCTGAGAACTCGGTCCA 446
| | | | |
Db 1578 CAGAGCAACAGACTGTAGTTAGTTTCAATCAACATGCCACGCTGAGAACTCGGTCCA 1637
QY 447 TCTGACAGGCTCCCATCGGCTGCCCTTTCGATGTTGGGCTGAAGATGTGACTTCCC 506
| | | | |
Db 1638 TCTGACAGGCTCCCATCGGCTGCCCTTTCGATGTTGGGCTGAAGATGTGACTTCCC 1697
QY 507 TGGCGAGTACAAAGATTACTTCTCCCACTACCAATCCGCCCTTGTGTGTGATCA 566
| | | | |
Db 1698 TGGCGAGTACAAAGATTACTTCTCCCACTACCAATCCGCCCTTGTGTGTGATCA 1757
QY 567 TGACCAAGCTTTCATGA----- 583
| | | | |
Db 1758 TGACCAAGCTTTCATGAAGTATGCTACGAGCTTATCTTCTTGGCTACCTTTGGCTA 1817
QY 584 -----AGACTGCTGAGAAATGCCCTTATTTGGTCCGAGGCTGAGCTACATT 627
| | | | |
Db 1818 ACCAATTCCTTTCGTAAGACTGCTGAGAAATGCTTACTTTGGTCCGAGGCTGAGCTACATT 1877
QY 628 ATCAAGAGAGGCTGAGATGCTCTCGGCTTCTCTAGTGGCTATGGCCAGTTCCATATC 687
| | | | |
Db 1878 ATCAAGAGAGGCTGAGATGCTCTCGGCTTCTCTAGTGGCTATGGCCAGTTCCATATC 1937
QY 688 CCTGTATCTGACGGCCAAAGTACTATTAAGCCGATGTAACCTGGCTTGCAGCCGAGGT 747
| | | | |
Db 1938 CCTGTATCTGACGGCCAAAGTACTATTAAGCCGATGTAACCTGGCTTGCAGCCGAGGT 1997
QY 748 GAGGACCAAGACCTGTGGGAGATGTATCATGTGCAACGAGACGCAATGGCTTTCCTT 807
| | | | |
Db 1998 GAGGACCAAGACCTGTGGGAGATGTATCATGTGCAACGAGACGCAATGGCTTTCCTT 2057
QY 808 AACGTCACGCCCCGCAAGTACGTTTCCGATTCCTTAACGCTGCGTGTCTGTG 867
| | | | |
Db 2058 AACGTCACGCCCCGCAAGTACGTTTCCGATTCCTTAACGCTGCGTGTCTGTG 2117
QY 868 CTCCTTACCTGTCGAGACACACTCTCCCAAGCTGAGAAATTCCTTCCAAAGTCAATGGC 927
| | | | |
Db 2118 CTCCTTACCTGTCGAGACACACTCTCCCAAGCTGAGAAATTCCTTCCAAAGTCAATGGC 2177
QY 928 TCTGATGCTGGTCTCCTTCAAGCCCCGTTTCAAGACCTTACCTTACCTTGTGTC 987
| | | | |
Db 2178 TCTGATGCTGGTCTCCTTCAAGCCCCGTTTCAAGACCTTACCTTACCTTGTGTC 2237
QY 988 GAGCGTTAGAGATCATTTAT----- 1008
| | | | |
Db 2238 GAGCGTTAGAGATCATTTATGATGATCCCTCCCTCTCAAGATGATGATCAAGAACTTA 2297
QY 1009 -----GACTTCAACAACTTTGCTGGGCAAGTCTTGACCTGGGCAACGTT 1053

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Db 2298 AGACTAACACTTGTAGACTTACACCACTTGTGCGCAGACTCTTGACCTGGCCAAAGTT 2357
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Qy 1054 GCTGAGACCAAGCAATGTCGGCGACGAGAGATGATAGCTCTGCGACTCGCAGAGATAGCGC 1113
    |||
Db 2358 GCTGAGACCAAGCAATGTCGGCGACGAGAGATGATAGCTCTGCGACTCTGCGAGGATGCGC 2417
    |||
Qy 1114 TTGCTGTCAGCTCTGTGCACTGTTGAGGACACAGCCAGGTCCCTCCACTCTCCGTGAC 1173
    |||
Db 2418 TTGCTGTCAGCTCTGTGCACTGTTGAGGACACAGCCAGGTCCCTCCACTCTCCGTGAC 2477
    |||
Qy 1174 GTTCTTTTCCCTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1233
    |||
Db 2478 GTTCTTTTCCCTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2537
    |||
Qy 1234 AAGGACACTACTGTATCAAGAGATGTTGGCTTGGCCGATGCAATAGAGAGAGAGAGAGAG 1293
    |||
Db 2538 AAGGACACTACTGTATCAAGAGATGTTGGCTTGGCCGATGCAATAGAGAGAGAGAGAGAG 2597
    |||
Qy 1294 AAGCCGAGCTCGGACACCGCTTGAAGTCTGAGAGCTGAGAACTCTCTGAGAGCTGAGAG 1353
    |||
Db 2598 AAGCCGAGCTCGGACACCGCTTGAAGTCTGAGAGCTGAGAACTCTCTGAGAGCTGAGAG 2657
    |||
Qy 1354 CACCCGCTGACACTTCACTTGTGACTTCAATCTCTCAAGGAACTGCTGCTGCTGCTGCT 1413
    |||
Db 2658 CACCCGCTGACACTTCACTTGTGACTTCAATCTCTCAAGGAACTGCTGCTGCTGCTGCT 2717
    |||
Qy 1414 CAGGTATGCTCTGAGAGTGTGCTTAAAGATGCTGCTGTTGAGAGAGAGAGAGAGAGAG 1473
    |||
Db 2718 CAGGTATGCTCTGAGAGTGTGCTTAAAGATGCTGCTGTTGAGAGAGAGAGAGAGAGAG 2777
    |||
Qy 1474 ACCCTGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1533
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Db 2778 ACCCTGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2837
    |||
Qy 1534 AACCTATTCACAGAGATTAACGACATGATGCTGATTTCAAGCTCAAGCCGATGAGAGAG 1593
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Db 2838 AACCTATTCACAGAGATTAACGACATGATGCTGATTTCAAGCTCAAGCCGATGAGAGAG 2897
    |||
Qy 1594 AAGGATATCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1653
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Db 2898 AAGGATATCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2957
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Qy 1654 TACACCGCAGAGACTTCCATGCTCGGCTGGAATCTTCCGCGAGTCCATCACTGCC 1713
    |||
Db 2958 TACACCGCAGAGACTTCCATGCTCGGCTGGAATCTTCCGCGAGTCCATCACTGCC 3017
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Qy 1714 CGAGTGCAGAGAGTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1773
    |||
Db 3018 CGAGTGCAGAGAGTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3077
    |||
Qy 1774 CTTGGAATCGAGAGATTA 1791
    |||
Db 3078 CTTGGAATCGAGAGATTA 3095
    |||

RESULT 8
AA227602
ID AA227602 standard; DNA; 3677 BP.
XX
AC AA227602;
XX
AC 16-DEC-1999 (first entry)
XX
DE Stachybotrys phenol oxidase genomic sequence.
XX
KW Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
XX fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
XX OS Stachybotrys chartarum.
XX
PN MO9949020-a2.
XX
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PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-US06327.
XX
PR 24-MAR-1998; 98US-0046969.
PR 22-DEC-1998; 98US-0218702.
PR 22-MAR-1999; 99US-0273957.
XX
PA (GENEV) GENENCOR INT INC.
XX
PI Amory A, Wang H, Dphase P, Lambrechts-Rongvaux A, Wang C;
XX
DR WPI: 1999-591088/50.
XX
DR P-PSDB: AAY39992.
XX
PT Novel enzyme for modifying coloured compounds used to prevent
PT dye-transfer.
XX
PS Claim 21; Fig 6; 64p; English.
XX
CC This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
CC of the invention. The invention is used to modify a coloured compound and
CC prevent dye transfer during fabric washing, or for stain bleaching or
CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC and food industries.
XX
SQ Sequence 3677 BP; 822 A; 1056 C; 849 G; 947 T; 3 other:
```

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Query Match 82.3%; Score 1474; DB 20; Length 3677;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
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```
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Db 1038 GTCAATATGCTGTTCAAGTATGCAACTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1097
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Qy 61 CTCGGCATCCCGATGAGACACCGGACGACCCCATTTGAGAGCTTTGATCCGAGTGAAG 120
    |||
Db 1098 CTCGGCATCCCGATGAGACACCGGACGACCCCATTTGAGAGCTTTGATCCGAGTGAAG 1157
    |||
Qy 121 ACTGAGTCTTCCGCTGACCTCCCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
    |||
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Qy 181 CCATACAACTTGGCTTAC-----
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Db 1218 CCATACAACTTGGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 198
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Qy 199 -----AGCAATGCCCTGCGCAATTTCAACCTGTCAAGAGAGAGAGAGAGAGAGAGAGAT----- 239
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Db 1278 TCTTATAGCAATGCCCTGCGCAATTTCAACCTGTCAAGAGAGAGAGAGAGAGAGAGAGAT 1337
    |||
Qy 240 -----GATCATTTACCAACCCCTGTAC 260
    |||
Db 1338 TTTCTAGAAAGCACTGCGGCCGAGCTAATGATTTCTAGAGATATTACCAACCCCTGTAC 1397
    |||
Qy 261 CGCAAGAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
    |||
Db 1398 CGCAAGAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1457
    |||
Qy 312 -----GATTTACCCACCTT 326
    |||
Db 1458 GCTCAGAAACCTTGTGTAATTAATCATTTGTAAGTCTGACCTTTTCAAGATTTTACCCACCTT 1517
    |||
Qy 327 GCGCCCTGCGCACTCTGCTGCGCTAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 386
    |||
Db 1518 GCGCCCTGCGCACTCTGCTGCGCTAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1577
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Qy 387 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 446
    |||
Db 1578 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1637
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Qy 447 TCTGCAAGGCTCCCATCGGCTGCCCTTTCGATGCTTGGCTGGAAGATGTGACTTCCC 506
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Db	1638	TTCTGACGAGGCTCCCACTACGCGTGGCCCTTTTCATGTTGGCTGAAGATGTACCTTCCC	1697
Qy	507	TGGCGAGTACAAGGATTACTACTTTTCCCACTACCAATCGCCCGCTTCTGTGTACCA	566
Db	1698	TGGCGAGTACAAGGATTACTACTTTTCCCACTACCAATCGCCCGCTTCTGTGTACCA	1757
Qy	567	TGACCAAGCTTTCATGA-----	583
Db	1758	TGACCAAGCTTTCATGAAGGATGTACAGAGCTTATCTTCTTGGCACTTTGGCTA	1817
Qy	584	-----AGACTGGTGAAGATAGCCTACTTTGGTGCAGGCTGGGCGCTACACT	627
Db	1818	ACCAACTTCTTCTTGTAGACTGCTGAGAAATGCTCTACTTTGGTGAAGCTGGCGCTACACT	1877
Qy	628	ATCAACGACGAGGCTGAGATATGCTTCGGCTCTTCTAGTGGCTATAGGCAATTCATATC	687
Db	1878	ATCAACGACGAGGCTGAGATATGCTTCGGCTCTTCTAGTGGCTATAGGCAATTCATATC	1937
Qy	688	CCTCTGATCTTGACGGCCAGTACTATACGCCGATGTATACCTGCGTTGCAACGAGGT	747
Db	1938	CCCTGTATCTTGACGGCCAGTACTATATACGCCGATGTATACCTGCGTTGCAACGAGGT	1997
Qy	748	GAGGACGAGGACCTGTGGGAGATATGCATCCATATGTCAAGGACAGCATAGGCTTCTCT	807
Db	1998	GAGGACGAGGACCTGTGGGAGATATGCATCCATATGTCAAGGACAGCATAGGCTTCTCT	2057
Qy	808	AACGTCAGCCCGCCAGTATCCGTTTCCGATTTCTCAACGCTAGCGGTGTCGTGCTTTGG	867
Db	2058	AACGTCAGCCCGCCAGTATCCGTTTCCGATTTCTCAACGCTAGCGGTGTCGTGCTTTGG	2117
Qy	868	CTCCTTACCTCTGTCAAGACCACTCTCCCAACGTCAGATTTCTTTCCAAAGTCAATTGCC	927
Db	2118	CTCCTTACCTCTGTCAAGACCACTCTCCCAACGTCAGATTTCTTTCCAAAGTCAATTGCC	2177
Qy	928	TCTATGTGTGTCCTTCAAGCCCGCGTTGACAGCTTAACCTTAACCTTAACCTTCTGTGTC	987
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Qy	988	GAGCGTTACGAGATCAATT-----	1008
Db	2238	GAGCGTTACGAGATCAATTATTTGGTATAGCCCTCCCTCTCAGCAATGAGTCAAGAACTTA	2297
Qy	1009	-----GACTTCACCAACTTTTGTGTGGCAGACTCTTGTACCTGTGGCAAGCTT	1053
Db	2298	AGACTTAACACTTGTATGACTTACCAACAATTGTGTGGCAGACTTGTACCTGTGGCAAGCTT	2357
Qy	1054	GCTGAGAACCAACGATGTGTGGCGACAGAGATGATATCGTTCGCACTCTCGAGTGTATGGCG	1113
Db	2358	GCTGAGAACCAACGATGTGTGGCGACAGAGATGATATCGTTCGCACTCTCGAGTGTATGGCG	2417
Qy	1114	TTTCTGTCGAGCTGTGGCACTGTTTGAAGCAACAGCAGAGTCCCTCCCACTCTCCGTGAC	1173
Db	2418	TTTCTGTCGAGCTGTGGCACTGTTTGAAGCAACAGCAGAGTCCCTCCCACTCTCCGTGAC	2477
Qy	1174	GTTCTCTTCCCTCTCTCAAGAAGAGGCCCGCGCGACAAACACTTCAAGTTTGAAGCAGAC	1233
Db	2478	GTTCTCTTCCCTCTCTCAAGAAGAGGCCCGCGCGACAAACACTTCAAGTTTGAAGCAGAC	2537
Qy	1234	AAGGACACTTACTGATCAACGATGTTGGCTTGGCCGATGTCAATGAGCGTGTCTGTGCC	1293
Db	2538	AAGGACACTTACTGATCAACGATGTTGGCTTGGCCGATGTCAATGAGCGTGTCTGTGCC	2597
Qy	1294	AAGCCGAGGCTCGGCAACCGTTGAGAGTCTGGAGAGTGAAGAACTCCCTGTGAGAGCTGGAGC	1353
Db	2598	AAGCCGAGGCTCGGCAACCGTTGAGAGTCTGGAGAGTGAAGAACTCCCTGTGAGAGCTGGAGC	2657
Qy	1354	CACCCGTCACATTCACCTGTTTGAATTCAGATCTCAACGCAACTGTGTGTGTGGC	1413
Db	2658	CACCCGTCACATTCACCTGTTTGAATTCAGATCTCAACGCAACTGTGTGTGTGGC	2717
Qy	1414	CAGGTCAATGCCCTTACAGATGTGCTGTCTTAAAGATGTCTGTGTTGGCAGGGGTGAC	1473

Db	2718	CAGGTCATGCCCTCTACAGATGCTGCTGGTCTTAAAGATGTGCTGTTGGGCAAGGGGTGAG	2777
Qy	1474	ACCCGTACCATCGAGGCCCACTACCAACCCCTGGACTGAGACTTACATGTGGCACTGTCAAC	1533
Db	2778	ACCCGTACCATCGAGGCCCACTACCAACCCCTGGACTGAGACTTACATGTGGCACTGTCAAC	2837
Qy	1534	AACTCATTCACGAGGATTAACGACATGATGTGCTGTATTCAAGCTCACGGCCATGGAAGAG	1593
Db	2838	AACTCATTCACGAGGATTAACGACATGATGTGCTGTATTCAAGCTCACGGCCATGGAAGAG	2897
Qy	1594	AAGGATATCTTTCAGAGGAGACTTCGAGGAGACCCCATACACCCCAAGTGGGCGCGCTTTCCT	1653
Db	2898	AAGGATATCTTTCAGAGGAGACTTCGAGGAGACCCCATACACCCCAAGTGGGCGCGCTTTCCT	2957
Qy	1654	TACAACCGCAACGACTTCATGTGCTCGCGCTGGAACCTTCCGCGAGATCATCTGCTCC	1713
Db	2958	TACAACCGCAACGACTTCATGTGCTCGCGCTGGAACCTTCCGCGAGATCATCTGCTCC	3017
Qy	1714	CGAGTGCAGAGGCTGCGCCGAGCAGAGACCGGTACACCGCTTGATGAGATCCTGGAGAT	1773
Db	3018	CGAGTGCAGAGGCTGCGCCGAGCAGAGACCGGTACACCGCTTGATGAGATCCTGGAGAT	3077
Qy	1774	CTTGGAAATCGAGGAGTAA	1791
Db	3078	CTTGGAAATCGAGGAGTAA	3095
RESULT 9			
AAA50018			
ID	AAA50018 standard; DNA: 3677 BP.		
XX			
XX	AAA50018;		
AC			
XX			
DT	10-OCT-2000 (first entry)		
XX			
DE	Stachybotrys chartarum phenol oxidising enzyme gene.		
XX			
KW	Phenol oxidising enzyme; detergent; bleaching; ds.		
XX			
OS	Stachybotrys chartarum.		
XX			
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FT		/*lag= a	1044..3095
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FT		/*tag= b	1044..1237
FT	Intron	/number= 1	1238..1285
FT		/*lag= c	1286..1324
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FT	Intron	/*lag= e	1450..1503
FT		/*tag= f	1504..1576
FT	exon	/number= 3	1577..1635
FT		/*lag= g	1636..1773
FT	Intron	/*tag= h	1774..1835
FT		/number= 4	1836..3095
FT	exon	/*lag= i	3096..3677
XX	MO2000039306-A2.		
XX	06-JUL-2000.		
PD	20-DEC-1999; 99MO-EP10287.		
PF			

XX 23-DEC-1998; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.
XX
XX (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
PA (HIND-) HINDOSTAN LEVER LTD.
XX
PI Bodie EA, Van Der Velden S, De Vries CH, Wang H;
XX WPI: 2000-514528/46.
DR P-PSDB; AAY95537.
XX
PT Detergent composition comprising novel phenol oxidising enzyme obtained
PT from fungus or bacteria, useful for pulp and paper bleaching, bleaching
PT color of stains on fabric and for anti-dye redeposition -
XX
XX Claim 1; Fig 1A-B; 45pp: English.
XX
XX The present sequence is that of the Stachybotrys chartarum MUC1 38898
CC phenol oxidising enzyme gene, including promoter and terminator
CC sequences. The gene was isolated from genomic DNA using primers
CC (see AAY50023-24) based on isolated peptides of the enzyme. The
CC gene codes for a 594 amino acid protein (see AAY95537). The invention
CC relates to detergent compositions comprising novel phenol oxidising
CC enzymes that are encoded by nucleic acids capable of hybridising to
CC the present DNA sequence, provided the enzymes are capable of
CC modifying the colour associated with dyes or coloured compounds, and
CC are produced from a bacterium, yeast or fungus (see AAY95538-40). The
CC phenol oxidising enzymes can be used for pulp and paper bleaching,
CC for bleaching the colour of stains on fabric and for anti-dye
CC transfer in detergent and textile applications. They may also be
CC capable of modifying the colour in the absence or presence of an
CC enhancer. Expression vectors and host cells comprising a nucleic
CC acid encoding a phenol oxidising enzyme, methods for producing the
CC phenol oxidising enzyme, and methods for constructing expression
CC hosts are provided.
XX
XX Sequence 3677 BP; 822 A; 1057 C; 849 G; 948 T; 1 other;
SQ
Query Match 82.3%; Score 1474; DB 21; Length 3677;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
OY 1 GTCATATAGCTTTCAGATGATGACATGGCAGCAGCCTCGGGCTCCTGTCGAGTC 60
DB 1038 GTCATATAGCTTTCAGATGATGACATGGCAGCAGCCTCGGGCTCCTGTCGAGTC 1097
OY 61 CTCGGCATCCCGATGAGACACCGGACGCCACCCATTGAGGCTGTGATCCCGAAGTGAAG 120
DB 1098 CTCGGCATCCCGATGAGACACCGGACGCCACCCATTGAGGCTGTGATCCCGAAGTGAAG 1157
OY 121 ACTGAGGCTTGGTGACTCCCTCTTGTGTCAGACGAGGATGACGATGGAGTACCT 180
DB 1158 ACTGAGGCTTGGTGACTCCCTCTTGTGTCAGACGAGGATGACGATGGAGTACCT 1217
OY 181 CCATFCAACTTCTTTAC----- 198
DB 1218 CCATFCAACTTCTTTACAGGTGAGACACCTTCCACCTGTTTTCTCCGATTAACTAAC 1277
OY 199 -----AGGAATGCCCTGGCAATTCACCTGTCAAGCAAGCCCAAGAT----- 239
DB 1278 TCTTATAGGAATGCCCTGGCAATTCACCTGTCAAGCAAGCCCAAGATTTTGTGAT 1337
OY 240 -----GATCATTTACCAACCTGTGAC 260
DB 1338 TTTCTACGAAGCAACTCGGCCCGCACTAATGATTTCTAGAGATCATTAACCAACCTGTGAC 1397
OY 261 CGGCAAGGACATTTGGTACTATAGATGAGATCAAGCAAGCATTTTCAGCAAG----- 311
DB 1398 CGGCAAGGACATTTGGTACTATAGATGAGATCAAGCAAGCATTTTCAGCAAGGATGATT 1457
OY 312 -----GATTTACCCCACTT 326

DB 1458 GCTCAGAAACCTTGTGTAATTATCATTTACTAGACCCTTTCAGATTAACCCACCTT 1517
OY 327 GGGCCCTGGCACTCTGTCGCGGTACAGATGGCATAGGCCCTGGCTCTACTTTCATGTTCC 386
DB 1518 GGGCCCTGGCACTCTGTCGCGGTACAGATGGCATAGGCCCTGGCTCTACTTTCATGTTCC 1577
OY 387 CAGAGACAGAGACTGTAGTTAGTTTCATCAACAAATGACACCGTGAGAACTCGGTCCA 446
DB 1578 CAGAGACAGAGACTGTAGTTAGTTTCATCAACAAATGACACCGTGAGAACTCGGTCCA 1637
OY 447 TCTGCAGGCTCCCATGCGGTGCCCTTTCGATGTTGGGCTGAAGATGTGACCTTCC 506
DB 1638 TCTGCAGGCTCCCATGCGGTGCCCTTTCGATGTTGGGCTGAAGATGTGACCTTCC 1697
OY 507 TGGGAGTACAAAGATTTACTTCCCACTACCAATCCCGGCGCTTGTGTGTACCA 566
DB 1698 TGGGAGTACAAAGATTTACTTCCCACTACCAATCCCGGCGCTTGTGTGTACCA 1757
OY 567 TGACCAGCTTTCATGA----- 583
DB 1758 TGACCAGCTTTCATGAAGGATGTGCTACGAGCCTTATCTTCTTGCGTACCTTTGGCTA 1817
OY 584 -----AGACTGCTGAGAAATGCTACTTGTGTCAGCGCTGGCGCTTACAT 627
DB 1818 ACCAACTTCTTTCGCTAGACTGCTGAGAAATGCTACTTGTGTCAGCGCTGGCGCTTACAT 1877
OY 628 ATCAACGAGGAGGAGGATGCTCGGTCTTCTAGGGCTATGGGAGTGGCATATTC 687
DB 1878 ATCAACGAGGAGGAGGATGCTCGGTCTTCTAGGGCTATGGGAGTGGCATATTC 1937
OY 688 CCTGTGATCTTGACGGCCAAAGTACTATAAGCGGATGTGATCCTGCTTTCAGACGAGGT 747
DB 1938 CCTGTGATCTTGACGGCCAAAGTACTATAAGCGGATGTGATCCTGCTTTCAGACGAGGT 1997
OY 748 GAGGACAGGACCTTGGGGAGTGTCAATGTCATCAACGAGACCATGECCTTTCCT 807
DB 1998 GAGGACAGGACCTTGGGGAGTGTCAATGTCATCAACGAGACCATGECCTTTCCT 2057
OY 808 AACGTCCAGCCCCGCAAGTACGTTTCGATTCCTCAACGCTGCCGTGTCTGTGCTGG 867
DB 2058 AACGTCCAGCCCCGCAAGTACGTTTCGATTCCTCAACGCTGCCGTGTCTGTGCTGG 2117
OY 868 CTCCTCTACCTGTGAGGACACGCTCTCCCAACGTCAGAAATCTTTCCAAATGCTTGGC 927
DB 2118 CTCCTCTACCTGTGAGGACACGCTCTCCCAACGTCAGAAATCTTTCCAAATGCTTGGC 2177
OY 928 TCTGATGCTGTCTCTTCAAGCCCCCGTTTCAGACCTTAACCTTACCTTGCCTTGGC 987
DB 2178 TCTGATGCTGTCTCTTCAAGCCCCCGTTTCAGACCTTAACCTTACCTTGCCTTGGC 2237
OY 988 GAGCGTTACGAGATCATTT----- 1008
DB 2238 GAGCGTTACGAGATCATTTATTTGATGCCCTCCCTTCACGAATGAGTCAAGAACTTA 2297
OY 1009 -----GACTTCAACAATTTGCTGGCGACACTTGTGACCTGGCAACGTT 1053
DB 2298 AGACTTAACACTTGTGAGCTTCAACAATTTGCTGGCGACACTTGTGACCTGGCAACGTT 2357
OY 1054 GCTGAGACCAACGATGTGGCGGACGAGAGATGATAGCTTCGACCTCGAGGTGATGGC 1113
DB 2358 GCTGAGACCAACGATGTGGCGGACGAGAGATGATAGCTTCGACCTCGAGGTGATGGC 2417
OY 1114 TTGCTGTGACGTCTGGGACCTGTTGAGGACAAACGACGAGTCCCTCACTCTCGGTGAC 1173
DB 2418 TTGCTGTGACGTCTGGGACCTGTTGAGGACAAACGACGAGTCCCTCACTCTCGGTGAC 2477
OY 1174 GTTCCCTTCCCTTCACAGAGAGCCCGCGGCAAGCAATTCAGTTTGAAGCGAGC 1233
DB 2478 GTTCCCTTCCCTTCACAGAGAGCCCGCGGCAAGCAATTCAGTTTGAAGCGAGC 2537
OY 1234 AACGACACTTACCTGATCAACGATGTGGCTTGGCGAATGTAAAGAGGTTGCTGACC 1293

Db	2538	AAGGACACATCACTGATCAACGATGTTGGCTTTGGCGATGTCAATGAGGCTGCTGGCC	2597
Oy	1294	AAGCCGAGCTCGGACACGTTTGAGGTCTGGGAGCTCGAAGCTCTCTGAGGCTGAGC	1355
Db	2598	AAGCCGAGCTCGGACACCGTTTGAGGTCTGGGAGCTCGAAGCTCTCTGAGGCTGAGC	2657
Oy	1354	CACCCGCTCCACATTCACCTTTGTTGACTTCAGATCCTCAAGCGAACTGGTGGTGGC	1413
Db	2658	CACCCGCTCCACATTCACCTTTGTTGACTTCAGATCCTCAAGCGAACTGGTGGTGGC	2717
Oy	1414	CAGGTCAATGCCCTGACGATGTGCGTGGTCTTAAAGATGTGTGTCGGTGGTGGGAGGGGTGAG	1473
Db	2718	CAGGTCAATGCCCTGACGATGTGCGTGGTCTTAAAGATGTGTGTCGGTGGTGGGAGGGGTGAG	2777
Oy	1474	ACCCTGACCATCGAGGGCCACTACCAACCTGTGACTGGAGCTTACATGTGGCATGTGCAC	1533
Db	2778	ACCCTGACCATCGAGGGCCACTACCAACCTGTGACTGGAGCTTACATGTGGCATGTGCAC	2837
Oy	1534	AACCTCATTCACGAGGATTAACGACATGATGGCTGTATTCAAGCTCACCGCCATGGAGAG	1593
Db	2838	AACCTCATTCACGAGGATTAACGACATGATGGCTGTATTCAAGCTCACCGCCATGGAGAG	2897
Oy	1594	AAGGATATCTTCAGAGAGACTTCGAGAGACCCCATAAACCCCAATGGGGGCCCTTCT	1655
Db	2898	AAGGATATCTTCAGAGAGACTTCGAGAGACCCCATAAACCCCAATGGGGGCCCTTCT	2957
Oy	1654	TACAAACGCAACGCACTTCGATGGCTCGGGCTGGAAACCTTCCGCGAGATCCATCACTGCC	1713
Db	2958	TACAAACGCAACGCACTTCGATGGCTCGGGCTGGAAACCTTCTCCGCGAGATCCATCACTGCC	3017
Oy	1714	CGAGTGCAGAGAGCTGGCCCGAGCAGAGAGCCGTACAAACCGCTCGATGAGATCTCTGGAGAT	1773
Db	3018	CGAGTGCAGAGAGCTGGCCCGAGCAGAGAGCCGTACAAACCGCTCGATGAGATCTCTGGAGAT	3077
Oy	1774	CTTGGAAATCGAGAGCTAA 1791	
Db	3078	CTTGGAAATCGAGAGCTAA 3095	

RESULT	ID	AAA51313	standard; DNA: 3677 BP.
XX	AC	AAA51313:	
XX	DT	09-OCT-2000	(first entry)
XX	DE	Stachybotrys chartarum	phenol oxidizing enzyme genomic DNA.
XX	KW	Phenol oxidizing enzyme;	colour; dye; modification; detergent; stain;
XX	KW	pulp; paper bleaching;	ds.
XX	OS	Stachybotrys chartarum.	
XX			
FH	Key	Location/Qualifiers	
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FT	exon	1836..2259
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FT	/tag= k	
FT	exon	2314..3095
FT	/tag= l	
FT	/partial	
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PN	MO200037654-A2.	
PD	29-JUN-2000.	
XX		
PF	20-DEC-1999;	99WO-USJ1009.
XX		
PR	23-DEC-1998;	98US-0220871.
PR	23-JUN-1999;	99US-0338723.
XX	(GENV) GENENCOR INT INC.	
PA		
PI	Wang H, Bodie EA;)
DR	WP1: 2000-452191/39.	
DR	P-PSDB; AAY96761.	
XX		
PT	New phenol oxidizing enzyme for modifying colors associated with dyes	
PT	or colored compounds, is obtained from fungus and is encoded by a	
PT	nucleic acid comprising a specific nucleotide sequence	
XX		
PS	Claim 10; Fig 1A-B; 45pp: English.	
XX		
CC	This genomic DNA encodes Stachybotrys chartarum phenol oxidizing enzyme.	
CC	Phenol oxidizing enzymes encoded by nucleic acid sequences which	
CC	hybridize to this DNA are claimed, as long as the enzyme is capable of	
CC	modifying the colour associated with dyes or coloured compounds. The	
CC	enzymes are useful in detergent compositions and for modifying colors	
CC	associated with dyes or colored compounds which occur in stains in a	
CC	sample. The enzymes are also useful for pulp and paper bleaching,	
CC	anti-dye transfer in detergent and other textile applications.	
XX		
SQ	Sequence 3677 BP: 822 A; 1057 C; 849 G; 948 T; 1 other:	
	Query Match	82.3%; Score 1474; DB 21; Length 3677;
	Best Local Similarity	87.0%; Pred. No. 0;
	Matches 1791; Conservative	0; Mismatches 0; Indels 267; Gaps
OY	I GTCAATATGCTGTTCATAAGCATGGCAACTGGCAGACGCTCCGGGCTCCTGTCTGGAGTC	60
Dd	1038 GTCAATATGCTGTTCATAAGCATGGCAAACTGGCAGACGCTCCGGGCTCCTGTCTGGAGTC	1097
OY	61 CTCGGCATCCCGATGGACACGCCGACGCCACCATTGAGAGCTGTTGCATCCCGAAGTGAG	120
Ddb	1098 CTCGGCATCCCGATGGACACGCCGACGCCACCATTGAGAGCTGTTGCATCCCGAAGTGAG	1157
OY	121 ACTGAGGTCCTTGCATGACTCCCTCTGCTGTCGACGAGGGCATGACACTGGAGTCACTT	180
Dd	1158 ACTGAGGTCCTTGCATGACTCCCTCTGCTGTCGACGAGGGCATGACACTGGAGTCACTT	1217
OY	181 CCATACAACTTCTTTC-----	198
Dd	1218 CCATACAACTTCTTTCACGAGTGAGACACCTGTCCACCTGTTTTCCATTAACATAAC	1277
OY	199 -----AGGAATGCCCTGGCAATTCACCTGTCACGACAGCACCCCAAGAT-----	239
Dd	1278 TCTTATAGGAATGCCCTGGCAATTCACCTGTCACGACAGCACCCCAAGATGTAATGCTTTGAT	1337
OY	240 -----GATCATTTACCAACCTGTGTAC	260
Dd	1338 TTTCACGAAGAAGCACTCGGCCCGACGACTAATGTAATTTCTAGAGATCATTAACAACCTGTGAC	1397
OY	261 CGGCAAGGACATTTGGTACTATGAGATGAGATCAAGCCATTTTCAGCAAG-----	311

Dd 1398 CGGCAAGACATTGGTACTATGAGATGCAAGATCAAGCCATTTCAGCAAGGGGTGAGTTT 1457
Qy 312 -----GATTTACCCACCTT 326
Dd 1458 GGTCAAGAAACCTTGtGTAATTATCATTTGTTACTGACCCTTTCAGATTTTACCCACCTT 1517
Qy 327 GCGCCCTGCCACTCTGTCGCTGCTACGATGGCAATGAGCCCTGCTCTACTTTCAATGTTCC 386
Dd 1518 GGGCCCTGCACTCTGTCGCTGCTACGATGGCAATGAGCCCTGCTCTACTTTCAATGTTCC 1577
Qy 387 CAGAGGAACAGAGACTGTAAGTATGATTCATCAACAATGCGACCGGAGNAACTGCTCA 446
Dd 1578 CAGAGGAACAGAGACTGTAAGTATGATTCATCAACAATGCGACCGGAGNAACTGCTCA 1637
Qy 447 TCTGCACGGCTCCCATCGCTGCTGCCCTTTCGATGGTGGCTGAAGATGACCTTCC 506
Dd 1638 TCTGCACGGCTCCCATCGCTGCTGCCCTTTCGATGGTGGCTGAAGATGACCTTCC 1697
Qy 507 TGGCAGATCAAGATTTACTTTTCCCACTACCAATCCGCCGCTTCTGTGTAACA 566
Dd 1698 TGGCAGATCAAGATTTACTTTTCCCACTACCAATCCGCCGCTTCTGTGTAACA 1757
Qy 567 TGACCAAGCTTTCATGA----- 583
Dd 1738 TGACCAAGCTTTCATGAAGCTTTCATGAAGCTTTCATTTCTTGCTAACCTTTGGCTA 1817
Qy 584 -----AGACTGCTGAGAAATGCTTACTTTGTCAGGCTGGCCCTACATT 627
Dd 1818 ACCAATTCTTTGTAAGACTGCTGGAATGCTTACTTTGGTCAAGCTGGCCCTACATT 1877
Qy 628 ATCAACGAGAGGCTGAGATGCTCTCGGTCTTCTAGTGGCTATGCGAGTTCCGATATC 687
Dd 1878 ATCAACGAGAGGCTGAGATGCTCTCGGTCTTCTAGTGGCTATGCGAGTTCCGATATC 1937
Qy 688 CCTTGATCTTACGAGCCCAAGTACTATTAAGCGCGATGGTACCCTGGCTTCGACCGAGGT 747
Dd 1938 CCTTGATCTTACGAGCCCAAGTACTATTAAGCGCGATGGTACCCTGGCTTCGACCGAGGT 1997
Qy 748 GAGGACCAAGACCTGTGGGAGATGTCATGTCACAGCAGAGCCATGGCTTTCCTT 807
Dd 1998 GAGGACCAAGACCTGTGGGAGATGTCATGTCACAGCAGAGCCATGGCTTTCCTT 2057
Qy 808 AACGTCCAGCCCCCGCAAGTACCCTTCGATTCCTCAACGCTGCCGTCTGTGCTTGG 867
Dd 2058 AACGTCCAGCCCCCGCAAGTACCCTTCGATTCCTCAACGCTGCCGTCTGTGCTTGG 2117
Qy 868 CTCCTCTACTCTGTGAGACAGCTCTCCCAAGCTCAGAAATTCCTTCCAAAGTCAATTGCC 927
Dd 2118 CTCCTCTACTCTGTGAGACAGCTCTCCCAAGCTCAGAAATTCCTTCCAAAGTCAATTGCC 2177
Qy 928 TCTGATGCTGTCTCTTCACAGCCCGCTTCAGACCTTCAACCTTCACTTCTGTTGCC 987
Dd 2178 TCTGATGCTGTCTCTTCACAGCCCGCTTCAGACCTTCAACCTTCACTTCTGTTGCC 2237
Qy 988 GAGCGTTAGGAATCATTT----- 1008
Dd 2238 GAGCGTTAGGAATCATTTGTAATGCCCTCCCTTCACGAATGAGTCAAGAACTCTA 2297
Qy 1009 -----GACTTCACCACTTTGCTGGCAGACTTGAACCTGGGCAACGTT 1053
Dd 2298 AGACTTACACTTTGTAATTCACCACTTTGCTGGCAGACTTGAACCTGGGCAACGTT 2357
Qy 1054 GCTGAGACCAACGATGTGCGGACGAGAGATGATGATGCTGCACTCTCGAGGTGATGCGC 1113
Dd 2358 GCTGAGACCAACGATGTGCGGACGAGAGATGATGATGCTGCACTCTCGAGGTGATGCGC 2417
Qy 1114 TTGCTGCTAGCTCTGCGCACTGTTAGAGACAACAGCAGAGTCCCTCACTCTCGTGAC 1173
Dd 2418 TTGCTGCTAGCTCTGCGCACTGTTAGAGACAACAGCAGAGTCCCTCACTCTCGTGAC 2477
Qy 1174 GTTCCCTTCCCTCTACAGGAAGGCCCGCGGACAACTTCATGAAGTTTGAAGCGACG 1233
Dd 2478 GTTCCCTTCCCTCTACAGGAAGGCCCGCGGACAACTTCATGAAGTTTGAAGCGACG 2537

Qy 1234 AACGACACTACCTGATATCAAGATGTTGGCTTTCGCGATGTCATGAGGCTGCTGGCC 1293
Dd 2538 AACGACACTACCTGATATCAAGATGTTGGCTTTCGCGATGTCATGAGGCTGCTGGCC 2597
Qy 1294 AAGCCCGAGCTGGCAGCCTGTTAGGTCTGGAGCTCGAGAACTCTCTGGAGCTGGAGC 1353
Dd 2598 AAGCCCGAGCTGGCAGCCTGTTAGGTCTGGAGCTCGAGAACTCTCTGGAGCTGGAGC 2657
Qy 1354 CACCCGTCACATTCACCTTGTGACTTCAGATTCCTCAACGGAACCTGGTGGTGGC 1413
Dd 2658 CACCCGTCACATTCACCTTGTGACTTCAGATTCCTCAACGGAACCTGGTGGTGGC 2717
Qy 1414 CAGTTCATGCCCCACAGATCTCTGCTTCTTAAAGATGTCGTGGTGGGAGGGGTGAG 1473
Dd 2718 CAGTTCATGCCCCACAGATCTCTGCTTCTTAAAGATGTCGTGGTGGGAGGGGTGAG 2777
Qy 1474 ACCCTGACCATGAGAGCCCACTACCAACCTTGAGCTTGAAGCTTATGTCAGTCTAC 1533
Dd 2778 ACCCTGACCATGAGAGCCCACTACCAACCTTGAGCTTGAAGCTTATGTCAGTCTAC 2837
Qy 1534 AACCTCATTCACAGAGATTAACGACATGATGGCTTATCAAGCTACCGCCATGGAGAG 1593
Dd 2838 AACCTCATTCACAGAGATTAACGACATGATGGCTTATCAAGCTACCGCCATGGAGAG 2897
Qy 1594 AAGGATATCTTCAGAGAGACTTCGAGAGCCCATGTAACCCCAAGTGGCGCCGTTCT 1653
Dd 2898 AAGGATATCTTCAGAGAGACTTCGAGAGCCCATGTAACCCCAAGTGGCGCCGTTCT 2957
Qy 1654 TACAAACCGAAGACTTCCATGCTGGCGCTGGAACCTTCCGCGGAGTCACTACCTGCC 1713
Dd 2958 TACAAACCGAAGACTTCCATGCTGGCGCTGGAACCTTCCGCGGAGTCACTACCTGCC 3017
Qy 1714 CGAGTGCAGAGCTGGCGCAGAGAGAGCCGTAACCCGCTGATGATGATCCCTGGAGAT 1773
Dd 3018 CGAGTGCAGAGCTGGCGCAGAGAGAGCCGTAACCCGCTGATGATGATCCCTGGAGAT 3077
Qy 1774 CTTGGAATGAGAGATTA 1791
Dd 3078 CTTGGAATGAGAGATTA 3095

RESULT 11
AAL47582
ID AAL47582 standard; DNA; 3677 BP.
XX
AC AAL47582;
XX
DT 13-SEP-2002 (first entry)
XX
DE S charitarum phenol oxidising enzyme gene.
XX
KW Phenol oxidising enzyme; fungus; redox reaction; detergent;
KW paper industry; pulp industry; textile; food industry; gene; ds.
XX
OS Stachybotrys charitarum.
OS
PN US6399329-B1.
PN
PD 04-JUN-2002.
PD
PF 21-DEC-1999; 99US-0468578.
PF
PR 12-DEC-1998; 98US-0220871.
PR
PR 23-JUN-1999; 99US-0338723.
PR
XX (GENEV) GENENCOR INT INC.
PA
XX Wang H, Bodie EA;
XX
XX
DR WPI: 2002-498835/53.
DR
XX P-PSDB; AAO18210.
XX

PT New polynucleotides encoding phenol oxidizing enzymes, useful for
PT preventing the transfer of dyes in solution from one textile to another
PT during detergent washing -

PS Claim 12; Fig 1; 37pp; English.

XX The present invention provides the protein and coding sequences of phenol
XX oxidizing enzymes from Stachybotrys chartarum, Bipolaris spoliifera and
XX Curvularia pallescens. These enzymes are useful in the textiles, paper,
XX pulp, detergent and food industries. In particular they are useful for
XX preventing the transfer of dyes in solution from one textile to another
XX during detergent washing (dye transfer inhibition). The present sequence
XX is the S. chartarum phenol oxidizing enzyme gene.

SO Sequence 3677 bp; 822 A; 1057 C; 849 G; 948 T; 1 other:

Query Match 82.3%; Score 1474; DB 24; Length 3677;

Best Local Similarity 87.0%; Pred. No. 0;

Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

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OY 1 GTCATATGCTGTTCAGTCATGCAACGCGAGAGAGCCCTCGGGCTCCTGTCGTGAGTC 60
DB 1038 GTCATATGCTGTTCAGTCATGCAACGCGAGAGAGCCCTCGGGCTCCTGTCGTGAGTC 1097
OY 61 CTCGGCATCCCGATGGACACCGGACCCCATTTGAGGCTTGGATCCGAAGTGAAG 120
DB 1098 CTCGGCATCCCGATGGACACCGGACCCCATTTGAGGCTTGGATCCGAAGTGAAG 1157
OY 121 ACTGAGTCTTGGTACTCCTCCTTGGTGAAGAGGGGATGAGACATGGGAGTCACT 180
DB 1158 ACTGAGTCTTGGTACTCCTCCTTGGTGAAGAGGGGATGAGACATGGGAGTCACT 1217
OY 181 CCATACAACTTGTCTTAC----- 198
DB 1218 CCATACAACTTGTCTTACAGTGAAGACACCTGTCCACCTGTTTTCCCTCGATTAAC 1277
OY 199 -----AGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGT----- 239
DB 1278 TCTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGTGTATGCTTTGAT 1337
OY 240 -----GATCATTTACCAACCCCTGTAC 260
DB 1338 TTTCTACGAAGCAACTGCGCCCGCACTAATGTATTCTAGATCATTAACCAACCTGTAC 1397
OY 261 CGGCAAGCAATTTGGTACTATAGATGAGATCAAGCATTTTCACCAAG----- 311
DB 1398 CGGCAAGCAATTTGGTACTATAGATGAGATCAAGCATTTTCACCAAGGGGTGAGTTT 1457
OY 312 -----GATTTACCCCACTT 326
DB 1458 GCTCAGAAACCTTGTGTAATTAATCATTTGTACGTACCCCTTCAGATTTTACCCCACTT 1517
OY 327 GCGCCCTGCCACTTCGTGCGGTACAGATGAGATGAGCCCTGTGCTCACTTTCAATGTTCC 386
DB 1518 GCGCCCTGCCACTTCGTGCGGTACAGATGAGATGAGCCCTGTGCTCACTTTCAATGTTCC 1577
OY 387 CAGAGAACAGAGATGTAGTATGTTATCAACAATGCGACCGGTGAGAACTCGGTCCA 446
DB 1578 CAGAGAACAGAGATGTAGTATGTTATCAACAATGCGACCGGTGAGAACTCGGTCCA 1637
OY 447 TCTGACAGGCTCCCATGCGGTGCGCTTTCGATGGTTGGGTGAAGATGTGACCTTCC 506
DB 1638 TCTGACAGGCTCCCATGCGGTGCGCTTTCGATGGTTGGGTGAAGATGTGACCTTCC 1697
OY 507 TGGCAGATACAGATTAATCACTTTCCCACTACCAATTCGCCCGCTTCTGTGATACA 566
DB 1698 TGGCAGATACAGATTAATCACTTTCCCACTACCAATTCGCCCGCTTCTGTGATACA 1757
OY 567 TGACCAACGCTTTCATGA----- 583
DB 1758 TGACCAACGCTTTCATGAAGTATGCTACAGAGCTTTATCTTTCTTGACCTACCTTTGGGCTA 1817
OY 584 -----AGACTGCTGAGAATGCTACTTGTGTGACAGCTGGCCCTTACATT 627
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DB 1818 ACCAATCTCTTTCCGTAGACTGCTGGAATGCTACTTTGTGTGAGGCTGGCGCTACATT 1877
OY 628 ATCAACGACGAGCTGAGATGCTCTCGGTCTTCTAGTGGCTATGCGAGATTCGATATC 687
DB 1878 ATCAACGACGAGCTGAGATGCTCTCGGTCTTCTAGTGGCTATGCGAGATTCGATATC 1937
OY 688 CCTGTATCTCGACGGCCAAAGTACTATTAACGGCGATGGTACCTGGGTGACCGGAGGT 747
DB 1938 CCTGTATCTCGACGGCCAAAGTACTATTAACGGCGATGGTACCTGGGTGACCGGAGGT 1997
OY 748 GAGGACACGAGACTGTGGGAGATGTCAATGTCACAGCAGACCATGGCTTTCCTT 807
DB 1998 GAGGACACGAGACTGTGGGAGATGTCAATGTCACAGCAGACCATGGCTTTCCTT 2057
OY 808 AACGTTCACCCCGCAGATTAACCGTTTCGATTCCTACACGCTGCGGTGTCTGCTTGG 867
DB 2058 AACGTTCACCCCGCAGATTAACCGTTTCGATTCCTACACGCTGCGGTGTCTGCTTGG 2117
OY 868 CTCCTCTACCTGTCGAGACCAAGCTCTCCCAAGTCAGAAATTCCTTCCAGTCATGTC 927
DB 2118 CTCCTCTACCTGTCGAGACCAAGCTCTCCCAAGTCAGAAATTCCTTCCAGTCATGTC 2177
OY 928 TCTGATGCTGTCTCCTTCAAGCCCGCTTTCAGACCTTAACCTTACCTTCTGTTGCC 987
DB 2178 TCTGATGCTGTCTCCTTCAAGCCCGCTTTCAGACCTTAACCTTACCTTCTGTTGCC 2237
OY 988 GAGCTTACGAGATCATTAAT----- 1008
DB 2238 GAGCTTACGAGATCATTAATGTTATGATCCCTCCCTCTCAGCAATGAGTCAAGAACTTA 2297
OY 1009 -----GACTTCAACAACTTGTGTCGGCAGACCTTGACCTGGGCAACGTT 1053
DB 2298 AGACTTAACACTTGTGATGACTTCAACAACTTGTGTCGGCAGACCTTGACCTGGGCAACGTT 2357
OY 1054 GCTGAGACCAAGATGTGCGGACGAGAGATGATGATAGCTGCGACTCTCGAGGTGATGCGC 1113
DB 2358 GCTGAGACCAAGATGTGCGGACGAGAGATGATGATAGCTGCGACTCTCGAGGTGATGCGC 2417
OY 1114 TTGCTGTCAGCTCTGCGACTGTGAGGACAACAGCAGGTCCCTCCATCTCCGTGAC 1173
DB 2418 TTGCTGTCAGCTCTGCGACTGTGAGGACAACAGCAGGTCCCTCCATCTCCGTGAC 2477
OY 1174 GTTCTTCCCTCCCTCAAGGAAGGCCCGCGCAACACCTTCAAGTTTGAAGGCAC 1233
DB 2478 GTTCTTCCCTCCCTCAAGGAAGGCCCGCGCAACACCTTCAAGTTTGAAGGCAC 2537
OY 1234 AACGACACTTACCTGATCAAGATGTTGGCTTGGCGATGTCAATGAGGCTGCTGGCC 1293
DB 2538 AACGACACTTACCTGATCAAGATGTTGGCTTGGCGATGTCAATGAGGCTGCTGGCC 2597
OY 1294 AAGCCGAGCTCGGACCGCTTGAAGTGTGGAGCTCGAGAACTCTTGGAGCTGAGAC 1353
DB 2598 AAGCCGAGCTCGGACCGCTTGAAGTGTGGAGCTCGAGAACTCTTGGAGCTGAGAC 2657
OY 1354 CACCCCGTCAATTCACCTTGTGACTTCAAGATCTTAACGCAACTGTGTGTGTGTC 1413
DB 2658 CACCCCGTCAATTCACCTTGTGACTTCAAGATCTTAACGCAACTGTGTGTGTGTC 2717
OY 1414 CAGGTATGCGCTTACGAGTCTGCTGCTTAAAGATGTGTGCTGTTGGGCGAGGGTGA 1473
DB 2718 CAGGTATGCGCTTACGAGTCTGCTGCTTAAAGATGTGTGCTGTTGGGCGAGGGTGA 2777
OY 1474 ACCCTGACCATGAGGCCCACTACCAACCCCTGAGCTGAGCTTACATGTGGCATGTGAC 1533
DB 2778 ACCCTGACCATGAGGCCCACTACCAACCCCTGAGCTGAGCTTACATGTGGCATGTGAC 2837
OY 1534 AACCTCATTCAGAGGATTAAGACATGATGGCTGTATTAACGTACACGCCATGAGAGAG 1593
DB 2838 AACCTCATTCAGAGGATTAAGACATGATGGCTGTATTAACGTACACGCCATGAGAGAG 2897
OY 1594 AAGGATATCTTCAGAGGACTTGAAGACCCCATGAACCCCAATGGGCGCCGTTCTT 1653
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Db	2898	AAGGATATATCTTCAGAGAGACTTCGACGACCCCATGAAACCCCAAGTGGCGCCCTTCT	2957
Qy	1654	TACAACCGCAACGACGATCTCCATGCTGCGCGTGGAAACTTCTCCGCGAGTCAATCACTGCC	1713
Db	2958	TACACACCGCAACGACGATCTCCATGCTGCGCGTGGAAACTTCTCCGCGAGTCAATCACTGCC	3017
Qy	1714	CGAGTGCAGAGACTTGCGCGAGCAGACCGCTTCAACACCGCTTCGATGAGATCTTGGAGAT	1773
Db	3018	CGAGTGCAGAGACTTGCGCGAGCAGACCGCTTCAACACCGCTTCGATGAGATCTTGGAGAT	3077
Qy	1774	CTTGGAAATCGAGAGATAA	1791
Db	3078	CTTGGAAATCGAGAGATAA	3095
RESULT 12			
ID	AAZ25735	standard; DNA; 2067 BP.	
XX	AAZ25735;		
XX	AA225735;		
DT	05-JAN-2000	(first entry)	
XX			
DE	Stachybotrys chartarum phenol oxidising enzyme PCR fragment.		
XX			
KW	Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;		
XX	detergent; anti-dye transfer; stain removal; bleaching; PCR primer; ss.		
OS	Synthetic.		
XX	Stachybotrys chartarum.		
PN	W09949010-A2.		
XX			
PD	30-SEP-1999.		
XX			
PE	23-MAR-1999; 99WO-EP02042.		
XX			
PR	24-MAR-1998; 98US-0046969.		
XX	22-DEC-1998; 98US-0218702.		
XX			
PA	(UNITL) UNILEVER NV.		
PA	(UNITL) UNILEVER PLC.		
XX			
PI	Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;		
XX	Wang C;		
DR	WPI: 1999-601211/51.		
XX			
PT	Detergent composition containing phenol oxidase from Stachybotrys, used		
XX	to bleach stains and prevent dye transfer		
PS			
XX	Example 17; Fig 9; 56pp: English.		
CC			
CC	The present invention describes a detergent composition containing a		
CC	purified phenol oxidising enzyme derived from Stachybotrys. The present		
CC	sequence represents a PCR fragment of Stachybotrys chartarum phenol		
CC	oxidising enzyme. The enzyme can be used to modify the colour of dyes		
CC	and other coloured compounds (e.g. for use in pulp and paper bleaching		
CC	also for removing stains, e.g. food, tea, blood etc., from fabrics) and		
CC	for preventing dye transfer during fabric washing.		
XX			
XX			
SO	Sequence 2067 BP; 445 A; 621 C; 500 G; 501 T; 0 other;		
Query Match 82.1%; Score 1470; DB 20; Length 2067;			
Best Local Similarity 87.0%; Pred. No. 0; Mismatches 0; Indels 267; Gaps			
Matches 1787; Conservative 0;			
Qy	4	AATATGCTGTTCAATCATGCGCACTGGCAGACGCTCGGGCTCTGCTGAGTCTTC	63
Db	7	AATATGCTGTTCAATCATGCGCACTGGCAGACGCTCGGGCTCTGCTGAGTCTTC	66
Qy	64	GGCATCCGAGTGCACCGCGACGCCACCCCATTTGAGCTGTTGATCCGAACTGAAGACT	123

Db	67	GGATCCCGATGAGACACCGGACGCCACCCCATTTGAGGCTGTTGATGCCGAAGTGAAGACT	126
Qy	124	GAGGCTCTCGCTGACTCCCTCTTGCTGACGAGGCGGATGAGAGCTGGAGTCCACCTCA	183
Db	127	GAGGCTCGCTGACTCCCTCTTGCTGACGAGGCGGATGAGAGCTGGAGTCCACCTCA	186
Qy	184	TACAACTTGGCTTAC-----	198
Db	187	TACAACTTGGCTTACAGGTGAGACACCTGTCCACCTGTTTTTCCCTGATTAACCTACTCT	246
Qy	189	---AGGAATGCCCTGACCAATTCACCTGTGAACGAGCCCAAGAT-----	239
Db	247	TATAGGAATGCCCTGACCAATTCACCTGTGAACGAGCCCAAGATGTATGTCTTTGATTTT	306
Qy	240	-----GATCATTTACCAACCTGTGCACGG	263
Db	307	CTACGAGCAACCTGGGCCGAGCTAATGTATCTTAGGATTCATTAACCAACCTGTGCACGG	366
Qy	264	CAAGACACTTTTGGTACTATGATCGAGATCAAGCAATTTCAAGCAAG-----	311
Db	367	CAAGACACTTTTGGTACTATGATCGAGATCAAGCAATTTCAAGCAAGGAGTTGCT	426
Qy	312	-----GATTTACCACCACTGTGCG	329
Db	427	CAGAAACCTTGTGTAAATTAATCATTTGTACTAGACCCCTTTCAGATTTTACCCACCTTGG	486
Qy	330	CCCTGCCACCTGCTCGCTGCGGCTACAGATGGCAAGACCCCTGCTCACTTTCAATGTTCCAG	389
Db	487	CCCTGCCACCTGCTCGCTGCGGCTACAGATGGCAAGACCCCTGCTCACTTTCAATGTTCCAG	546
Qy	390	AGGAACAGAGACTGTAGTTAGGTTCAACAATGCGACCGTGGAGAGACTCGGTCCATCT	449
Db	547	AGGAACAGAGACTGTAGTTAGGTTCAACAATGCGACCGTGGAGAACTCGGTCCATCT	606
Qy	450	GCAGCGCTCCCAATCGGCTGCGCCCTTTCGATGGTTGGGCTGAAGATGTACACTTCCCTGG	509
Db	607	GCAGCGCTCCCAATCGGCTGCGCCCTTTCGATGGTTGGGCTGAAGATGTACACTTCCCTGG	666
Qy	510	CGAGTACAGAGATTACTACTTTCCCACTACCAATCCGCCGCTCTGTGGTACCATGA	569
Db	667	CGAGTACAGAGATTACTACTTTCCCACTACCAATCCGCCGCTCTGTGGTACCATGA	726
Qy	570	CCAGCTTTTCATGA-----	583
Db	727	CCACGCTTTCATGAAGGTATGCTACGAGCCTTATCTTCTTGGCTACCTTGGCTAAC	786
Qy	584	-----AGACTGCTGAGAAATGCTACTTTGTGTACAGGCTGGCCCTACATATAC	630
Db	787	AACCTTCTTTTGTGTAGACTGTGGAATAAGCTCACTTTGTGTAGGCTGGCCCTACATATATC	846
Qy	631	AACGACGAGGCTGAGAGATGCTGTGGCTCTCTAGTGGCTATGAGGAGTTTCATATTCCT	690
Db	847	AACGACGAGGCTGAGAGATGCTGTGGCTCTCTAGTGGCTATGAGGAGTTTCATATTCCT	906
Qy	691	CTGATCTGACGGCCCAAGTACTATTAACGCCAGATGTAACCTGTGCTCGAACGAGGCTGAG	750
Db	907	CTGATCTGACGGCCCAAGTACTATTAACGCCAGATGTAACCTGTGCTCGAACGAGGCTGAG	966
Qy	751	GACCAAGACCTGTGGGGAAGATGTATCATATGTCAACGGACAGCATGGCTTTCCTTAAC	810
Db	967	GACCAAGACCTGTGGGGAAGATGTATCATATGTCAACGGACAGCATGGCTTTCCTTAAC	1026
Qy	811	GTCCAGCCCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCGGTGTCTGTGCTGGGCTC	870
Db	1027	GTCCAGCCCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCGGTGTCTGTGCTGGGCTC	1086
Qy	871	CTTCACTCTGTGACAGACAGCTGTCCCAAGTCAAGATTTCTTTTCCAAATGCAATTCCTCT	930
Db	1087	CTTCACTCTGTGACAGACAGCTGTCCCAAGTCAAGATTTCTTTTCCAAATGCAATTCCTCT	1146
Qy	931	GATGCTGTCTCTTTCAAGCCCCCGTTCAAGCTCTTAACCTCTACCTTGTGTTGCCGAG	990
Db	1147	GATGCTGTCTCTTTCAAGCCCCCGTTCAAGCTCTTAACCTCTACCTTGTGTTGCCGAG	1208

QY	991	CGTTACGAGTCACTTAT	-----1008
Db	1207	CGTTACGAGTCACTTAT	
QY	1009	-----TACTTCAACCACTTTGGTGGCCAGACTCTTGACCAATGAGTCAAGAACTTAAGA	1266
Db	1267	CTAACACTTGTAGACTTCACCAACTTTGGCTGGCCAGACTCTTGACCTGGCAAGCTTGCT	1326
QY	1057	GAGACCAAGCATGTCCGGCCAGCAGGATGAGTACGCTCGCACTCTCGAGGTGATGCGCTTC	1116
Db	1327	GAGACCAAGCATGTCCGGCCAGCAGGATGAGTACGCTCGCACTCTCGAGGTGATGCGCTTC	1386
QY	1117	GTCCTCAGCTCTGGCACTGTTGGAGCAACAGCAGAGTCCCTCCACATCCGTGAGCTT	1176
Db	1387	GTCCTCAGCTCTGGCACTGTTGGAGCAACAGCAGAGTCCCTCCACATCTCCGTGAGCTT	1446
QY	1177	CCCTTCCCTCCTGACAAAGGAAGGCCCGCCGCGACAAAGCAGCTTCAAGTTTGAACGAGCAAC	1236
Db	1447	CCCTTCCCTCCTGACAAAGGAAGGCCCGCCGCGACAAAGCAGCTTCAAGTTTGAACGAGCAAC	1506
QY	1237	GGACACTACCTGATCAACGATGTTGGCTTTGGCGATGTAATGACCGTGTCTGGCCAAAG	1286
Db	1507	GGACACTACCTGATCAACGATGTTGGCTTTGGCGATGTAATGACCGTGTCTGGCCAAAG	1566
QY	1297	CCCGAGCTCGGCACCCGTTGAGTGCTGGAGGCTCGAAGAACCTCTCGAGAGGCTGGAGCCAC	1356
Db	1567	CCCGAGCTCGGCACCCGTTGAGTGCTGGAGGCTCGAAGAACCTCTCGAGAGGCTGGAGCCAC	1626
QY	1357	CCCGTCACACTTACCTTGTGACTTCAAGATCTCTCAAGCGAAGCTGAGTGTGTCGACAG	1416
Db	1627	CCCGTCACACTTACCTTGTGACTTCAAGATCTCTCAAGCGAAGCTGAGTGTGTCGACAG	1686
QY	1417	GTCATGCCATCAGCAGTCTGCTGGTCTTAAGATGTCGTGTGGTGGCCAGAGGGGTGAGACC	1476
Db	1687	GTCATGCCATCAGCAGTCTGCTGGTCTTAAGATGTCGTGTGGTGGCCAGAGGGGTGAGACC	1746
QY	1477	CTGACACTCGAGGCCCACTACCAACCTCGAGCTGAGCTTACATGTGGCACATGTCACAAAC	1536
Db	1747	CTGACACTCGAGGCCCACTACCAACCTCGAGCTGAGCTTACATGTGGCACATGTCACAAAC	1806
QY	1537	CTCATTTACAGAGATTAACGATGATGCTGTATTCAACGTCACCCGCAATGGAGAGAGAG	1596
Db	1807	CTCATTTACAGAGATTAACGATGATGCTGTATTCAACGTCACCCGCAATGGAGAGAGAG	1866
QY	1597	GGATATCTTACGAGAGGACTTCGAGGAGCCCATGAACCCCAAGTGGCGCGCTTCCTTAC	1656
Db	1867	GGATATCTTACGAGAGGACTTCGAGGAGCCCATGAACCCCAAGTGGCGCGCTTCCTTAC	1926
QY	1657	AACCGCAAGCACTTCATGCTCGCGCTGGAAACTTCTCCGCGAGATCCATCACTGCCGA	1716
Db	1927	AACCGCAAGCACTTCATGCTCGCGCTGGAAACTTCTCCGCGAGATCCATCACTGCCGA	1986
QY	1717	GTCGAGAGAGCTGGCCGAGCAGAGGAGCCGTCAACACCGCTCGATGAGATCCTGGAGATCTT	1776
Db	1987	GTCGAGAGAGCTGGCCGAGCAGAGGAGCCGTCAACACCGCTCGATGAGATCCTGGAGATCTT	2046
QY	1777	GGAAATCGAGAGATA 1790	
Db	2047	GGAAATCGAGAGATA 2060	
RESULT 13			
AA227609 standard; DNA; 2067 BP.			
AC	AA227609:		
AC	AA227609:		
DT	16-DEC-1999 (first entry)		
XX	Stachybotrys phenol oxidase coding sequence.		
DE	Phenol oxidase; enzyme; coloured compound; dye transfer prevention;		
XX			

XX	fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
XX	
OS	Stachybotrys chartarum.
XX	
PN	WO9949020-A2.
XX	
PD	30-SEP-1999.
XX	
PF	23-MAR-1999; 99WO-US06327.
XX	
PR	24-MAR-1998; 98US-0046969.
XX	
PR	22-DEC-1998; 98US-0218702.
XX	
PR	22-MAR-1999; 99US-0273957.
XX	
PA	(GENEV) GENENCOR INT INC.
XX	
PI	Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;
XX	
DR	WPI; 1999-591088/50.
XX	
PT	Novel enzyme for modifying coloured compounds used to prevent
XX	dye-transfer.
XX	
PS	Example 17; Fig 9; 64pp; English.
XX	
CC	This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
XX	of the invention. The invention is used to modify a coloured compound and
CC	prevent dye transfer during fabric washing, or for stain bleaching or
XX	anti-dye transfer. It is useful in the detergent, paper and pulp, textile
XX	and food industries.
XX	
SO	Sequence 2067 BP; 445 A; 621 C; 500 G; 501 T; 0 other;

	Query Match	Best Local	Similarity	82.1%	Score 1470:	DB 20:	Length 2067:
	Matches 1787:	Conservative	0:	Mismatches	0:	Indels	267:
							Gaps
QY	4	AATATGCTGTTCAAGTACATGAGCAACTGGCAGACGACCTCCGGGGCTCCTGTGTGAGTCC	63				
Db	7	AATATGCTGTTCAAGTACATGAGCAACTGGCAGACGACCTCCGGGGCTCCTGTGTGAGTCC	66				
QY	64	GGCATCCCGATGGACACCCGGGAGCCACCCTATGAGGCTGTGATCCCGAAGTGAAGACT	1233				
Db	67	GGCATCCCGATGGACACCCGGGAGCCACCCTATGAGGCTGTGATCCCGAAGTGAAGACT	1260				
QY	124	GAGATCTTCGCTGACCTCCCTCCTTGGTGCAGCAGAGCGCATGACGACTGGAGTACCTCCA	1833				
Db	127	GAGATCTTCGCTGACCTCCCTCCTTGGTGCAGCAGAGCGCATGACGACTGGAGTACCTCCA	1866				
QY	184	TACAACCTTGCTTTAC-----	1988				
Db	187	TACAACCTTGCTTTACAGGTGAGACACCTGTCCACCTGTTTCCCTGGATACACTCT	2464				
QY	199	---AGGAATGCCCTGGCCAAATTCACCTGTCAAGCAGCCCAAGAT-----	2399				
Db	247	TATAGGAATGCCCTGGCCAAATTCACCTGTCAAGCAGCCCAAGATGTATGCTTTGATTTT	3066				
QY	240	-----GATCATTAACCAACCTGTCAACCGG	2633				
Db	307	CTACGAAGCAACTGGCCCCGACCTAATGTATTTCTAGAGATTAATTAACCAACCTGTCAACGG	3666				
QY	264	CAAGACATTTGGTACTATGATGAGATCGAGATCAAGCCATTTTCAGCAAG-----	3111				
Db	367	CAAGACATTTGGTACTATGATGAGATCGAGATCAAGCCATTTTCAGCAAGAGGTGAGTTTGT	4266				
QY	312	-----GATTTTACCCACCTTTGGG	3299				
Db	427	CAGAAACCTTGTTGTAATTAATCATTTGTACTGACCTCTTAATTAATTAACCCACCTTGGG	4866				
QY	330	CCCTGGCACTCTCGTGGGTCATACATGGCAGAGACCCCTGGTCTCACTTCAATGTTCACG	3899				
Db	487	CCCTGGCACTCTCGTGGGTCATACATGGCAGAGACCCCTGGTCTCACTTCAATGTTCACG	5466				

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QY 390 AGAAGACAGACTAGTATAGTTCATCAACAATGCCACCGTGGAGACTCGTCCATCT 449
    |||
Db 547 AGGACAGAGACTAGTATAGTTCATCAACAATGCCACCGTGGAGAACTCGGTCCATCT 606
QY 450 GACAGGCTCCCATGCGCGCCCTTGGATGGTGGGCTGAAGATGATACCTTCCCTGG 509
    |||
Db 607 GACAGGCTCCCATGCGCGCCCTTGGATGGTGGGCTGAAGATGATACCTTCCCTGG 666
QY 510 CGAGTACAAGATTAATCTACTTCCCACTAACCAATCCGCCCTTCTGTGTACCATGA 569
    |||
Db 667 CGAGTACAAGATTAATCTACTTCCCACTAACCAATCCGCCCTTCTGTGTACCATGA 726
QY 570 CCACGCTTTCANGA----- 583
    |||
Db 727 CCACGCTTTCANGAAGGTATGCTACAGCGCTTATCTTCTTGGCTACCTTGGCTAAC 786
QY 584 -----AGACACTGAGAAATGCTTACTTGGTACAGGCTGGCGCCATCAATTATC 630
    |||
Db 787 AACCTTCCTTTCGTAGACTGTGAGAAATGCTTACTTGGTACAGGCTGGCGCCATCAATTATC 846
QY 631 AACGACGAGGCTGAGGATGCTCGGCTTCTAGTGGCTATGCGAGTTCGATATCCCT 690
    |||
Db 847 AACGACGAGGCTGAGGATGCTCGGCTTCTAGTGGCTATGCGAGTTCGATATCCCT 906
QY 691 CTGATCTGAGCGGCCAAGTACTATAACGCCGATGGTACCCTGGCTTGCACCGAGGCTAG 750
    |||
Db 907 CTGATCTGAGCGGCCAAGTACTATAACGCCGATGGTACCCTGGCTTGCACCGAGGCTAG 966
QY 751 GACCAAGGACTGTGGGGGAATGTCATCATGTCACAGGACGATGGCTTTCCTTAAC 810
    |||
Db 967 GACCAAGGACTGTGGGGGAATGTCATCATGTCACAGGACGATGGCTTTCCTTAAC 1026
QY 811 GTCCAGCCCCGGAAGTACCGTTCGATTCCTCAACGCTGCGGTGTCTGTGCTTGGCTC 870
    |||
Db 1027 GTCCAGCCCCGGAAGTACCGTTCGATTCCTCAACGCTGCGGTGTCTGTGCTTGGCTC 1086
QY 871 CTCTACCTGTGACGACCAAGCTCTCCCAACGTCAGATTCTTTTCCAACTATGCTCT 930
    |||
Db 1087 CTCTACCTGTGACGACCAAGCTCTCTCCCAACGTCAGATTCTTTTCCAACTATGCTCT 1146
QY 931 GATGCGGTCTGCTTCAACCCCGCTTGCAGCCTTCAACCTGCTGCTGTGGCGAG 990
    |||
Db 1147 GATGCGGTCTCTTCAACCCCGCTTGCAGCCTTCAACCTGCTGCTGTGGCGAG 1206
QY 991 CGTTACGAGATCATTAAT----- 1008
    |||
Db 1207 CGTTACGAGATCATTAATGATGCCCTCCCTCTCAGCAATGATCAAGAACTCTAAGA 1266
QY 1009 -----GACTTCACCAACTTGTGCTGGCGAGACTCTTGACCTGGCAACGTTGCT 1056
    |||
Db 1267 CTAAACACTTGTAGACTTCAACAACTTGTGCGCAAGACTCTTGACCTGGCAACGTTGCT 1326
QY 1057 GAGACCAAGGATGGCGGACGAGGATGATAGCGTGCAGACTGTGAGGTGGCTGCTC 1116
    |||
Db 1327 GAGACCAAGGATGGCGGACGAGGATGATAGCGTGCAGACTGTGAGGTGGCTGCTC 1386
QY 1117 GTGCTAGCTCTGGCACTGTGAGGACAACAGCAGAGTCCCTCCACTCTCCGTGACGTT 1176
    |||
Db 1387 GTGCTAGCTCTGGCACTGTGAGGACAACAGCAGAGTCCCTCCACTCTCCGTGACGTT 1446
QY 1177 CCTTTCCTCTCTACAGGAAGGCCCGCGCAACAGCACTTCAAGTTTGAAGCGACAAAC 1236
    |||
Db 1447 CCTTTCCTCTCTACAGGAAGGCCCGCGCAACAGCACTTCAAGTTTGAAGCGACAAAC 1506
QY 1237 GGACACTACTCTATCAAGCATGTGGCTTGGCGAGTGAATGAGCGGTCTCCGTGGCAAG 1296
    |||
Db 1507 GGACACTACTCTATCAAGCATGTGGCTTGGCGAGTGAATGAGCGGTCTCCGTGGCAAG 1566
QY 1297 CCGGAGCTGGGACCGTGTAGGCTGGAGACTGAGAACTCCTCTGGAGGCTGAGACCAAC 1356
    |||
Db 1567 CCGGAGCTGGGACCGTGTAGGCTGGAGACTGAGAACTCCTCTGGAGGCTGAGACCAAC 1626
QY 1357 CCGGTCACATTACCTTGTGACTTCAAGATTCCTCAAGCAAGAACTGGTGGTGGCCAG 1416

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Db 1627 CCGGTCACATTACCTTGTGACTTCAAGATTCCTCAAGCAAGTGGTGGTGGCCAG 1686
QY 1417 GTGATGCCCTTACGAGTCTCTGTGCTTAAAGATGTCGTGGTGGGCGAGGGGTGAGACC 1476
    |||
Db 1687 GTGATGCCCTTACGAGTCTCTGTGCTTAAAGATGTCGTGGTGGGCGAGGGGTGAGACC 1746
QY 1477 CTGACCATGAGGCGCCACTACCAACCCCTGAGCTGAGCTTACATGTGGCATGTGCACAAAC 1536
    |||
Db 1747 CTGACCATGAGGCGCCACTACCAACCCCTGAGCTGAGCTTACATGTGGCATGTGCACAAAC 1806
QY 1537 CTGATTCACGAGGATTAACCATGATGGCTGTATTCAACGTACACGGCCATGAGAGGAAG 1596
    |||
Db 1807 CTGATTCACGAGGATTAACCATGATGGCTGTATTCAACGTACACGGCCATGAGAGGAAG 1866
QY 1597 GGATATCTTCAGAGAGACTTCGAGGACCCCATGAAACCCCAAGTGGGCGCGCTTCCCTTAC 1656
    |||
Db 1867 GGATATCTTCAGAGAGACTTCGAGGACCCCATGAAACCCCAAGTGGGCGCGCTTCCCTTAC 1926
QY 1657 AACCGCAACGACTTCCATGCTCGCGCTGGAAACTTCTCCCGAGTCAATCACTGCCCCGA 1716
    |||
Db 1927 AACCGCAACGACTTCCATGCTCGCGCTGGAAACTTCTCCCGAGTCAATCACTGCCCCGA 1986
QY 1717 GTGCAAGACTGGCGGACGAGCAAGCCGTCACACCGCTCGATGATGATCTTGGAGATCTT 1776
    |||
Db 1987 GTGCAAGACTGGCGGACGAGCAAGCCGTCACACCGCTCGATGATGATGATCTTGGAGATCTT 2046
QY 1777 GGATGAGAGAGTA 1790
    |||
Db 2047 GGATGAGAGAGTA 2060

RESULT 14
AAZ61243
ID AAZ61243 standard; DNA; 2110 BP.
XX
AC AAZ61243:
XX
DT 30-MAY-2000 (first entry)
XX
DE DNA encoding a phenol oxidizing enzyme.
XX
KW Phenol oxidizing enzyme; fungus; redox reaction; detergent; bleaching;
KW fabric; pulp; paper; decolorisation; plant-derived food product;
KW coloured compound; porphyrin; tannin; polyphenol; carotenoid;
KW anthocyanin; Maillard reaction product; ss.
XX
OS Acremonium murorum.
XX
FH Key
FH CDS Location/Qualifiers
FT 135..1943
FT /*tag= a
FT /product= "phenol oxidizing enzyme"
XX
PN WO200005349-A1.
XX
PD 03-FEB-2000.
XX
PF 13-JUL-1999; 99WO-EP04922.
XX
PR 21-JUL-1998; 98EP-0202454.
XX
PA (UNITE ) UNILEVER NV.
PA (UNITE ) UNILEVER PLC.
PA (HIND-) HINDUSTAN LEYER LTD.
XX
PI Convents D, Gouka RJ, Van Der Heiden M, Swarthoff T, Verrips CT;
XX
DR WPI: 2000-195101/17.
XX
P-PsDB: AA69204.
XX
PT Phenol-oxidizing enzyme from Acremonium, used in detergent compositions
PT for bleaching stains on fabrics

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Example 2: Page 37-40; 45pp: English.

The present sequence encodes a phenol oxidizing enzyme from the fungus *Acremonium murorum*. The enzyme has the CBS accession number 157.72. The enzyme catalyses redox reactions and is specific for molecular oxygen as the electron acceptor. The phenol oxidizing enzyme is specifically used in detergents for bleaching strains on fabrics, but also for bleaching pulp and paper and for decolourisation of plant-derived food products. The enzyme has a pH optimum in the alkaline to neutral range and can bleach a wide variety of coloured compounds, e.g. porphyrins, tannins, polyphenols, carotenoids, anthocyanins and Maillard reaction products.

Sequence 2110 BP: 400 A; 732 C; 556 G; 422 T; 0 other;

Query Match 38.3%; Score 685.8; DB 21; Length 2110;
Best Local Similarity 65.6%; Pred. No. 5.6e-174;
Matches 1043; Conservative 0; Mismatches 527; Indels 21; Gaps 2;

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QY 188 ACCTGCTTACAGGATGCCCTGCCAATCCACCTGTCAAGAGCCCAAGATGATCATTA 247
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 337 AACGCTGTTCCAGAGGCGCGCTGTGATCCCTCCGAAGAGCCTCTTCAACCGTCA 396
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 248 CCAACCCCTGTCAACGGCAAGACATTTGGTACTAGATCGAGATCAAGCATTTTCAGC 307
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 397 CCAACCCGTTACAAGGTGGGAGATGACTACTATGATGATCGATCAAGCATTTCTCG 456
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 308 AAAGATTTACCCCACTTGGCCCTCCCACTCTGCTGGCTACGATGGCATGAGCCCTG 367
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 457 AACAGTCTTCCCTGACCTGCGGCGCTGACCTCTGCGTACGACGATCTCCGCCG 516
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 368 GTCCTACTTCAATGTTCCCAAGAGAACAGACTGATTTAGTTCATCAACAATGCCA 427
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 517 GTCTACTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 428 CCGTGGAGAACTGCTGCTCATCTGACAGGCTCCCATCGCTGCGCTTTCATGTTGGG 487
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 577 CTTGTGAGAGCTTCATTCATCTTCAAGGCTCGTTCAGCGCTGCGCTTGGAGCGCTGG 636
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 488 CTGAAGATGTGACTTCCCTGGCGAGTACAGAGATTACTTTCCCAACTCAATCCG 547
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 637 CTGAGAGATGTCAACAAACCGGCGAGTACAGAGACTACTATCCCAATGCGCAGCGG 696
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 548 CCCGCTTCTGTTGATACCATATGACCAAGCTTTCATGAAAGCTGCTGATGCTACTTGG 607
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 697 GCGGCTTCTGTTGATACCATATGACCAAGCTTTCATGAAAGCTGCTGATGCTACTTGG 756
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 608 GTGAGGCTGGCGCTACATATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 757 GCCAGGCTGGTGGTATCATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 816
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 668 GCTATGGCGAGTTGCATATCCCTGTGATCTTGAAGGCGCAAGTACTATTAAGCCGATGTA 727
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 817 GATATGAGAGATGACATATCCCTGTGATCTTGAAGGAGTACTATTAAGCCGATGTA 876
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 728 CCTGCGTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 877 CTCTCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 788 GACAGCATGAGCTTTCCTTAAAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 937 GAGTCCCGTGGCTACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 996
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 848 CTGCGGTGCTGCTGGCTGCTCTTACCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 997 CCGCGGTGCTGCTGCTCTTACCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1056
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 908 TTCCTTCCAAAGTCAAGTCTGATGCTGAGTCTTAAAGAGAGAGAGAGAGAGAGAGAG 967
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1057 TCCGCTTCCAGGATCAAGCTGCTGAGTCTTCCGAGAGAGAGAGAGAGAGAGAGAGAG 1116
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 968 ACCTTACCTTCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
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DB 1117 AGCTGCTCTTCCATATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1176
QY 1028 GCCAGACTCTTGAACCTGCGCAAGCTTGTGAGACACAGATGTGCGGACAGAGATGAT 1087
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1177 GCAAGACCATTCAGAGCTCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1236
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1088 AGCGTGCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1141
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1237 ACAGACAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1296
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1142 ACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1201
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1297 AACAGCTCGTGGTCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1356
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1202 CCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1261
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1357 CCATCGACCACTCTGCTCCCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1416
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1262 GCTTGGCGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1417 CTTTCTCGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1476
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QY 1322 GGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1381
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QY 1477 GGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1536
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QY 1382 TCAGATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1426
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QY 1487 AGGCGCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1546
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QY 1727 TGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1757
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 1897 TGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1927
DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
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RESULT 15
AA047790 standard; DNA; 1959 BP.

AA047790;

24-FEB-1994 (first entry)

Billrubin oxidase gene.

Billrubin: oxidase; analytical. BO: expression vector. PCR;

polymerase chain reaction; ss.

Myrothecium verticaria.

Key Location/Qualifiers
CDS 66..1784

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 20:53:21 : Search time 57.3199 Seconds
(without alignments)
9582.334 Million cell updates/sec

Title: US-09-218-702-1

Perfect score: 1791
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1474	82.3	3677	4	US-09-218-702-3
5	1470	82.1	2067	4	US-09-218-702-5
6	503.4	28.1	2905	4	US-09-468-578-3
7	502.8	28.1	2063	4	US-09-468-578-6
8	460.4	25.7	1958	4	US-09-401-476-1
9	460.4	25.7	2095	4	US-09-401-476-3
10	188.6	10.5	858	4	US-09-468-578-8
11	54.6	3.0	7218	1	US-08-232-463-14
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13	45.8	2.6	6441	4	US-08-669-785-1
14	45.8	2.6	6443	6	5183745-5
15	45.6	2.5	5118	4	US-08-669-785-3
16	43	2.4	5468	4	US-09-535-008-66
17	43	2.4	5477	4	US-09-535-008-74
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24	42.6	2.4	5567	4	US-09-535-008-64
25	42.6	2.4	5576	4	US-09-535-008-72
26	41.8	2.3	390	4	US-09-197-649-7
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	29	38.8	2.2	4108	4	US-08-981-729-8	Sequence 8, Appl
	30	38.8	2.2	4108	4	US-08-981-446B-1	Sequence 1, Appl
	31	38.6	2.2	686	4	US-08-998-416-715	Sequence 715, App
C	32	38.2	2.1	4403765	4	US-09-103-840A-2	Sequence 2, Appl
	33	38.2	2.1	4411529	4	US-09-103-840A-1	Sequence 1, Appl
C	34	37.8	2.1	1872	2	US-08-743-637B-17	Sequence 17, Appl
	35	37.8	2.1	1872	3	US-08-526-840B-17	Sequence 17, Appl
C	36	37.2	2.1	969	4	US-09-134-001C-109	Sequence 109, App
	37	36.4	2.0	2923	1	US-08-243-542-6	Sequence 6, Appl
C	38	36.4	2.0	2923	1	US-08-477-407-6	Sequence 6, Appl
C	39	36.4	2.0	2923	1	US-08-484-355-6	Sequence 6, Appl
C	40	36.4	2.0	44377	2	US-08-804-227C-7	Sequence 7, Appl
C	41	36.4	2.0	44377	2	US-08-804-198-1	Sequence 1, Appl
C	42	35.6	2.0	49372	1	US-08-614-770A-1	Sequence 1, Appl
	43	35.4	2.0	3468	1	US-07-951-715A-2	Sequence 2, Appl
	44	35.4	2.0	3468	1	US-07-951-715A-4	Sequence 4, Appl
	45	35.4	2.0	3468	2	US-08-459-448A-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-468-578-5
: Sequence 5, Appl 539329
: Patent No. 6399329
: GENERAL INFORMATION:
: APPLICANT: Wang, Huaming
: APPLICANT: Bodie, Elizabeth A.
: TITLE OF INVENTION: Phenol Oxidizing Enzymes
: FILE REFERENCE: GC561-3
: CURRENT APPLICATION NUMBER: US/09/468,578
: CURRENT FILING DATE: 1999-12-21
: PRIOR APPLICATION NUMBER: US 09/220,871
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: US 09/338,723
: PRIOR FILING DATE: 1999-06-23
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 1791
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: cDNA
US-09-468-578-5

Query Match      100.0%: Score 1791; DB 4; Length 1791;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCATATGCTGTTCAAGTCATGCACTGGCAGCAGCCCTCCGGCTCTGTCGAGTC 60
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DB 1 GTCATATGCTGTTCAAGTCATGCACTGGCAGCAGCCCTCCGGCTCTGTCGAGTC 60
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QY 61 CTCGGCATCCCGATGACACCGGACCCATTCGAGGCTGTATCCCAAGTGAAG 120
    |||
DB 61 CTCGGCATCCCGATGACACCGGACCCATTCGAGGCTGTATCCCAAGTGAAG 120
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QY 121 ACTGAGGTCTTGCCTGACCTCCCTTGTGTCAGCAGGGATGACGACTGGAGTACCT 180
    |||
DB 121 ACTGAGGTCTTGCCTGACCTCCCTTGTGTCAGCAGGGATGACGACTGGAGTACCT 180
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QY 181 CCATTAACCTTGGTTTACAGGAATGCCCTGCCAATTCCACTCTGTAAGCAGCCCAAGATG 240
    |||
DB 181 CCATTAACCTTGGTTTACAGGAATGCCCTGCCAATTCCACTCTGTAAGCAGCCCAAGATG 240
    |||

QY 241 ATCATTAACCAACCTGTACACCGGACGAGATTTGGTACTATGAGATGATCAAGATCAAGCA 300
    |||
DB 241 ATCATTAACCAACCTGTACACCGGACGAGATTTGGTACTATGAGATGATCAAGATCAAGCA 300
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QY 301 TTTCAGCAAGATTTACCCACCTTGGCGCCCTGCCACTCTGCTGCTAGCATGTGATG 360
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Db 301 TTTCAGCAAGATTTACCCCACTTGCCGCTGCACATCTCGTGGCTACGATGCGATG 360
QY 361 ACCCCGCGCTACTTTCAATGTGCCAGAGAACAGACGTAGTTAGTTTCACTCAAC 420
Db 361 ACCCCGCGCTACTTTCAATGTGCCAGAGAACAGACGTAGTTAGTTTCACTCAAC 420
QY 421 AATGCCACGCTGAGAACATCGGCTCATCTGCAGGCTCCCTACGCTGCCCTTTCAT 480
Db 421 AATGCCACGCTGAGAACATCGGCTCATCTGCAGGCTCCCTACGCTGCCCTTTCAT 480
QY 481 GGTGGGCTGAAGATGTGACCTTCCCTGCGAGTACAGAGATTACTATTTCCCACTAC 540
Db 481 GGTGGGCTGAAGATGTGACCTTCCCTGCGAGTACAGAGATTACTATTTCCCACTAC 540
QY 541 CAATCGCGCGCTCTGTGTGATCCATGACCAACGCTTTCATGAAGCTGTGAGATGCC 600
Db 541 CAATCGCGCGCTCTGTGTGATCCATGACCAACGCTTTCATGAAGCTGTGAGATGCC 600
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Db 601 TACTTTGGTCAGGCTGGCCCTACATTAACAAGAGAGGCTGAGATGCTCGCTTT 660
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Db 661 CCTAGTGGCTATGGGAGTTTCGATATCCCTCTGATCTGAACGGCCAAAGTATTAAGCC 720
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Db 721 GATGTAACCTCGTTCGACCGGAGGAGAACAGGACCTGTGGGAGATGATCAATCA 780
QY 781 GTCAACGAGACAGCATGCGCTTCTTAACGTCACAGCCCGCAAGTACCGTTCCGATT 840
Db 781 GTCAACGAGACAGCATGCGCTTCTTAACGTCACAGCCCGCAAGTACCGTTCCGATT 840
QY 841 CTCACGCTGCGGTGTCTGTGCTTGGCTCTTACCTGTCAGAACAGCTCTCCCAAC 900
Db 841 CTCACGCTGCGGTGTCTGTGCTTGGCTCTTACCTGTCAGAACAGCTCTCCCAAC 900
QY 901 GTGAGAAATTCCTTTCACAGCATGCTGCTGATGCTGGTCTCCCTTAAGCCCGGTTCA 960
Db 901 GTGAGAAATTCCTTTCACAGCATGCTGCTGATGCTGGTCTCCCTTAAGCCCGGTTCA 960
QY 961 ACCTCTAACCTCTACCTTCTGTGGCGAGCGTTTACAGATCAATTAATGACTTCAACAC 1020
Db 961 ACCTCTAACCTCTACCTTCTGTGGCGAGCGTTTACAGATCAATTAATGACTTCAACAC 1020
QY 1021 TTTTGTGGCCAGACTTTGACTGCGCAACGTTGCTGAGAACAGATGTGCGGACGAG 1080
Db 1021 TTTTGTGGCCAGACTTTGACTGCGCAACGTTGCTGAGAACAGATGTGCGGACGAG 1080
QY 1081 GATGATGAGCTGCGACCTCCGAGTGATGCGGTTGCTGTCAGCTGTGGACATGTTGAG 1140
Db 1081 GATGATGAGCTGCGACCTCCGAGTGATGCGGTTGCTGTCAGCTGTGGACATGTTGAG 1140
QY 1141 GACACAGCAGGATGCCCTCCACTCTCCGTGACGTTCTTCCCTCCTCAACAAGAGAGG 1200
Db 1141 GACACAGCAGGATGCCCTCCACTCTCCGTGACGTTCTTCCCTCCTCAACAAGAGAGG 1200
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Db 1201 CCCGCGGACAGACTTCAAGTTTGAACGACAGACGACACTACTGATCAACGATGTT 1260
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Db 1261 GGGTTTGGCGATGTCAATGAGCGTGTCTGAGCCAAAGCCGAGGTGGGCAACCGTTGAGT 1320
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Db 1381 TTTCAGATCCTCAAGGAACTGGTGTCTGTGCGCAGGTCAATGCTCAAGATCTGTGCT 1440
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Db 1441 CTTAAGATGTGCTGTGTTGGGACAGGGGTGAGACCTGACCATGAGGCCCACTACCA 1500
QY 1501 CCCGTGACTGGAGCTTACATGTGGCACTGTCAACACCTCAATTCACAGAGATTAACAGAT 1560
Db 1501 CCCGTGACTGGAGCTTACATGTGGCACTGTCAACACCTCAATTCACAGAGATTAACAGAT 1560
QY 1561 ATGCTGTATTTACAGTCAACCGCATGAGAGAGAGAGATATCTTTAGAGACACTTCGAG 1620
Db 1561 ATGCTGTATTTACAGTCAACCGCATGAGAGAGAGAGATATCTTTAGAGACACTTCGAG 1620
QY 1621 GACCCCATGACCCCAAGAGGGCGCGCTTCCCTTACACCGCAACGACATTCATGCTGCC 1680
Db 1621 GACCCCATGACCCCAAGAGGGCGCGCTTCCCTTACACCGCAACGACATTCATGCTGCC 1680
QY 1681 GCTGAAACCTTCTCCGCGAGTCCATCACTGCCGAGTGCAGAGAGCTGGCCGAGAGAG 1740
Db 1681 GCTGAAACCTTCTCCGCGAGTCCATCACTGCCGAGTGCAGAGAGCTGGCCGAGAGAG 1740
QY 1741 CCGTACACCCGCTCGATGAGATCTGAGAGATCTTGGAAATGAGAGATTA 1791
Db 1741 CCGTACACCCGCTCGATGAGATCTGAGAGATCTTGGAAATGAGAGATTA 1791

RESULT 2
US-09-218-702-1
; Sequence 1, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huang
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218/702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Stachybotrys sp.
US-09-218-702-1

Query Match 100.0%; Score 1791; DB 4; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAATATGCTGTTCAGTCAATGGAACAGTGGACAGAGCTCCGCGCTCTGTCGAGTTC 60
Db 1 GTCAATATGCTGTTCAGTCAATGGAACAGTGGACAGAGCTCCGCGCTCTGTCGAGTTC 60
QY 61 CTCGGCATCCGATGAGACACCGGACAGCACCCCATTTGAGGCTGTGATCCCGAAGTGAAG 120
Db 61 CTCGGCATCCGATGAGACACCGGACAGCACCCCATTTGAGGCTGTGATCCCGAAGTGAAG 120
QY 121 ACTGAGGTCTGCTGACTACCTCCCTTGGTGCAGAGGGATGAGACATGGGAGTCACT 180
Db 121 ACTGAGGTCTGCTGACTACCTCCCTTGGTGCAGAGGGATGAGACATGGGAGTCACT 180
QY 181 CCATACAACTTGTCTTACAGGAATGCTGCAATTTCACTCTCAAGCAGGCCAAGATG 240
Db 181 CCATACAACTTGTCTTACAGGAATGCTGCAATTTCACTCTCAAGCAGGCCAAGATG 240
QY 241 ATCATTAACAACCTGTCAACCGGCAAGAGACATTTGGTACTATGAGATCGAAGATCAAGCA 300
Db 241 ATCATTAACAACCTGTCAACCGGCAAGAGACATTTGGTACTATGAGATCGAAGATCAAGCA 300
QY 301 TTTCAGCAAAAGATTTACCCCACTTGGCCCTGACACTCTGTGCGTACGATGGCATG 360
Db 301 TTTCAGCAAAAGATTTACCCCACTTGGCCCTGACACTCTGTGCGTACGATGGCATG 360
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OY	361	AGCCTGTCCTACTTTCATGTGTTCCACAGAGAACGAACTGTAGTTACATCAAC	420
Db	361	AGCCCTGGTCTACTTTCATGTGTTCCAGAGAACGAACTGTAGTTACATCAAC	420
OY	421	AATGCCACCGGAGAACTGTGTCACATCTGCACAGGCTGCCCAATCGGCGCCCTTCGAT	480
Db	421	AATGCCACCGTGGAGAACTGTGTCACATCTGTCACAGGCTGCCCAATCGGCGTTCGAT	480
OY	481	GTTGGGCTGAAGATGTGACCTTCCCTGGGAGATACMAAGATTACTCTTCCCAATAC	540
Db	481	GTTGGGCTGAAGATGTGACCTTCCCTGGGAGATACMAAGATTACTCTTCCCAATAC	540
OY	541	CAATCCGCCCGCCCTCTCTGTGTGTACATGACACACGCTTTATGAAGACTGTGAGATGCC	600
Db	541	CAATCCGCCCGCCCTCTCTGTGTGTACATGACACACGCTTTATGAAGACTGTGAGATGCC	600
OY	601	TACTTTGGTCAGGCTGGCGCTACATTATCAAGACGAGGCTGAGAGATGCTCGGTGTT	660
Db	601	TACTTTGGTCAGGCTGGCGCTACATTATCAAGACGAGGCTGAGAGATGCTCGGTGTT	660
OY	661	CCCTGTGGCTATGGCGAGTTCGATATCCCTCTGATCCTACAGCCGCAAGTACTATACGCC	720
Db	661	CCCTGTGGCTATGGCGAGTTCGATATCCCTCTGATCCTACAGCCGCAAGTACTATACGCC	720
OY	721	GATGGTACCTCGCTGTGACCCGAGGGTGAAGACACGACTCTGGGGAGATGTCAATCAT	780
Db	721	GATGGTACCTCGCTGTGACCCGAGGGTGAAGACACGACTCTGGGGAGATGTCAATCAT	780
OY	781	GTCACAGGACAGCGCATGGCCCTTCCTTAAAGTCACACCCGCGACATCCGTTCCGATTC	840
Db	781	GTCACAGGACAGCGCATGGCCCTTCCTTAAAGTCACACCCGCGAAGTACCGTTCCGATTC	840
OY	841	CTCAACGCTGCGCGTGTCTCGTGTGGCTCTCTACTCTGTGAGAACGACTCTCCCAAC	900
Db	841	CTCAACGCTGCGCGTGTCTCGTGTGGCTCTCTACTCTGTGAGAACGACTCTCCCAAC	900
OY	901	GTCAGAAATCCCTTTCCAAGTCATTTGCCCTGTGATGTCGTCTCTTCAAGCCCGCCGTACG	960
Db	901	GTCAGAAATCCCTTTCCAAGTCATTTGCCCTGTGATGTCGTCTCTTCAAGCCCGCCGTACG	960
OY	961	ACGCTTAACCTTAACCTTGTGTTGGCCGAGCGTTACGAAATATTATTGACTTCAACCAAC	1020
Db	961	ACGCTTAACCTTAACCTTGTGTTGGCCGAGCGTTACGAAATATTATTGACTTCAACCAAC	1020
OY	1021	TTTCTGTGGCAGACTCTTGACCTGCGCCACAGCTGTGAGAACCAAGATGTGGCGACAG	1080
Db	1021	TTTCTGTGGCAGACTCTTGACCTGCGCCACAGCTGTGAGAACCAAGATGTGGCGACAG	1080
OY	1081	GATGAGTACGCTGCGACTCTGAGGATGATGCGCTTCGTGTCAGCTGTGGCACTGTGGAG	1140
Db	1081	GATGAGTACGCTGCGACTCTGAGGATGATGCGCTTCGTGTCAGCTGTGGCACTGTGGAG	1140
OY	1141	GACAAACGCCAGTCCCTCTCACTCTCCGTGACGTTCTTTCCCTCTCACAAAGAGAGC	1200
Db	1141	GACAAACGCCAGTCCCTCTCACTCTCCGTGACGTTCTTTCCCTCTCACAAAGAGAGC	1200
OY	1201	CCGCGCAACAAGCACTTCAAGTTTGAACGACAGAACGACACTACTCTGATCAAGATTT	1260
Db	1201	CCGCGCGAACAAGCACTTCAAGTTTGAACGACGACGACACTACTGATCAAGATTT	1260
OY	1261	GCGCTTTCGCGATGTCAATGAGCGCTGTCGGCCAAAGCCCGAGCTCGGACCGTGTGAGGTC	1320
Db	1261	GCGCTTTCGCGATGTCAATGAGCGCTGTCGGCCAAAGCCCGAGCTCGGACCGTGTGAGGTC	1320
OY	1321	TGGGAGCTCGAGAACTCTCTCTGAGGCTGTGAGACACCCCGTCAACATTCACCTTGTGTAC	1380
Db	1321	TGGGAGCTCGAGAACTCTCTCTGAGGCTGTGAGACACCCCGTCAACATTCACCTTGTGTAC	1380
OY	1381	TTTCAAGATCCCAAGGCAACTGTGTCGCGGCGAGGCTATGCGCTACGAGGTCTGCTGGT	1440
Db	1381	TTTCAAGATCCCTCAAGGCAACTGTGTCGCGGCGAGGCTATGCGCTACGAGGTCTGCTGGT	1440
OY	1441	CTTAAAGATGTCTGTGGTTGGGACAGGGGTGAGACCTGTACCATTGAGAGCCCACTACCA	1500

D _b	1441	CTTAGAGATGCTGCTTGTTGGCAGGGGAGAACCTTACCATCGAGGCCACACTACCA	15000
Q _y	1501	CCCTGAGACTGAGGCTTACATGTGGCACTGTGCACAACCTGATTCACAGAGATTAA	15600
D _b	1501	CCCTGAGACTGAGGCTTACATGTGGCACTGTGCACAACCTGATTCACAGAGATTAA	15600
Q _y	1561	ATGCGCTGATTCAACGTCACCGCCCATGAGAGAGAGGATATCTTCAGAGACTTCG	16200
D _b	1561	ATGCGCTGATTCAACGTCACCGCCCATGAGAGAGAGGATATCTTCAGAGACTTCG	16200
Q _y	1621	GACCCCATGAAACCCCAAGTGGGGCGCGCTTCCTTACAACCGCAAGACTCCATGCTGC	16800
D _b	1621	GACCCCATGAAACCCCAAGTGGGGCGCGCTTCCTTACAACCGCAAGACTCCATGCTGC	16800
Q _y	1681	GCTGGAACCTTCTCCGCCGAGTGCATCTACTGCCCCAGTGCAGAGACTGGCGAGCAGG	17400
D _b	1681	GCTGGAACCTTCTCCGCCGAGTGCATCTACTGCCCCAGTGCAGAGACTGGCGAGCAGG	17400
Q _y	1741	CCGTACACACCGCCTCATGTAGAGATCTTGAGAACTTGAGAGAGTAA	1791
D _b	1741	CCGTACACACCGCCTCATGTAGAGATCTTGAGAACTTGAGAGAGTAA	1791

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RESULT 3
US-09-468-578-1
Sequence 1, Application US/09468578
Patent No. 6399329
GENERAL INFORMATION:
APPLICANT: Wang, Huaming
APPLICANT: Bodie, Elizabeth A.
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GC561-3
CURRENT APPLICATION NUMBER: US/09/468,578
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 09/220,871
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 09/338,723
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3677
TYPE: DNA
ORGANISM: Stachybotrys chartarum
US-09-468-578-1

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Query Match	82.3%	Score 1474;	DB 4;	Length 3677;
Best Local Similarity	87.08;	Pred. No. 0;		
Matches 1791; Conservative	0;	Mismatches 0;	Indels 267;	Gaps 5;

Qy	1	GTAAATATGCTGTTCAAGTACGTACGGCAACTCGGGAGACCTCCGGGGCTCCTGTCTGAGATC	60
Db	1038	GTCAATATGCTGTTCAAGTACGTATGGCAACTGGCAGACACCTCCGGGGCTCCTGTCTGAGATC	109
Qy	61	CTCGCATCCCGATGGAGACACGGAGCGACCCCAATTGAGAGCTTTGATATCCGAAGTGAAG	120
Db	1098	CTCGGCATCCCGATGGAGACACGGAGCGACCCCAATTGAGAGCTTTGATATCCGAAGTGAAG	115
Qy	121	ACTGAGGCTCTTCGCTGACCTCCCTTCCTTGTCGACAGCAGGCGATAGACGATCGGAGTACCT	180
Db	1158	ACTGAGGCTCTTCGCTGACCTCCCTTCCTTGTCGACAGCAGGCGATAGACGATCGGAGTACCT	121
Qy	181	CCATACCACTGCTTAC-----	198
Db	1218	CCATACCAACTGCTTACAGGTGAGACACCTGTCACCACTGTTTTCCCTCGATTAACTAAC	127
Qy	199	-----AGGAATGCCCTGSCCAATTCACCTGTGCAGAGGCCCAAGAT-----	239
Db	1278	TCCTTATAGGAATGCCCTGSCCAATTCACCTGTGCAGAGGCCCAAGATGTAATGCTTTGAT	133
Qy	240	-----GATCATTCACCAACCTGTCAC-----	260

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Db 1338 TTTTACGAGCAACTGGCCCCGACTAATGTATTCAGATCATTAACCAACCCGTGTAC 1397
Oy 261 CGGCAAGACATTTGGTACTATGATGAGATCGAGATTCAGACCATTTTCAGCAAA----- 311
Db 1398 CGGCAAGACATTTGGTACTATGATGAGATCGAGATTCAGACCATTTTCAGCAAAAGGCTGAGTTT 1457
Oy 312 -----GATTTTACCCACCTT 326
Db 1458 GCTCAGAAACCTTGTGTATTAATCATTTTACTGACCCCTTTCAAGATTTTACCCACCTT 1517
Oy 327 GGGCCCTGGCAGCTCTGCTGGGCTAGCATGAGCATGAGCCCTGGCTGCTTCAATTTTCC 386
Db 1518 GGGCCCTGGCAGCTCTGCTGGGCTAGCATGAGCATGAGCCCTGGCTGCTTCAATTTTCC 1577
Oy 387 CAGAGGAAGAGACTGTAGTTAGTTCAACAATGCGACCGCTGAGAAACCGGTCCA 446
Db 1578 CAGAGGAAGAGACTGTAGTTAGTTCAACAATGCGACCGCTGAGAAACCGGTCCA 1637
Oy 447 TCTGCAGGCTCCCATGCGGTGCCCCCTTTCGATGGTGGGCTGAAGATGTGACCTTCCC 506
Db 1638 TCTGCAGGCTCCCATGCGGTGCCCCCTTTCGATGGTGGGCTGAAGATGTGACCTTCCC 1697
Oy 507 TGGCGAGTCAAGGATTAATCTTCCCAACTACCAATCGGCCGCTCTGTGTACCA 566
Db 1698 TGGCGAGTCAAGGATTAATCTTCCCAACTACCAATCGGCCGCTCTGTGTACCA 1757
Oy 567 TGACCAAGCTTTCATGA----- 583
Db 1758 TGACCAAGCTTTCATGAAGTATGCTACGAGCCTTATCTTTCTTGGCTAACCTTTGGCTA 1817
Oy 584 -----AGACTGCTGAGAAATGCCCTACTTTGGTACAGCTGGCCCTTACATT 627
Db 1818 ACCAACTTCCTTTCGATGAGCTGCTGAGAAATGCCCTACTTTGGTACAGCTGGCCCTTACATT 1877
Oy 628 ATCAACGAGAGAGCTGAGATGCTGCGGCTCTAGTGGCTATGGCGAGTTCGATATC 687
Db 1878 ATCAACGAGAGAGCTGAGATGCTGCGGCTCTAGTGGCTATGGCGAGTTCGATATC 1937
Oy 688 CCTGTGATCTGAGGCGCAAGTACTATTAACGCCGATGATACCTGCGTTTCGACGAGAGT 747
Db 1938 CCTGTGATCTGAGGCGCAAGTACTATTAACGCCGATGATACCTGCGTTTCGACGAGAGT 1997
Oy 748 GAGAGACGAGACTGTGGGAGATGTATCATCATGTCAACGAGACGCTATGGCTTTCTT 807
Db 1998 GAGAGACGAGACTGTGGGAGATGTATCATCATGTCAACGAGACGCTATGGCTTTCTT 2057
Oy 808 AACGTCAGCCCCGCAAGTACGCTTCGATTCGATTCGATTCGATTCGATTCGATTCG 867
Db 2058 AACGTCAGCCCCGCAAGTACGCTTCGATTCGATTCGATTCGATTCGATTCGATTCG 2117
Oy 868 CTCCTCTACCTGCTCAGACCAAGCTCTCCCAACGTCAGAAATTCCTTTCGAAGTCATTTGCC 927
Db 2118 CTCCTCTACCTGCTCAGACCAAGCTCTCCCAACGTCAGAAATTCCTTTCGAAGTCATTTGCC 2177
Oy 928 TCTGATGCTGTCTCTTCAAGCCCCGTTTCAGACTCTTAACCTTCACTGCTGTTGCC 987
Db 2178 TCTGATGCTGTCTCTTCAAGCCCCGTTTCAGACTCTTAACCTTCACTGCTGTTGCC 2237
Oy 988 GAGCGTTAGAGATCATTAAT----- 1008
Db 2238 GAGCGTTAGAGATCATTAATTTT----- 1008
Oy 1009 -----GACTTACCAACTTTGCTGGCCAGACTTGTAGCTGGCCAGACTT 1053
Db 2298 AGACTAACACTTGTAGACTTTCACCAACTTTGCTGGCCAGACTTGTAGCTGGCCAGACTT 2357
Oy 1054 GCTGAGACCAAGATGTGGCGACGAGATGATGATGATGATGATGATGATGATGATGATG 1113
Db 2358 GCTGAGACCAAGATGTGGCGACGAGATGATGATGATGATGATGATGATGATGATGATG 2417
Oy 1114 TTGCGTGTAGCTGTGGCACTGTTGAGGACANAGCAGAGTCCGCTCCCTCCCTCCCTGAGC 1173
Db 2418 TTGCGTGTAGCTGTGGCACTGTTGAGGACANAGCAGAGTCCGCTCCCTCCCTCCCTGAGC 2477
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Oy 1174 GTTCTCTTCCCTCCTTCACAAGGAGGCCCGCGACAGCACTTCAAGTTTGAAGCCAGC 1233
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Oy 1234 AACGACACTTACCTGATFCAACGATGTTGGCTTTGGCGATGTCAATAGAGTGTCTGCGCC 1293
Db 2538 AACGACACTTACCTGATFCAACGATGTTGGCTTTGGCGATGTCAATAGAGTGTCTGCGCC 2597
Oy 1294 AAGCCGAGCTGGCGCCGCTTGAAGTCTGAGAGCTGAGAACTCTCTGAGAGCTGGAGC 1353
Db 2598 AAGCCGAGCTGGCGCCGCTTGAAGTCTGAGAGCTGAGAACTCTCTGAGAGCTGGAGC 2657
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Db 2658 CACCCCGTCACATTCACCTTGTGACTTCAAGATCCTCAAGGAACTGATGCTGTGCG 2717
Oy 1414 CAGGTATGCCCCACAGATCTGCTGTTAAGATGTGTCTGTTGGGAGAGGCTGAG 1473
Db 2718 CAGGTATGCCCCACAGATCTGCTGTTAAGATGTGTCTGTTGGGAGAGGCTGAG 2777
Oy 1474 ACCCTGACATCGAGGCCCACTACCAACCTGAGCTGAGACTTACATGTGGCACTGTAC 1533
Db 2778 ACCCTGACATCGAGGCCCACTACCAACCTGAGCTGAGACTTACATGTGGCACTGTAC 2837
Oy 1534 AACCTGATTCACAGAGATTAACGATGATGCTGTATTCACGTCACCGCCATGAGAGAG 1593
Db 2838 AACCTGATTCACAGAGATTAACGATGATGCTGTATTCACGTCACCGCCATGAGAGAG 2897
Oy 1594 AAGGATATCTTCAGAGAGACTTCGAGAGACCCCATBAACCCCAAGTGGGCGGCTTCT 1653
Db 2898 AAGGATATCTTCAGAGAGACTTCGAGAGACCCCATBAACCCCAAGTGGGCGGCTTCT 2957
Oy 1654 TACAAACGCAAGACTTCCATGCTCGCGTGAACCTTCTCGCGAGTCCATCACTGCG 1713
Db 2958 TACAAACGCAAGACTTCCATGCTCGCGTGAACCTTCTCGCGAGTCCATCACTGCG 3017
Oy 1714 CGAGTCCAGAGCTGGCCGAGAGAGCCGTACCAACCGCTCGATGATGATCTGAGAGAT 1773
Db 3018 CGAGTCCAGAGCTGGCCGAGAGAGCCGTACCAACCGCTCGATGATGATCTGAGAGAT 3077
Oy 1774 CTTGGAATGAGAGATTA 1791
Db 3078 CTTGGAATGAGAGATTA 3095
RESULT 4
US-09-218-702-3
; Sequence 3, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el phenol oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-218-702-3
Query Match 82.3%; Score 1474; DB 4; Length 3677;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
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Db 1098 CTCGGCATCCCGATGGACACCGGCAGCACCCCATTTGAGCGCTGTGATCCCGAAGGAAG 1157
QY 121 ACTGAGTCTTGCTGCTACTCCCTCTTGGTGCAGCAGCGGATATGAGCTGGAGTCACT 180
Db 1158 ACTGAGGTCTTGCTGCTACTCCCTCTTGGTGCAGCAGCGGATATGAGCTGGAGTCACT 1217
QY 181 CCATACACCTGGCTTAC----- 198
Db 1218 CCATACACCTGGCTTACAGGTGAGACACCTGTCCACCTGTTTCCCTCGATTAACTAAC 1277
QY 199 -----AGGAATGCCCTGGCAATTTCCACCTGTTCAGACGCCCAAGAT----- 239
Db 1278 TCTTATAGGAATGCCCTGGCAATTTCCACCTGTTCAGACGCCCAAGATTAATGCTTTGAT 1337
QY 240 -----GATATTACCAACCTGTGAC 280
Db 1338 TTTCTACGAGAACACTGGGCCCGGACTAATGTATTCAGATCATTAACCAACCTGTGAC 1397
QY 261 CGGCAAGGACATTTGGTACTAGATGAGATCAAGCCATTTCAGCAAG----- 311
Db 1398 CGGCAAGGACATTTGGTACTAGATGAGATCAAGCCATTTCAGCAAGGGGTGAGTTT 1457
QY 312 -----GATTTACCCCACTT 326
Db 1458 GCTCAGAAACCTTGTGTAATTATCATTTGTACTGACCCCTTTCAGATTTTACCCCACTT 1517
QY 327 GGGCCCTGGCACCTCTCTGTGGCTAGATGAGCCCTGGTCTTCAATTTTCC 386
Db 1518 GGGCCCTGGCACCTCTCTGTGGCTAGATGAGCCCTGGTCTTCAATTTTCC 1577
QY 387 CAGAGAACAGAGACTGTATTAGTTTCATCAACATGACACCGTGGAGAACCGGTCCA 446
Db 1578 CAGAGAACAGAGACTGTATTAGTTTCATCAACATGACACCGTGGAGAACCGGTCCA 1637
QY 447 TCTGCAGGCTCCCATCGCGTCCCTTTCGATGGTGGGCTGAAGATGTACCTTCC 506
Db 1638 TCTGCAGGCTCCCATCGCGTCCCTTTCGATGGTGGGCTGAAGATGTACCTTCC 1697
QY 507 TGGCGAGTCAAGAGATTAATCTTTCCCACTACCAATCCGCCCTTCTGTGTACCA 566
Db 1698 TGGCGAGTCAAGAGATTAATCTTTCCCACTACCAATCCGCCCTTCTGTGTACCA 1757
QY 567 TGACCAAGCTTTCATGA----- 583
Db 1758 TGACCAAGCTTTCATGAAGATTAATCTTTCTTTTGGCTAACCTTTGGCTA 1817
QY 584 -----AGACTGCTGAGAAATGCCCTACTTTGCTGAGGCTGGCGCTACATT 627
Db 1818 ACCAACTTCTTTCGTAAGACTGCTGAGAAATGCCCTACTTTGGTGAAGCTGGCGCTACATT 1877
QY 628 ATCAACAGAGAGGCTGAGATGCTCTCGGTCTTCTAGTGGCTATATGGCAATTCATATC 687
Db 1878 ATCAACAGAGAGGCTGAGATGCTCTCGGTCTTCTAGTGGCTATATGGCAATTCATATC 1937
QY 688 CCTCTGATCTGAGGCGCAAGTACTATAACGCCGATGATACCTTGGCTTCGACGAGGGT 747
Db 1938 CCTCTGATCTGAGGCGCAAGTACTATAACGCCGATGATACCTTGGCTTCGACGAGGGT 1997
QY 748 GAGGACAGGAGCTGTGGGAGATGTATCATATGTCACGACAGCCATGGCTTTCCTT 807
Db 1998 GAGGACAGGAGCTGTGGGAGATGTATCATATGTCACGACAGCCATGGCTTTCCTT 2057
QY 808 AACGTTCACGCCCGCAAGTACCGTTCCGATTCCTAACGCTGCGGTCTGTGCTTGG 867
Db 2058 AACGTTCACGCCCGCAAGTACCGTTTCGATTCCTAACGCTGCGGTCTGTGCTTGG 2117
QY 868 CTCCTCTACCTGCTGAGACAGCTCTCCCAAGGTAGATTCCTTCCAAAGTCATGGC 927
Db 2118 CTCCTCTACCTGCTGAGACAGCTCTCCCAAGGTAGATTCCTTCCAAAGTCATGGC 2177
QY 928 TCTGATGTGCTCTCTTCAAGCCCGCTTCAGACCTTAACCTTAACCTTGTGCTTGGC 987
|||||

Db 2178 TCTGATGTGCTCTCTTCAAGCCCGCTTCAGACCTTAACCTTAACCTTGTGCTTGGC 2237
QY 988 GAGCGTTAGAGATCATTAAT----- 1008
Db 2238 GAGCGTTAGAGATCATTAATGATATGCCCTCCCTCTCAGCAATGATGTCACAACTTA 2297
QY 1009 -----GACCTTCACCACTTTGCTGGCAGACTCTTGAACCGCCCAAGTT 1053
Db 2298 AGACTTAACCTTATAGACTTCACCACTTTGCTGGCAGACTCTTGAACCGCCCAAGTT 2357
QY 1054 GCTGAGACCAAGCATGTGCGCGAGAGATGATAGCTGSCACTCTCGAGTGAATGCGC 1113
Db 2358 GCTGAGACCAAGCATGTGCGCGAGAGATGATAGCTGSCACTCTCGAGTGAATGCGC 2417
QY 1114 TTGCTGTACGCTCTGCGACTGTGAGAGAACAGCAGTCCCTTCACCTCTGCTGAC 1173
Db 2418 TTGCTGTACGCTCTGCGACTGTGAGAGAACAGCAGTCCCTTCACCTCTGCTGAC 2477
QY 1174 GTTCCTTCCCTCTCTCACAAGGAAGCCCGCGACAAAGCACTTCAAGTTTGAAGCAGC 1233
Db 2478 GTTCCTTCCCTCTCTCACAAGGAAGCCCGCGACAAAGCACTTCAAGTTTGAAGCAGC 2537
QY 1234 AACGACACTACCTGATCAACGATGTGGCTTGGCGATGTCAATGAGCGTGTCTGGCC 1293
Db 2538 AACGACACTACCTGATCAACGATGTGGCTTGGCGATGTCAATGAGCGTGTCTGGCC 2597
QY 1294 AACCCGAGCTCGGCACCGTTGAGGTGTGGAGCTGAGAACCTCTCTGAGGCTGGAGC 1353
Db 2598 AACCCGAGCTCGGCACCGTTGAGGTGTGGAGCTGAGAACCTCTCTGAGGCTGGAGC 2657
QY 1354 CACCCGTCACATTCACCTGTGTGACTTCAAATCTCAAGGAACCTGCTGTGCTGCGC 1413
Db 2658 CACCCGTCACATTCACCTGTGTGACTTCAAATCTCAAGGAACCTGCTGTGCTGCGC 2717
QY 1414 CAGTCAATGCCCTACAGAGTCTGCTGTCTTAAGATGTGCTGTGGTGGAGAGGGGTGAG 1473
Db 2718 CAGTCAATGCCCTACAGAGTCTGCTGTCTTAAGATGTGCTGTGGTGGAGAGGGGTGAG 2777
QY 1474 ACCCTGACATCGAGGCCCACTACCAACCTTGAGCTGAGACTTACATGTGTGCACTGTAC 1533
Db 2778 ACCCTGACATCGAGGCCCACTACCAACCTTGAGCTGAGACTTACATGTGTGCACTGTAC 2837
QY 1534 AACCTATTCAGAGGATTAACGATGATGGCTGTTCAAAGTCAACCGCATGGAGGAG 1593
Db 2838 AACCTATTCAGAGGATTAACGATGATGGCTGTTCAAAGTCAACCGCATGGAGGAG 2897
QY 1594 AAGGATATCTTCAGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCTTCT 1653
Db 2898 AAGGATATCTTCAGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCTTCT 2957
QY 1654 TACAAACGCAAGACTTCATGCTCGCGCTGGAATCTTCGCGCGAGTCCATCTGCGC 1713
Db 2958 TACAAACGCAAGACTTCATGCTCGCGCTGGAATCTTCGCGCGAGTCCATCTGCGC 3017
QY 1714 CGAGTCAAGAGCTGGCCGAGGAGGAGCGGTACAAACGCTGATAGATTCGAGGAGAT 1773
Db 3018 CGAGTCAAGAGCTGGCCGAGGAGGAGCGGTTCAAACGCTGATAGATTCGAGGAGAT 3077
QY 1774 CTTGGAATCGAGAGATTA 1791
Db 3078 CTTGGAATCGAGAGATTA 3095

RESULT 5.
US-09-218-702-5
; Sequence 5, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22

Db 2040 CGCTGAGCAGCCTTACAGCGACTCG 2066

RESULT 7
US-09-468-578-6
; Sequence 6, Application US/09468578
; Patent No. 639329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Curvularia pallescens
US-09-468-578-6

Query Match 28.1%; Score 502.8; DB 4; Length 2063;
Best Local Similarity 60.4%; Pred. No. 1.2e-128;
Matches 1000; Conservative 0; Mismatches 522; Indels 134; Gaps 5;

QY 244 ATTACCAACCTGTCCACCGGCAAGACATTTGGTACTAGATGATCAACCATTT 303
Db 310 ATGACCAAACTCTGTCAACAACAGAGATCTGTACTACGAGATGTCAACACCTTT 369
QY 304 CAGCAAGATTTTACCCCACTTGGCCCTGCCACTCTGCGCTACGATGCGATGAGC 363
Db 370 AACCAACAGTCTATCAAGTCTAGCTCTGCTGCTTGTGATGATGATGATTTA 429
QY 364 CCTGTCTACTTCAATGTTCCACAGAGACAGACATGTAGTTGATTCATCAACAT 423
Db 430 CCAGGCCCTACAGTCTGTGCGGAGAGACAGACAGCGGTTGTAGATTCGTAACCG 489
QY 424 GCCACCGTGGAGACTCGGTCTGACAGCGCTCCCAATCGCGTCCCTTTGATGCT 483
Db 490 GGTGATCGGAGAGTTCGATTCATCTTCATGTTCCCTCCCGTCCCTTTGAGGGA 549
QY 484 TGGGCTGAAGATGTGACCTTCCCTGCGGAGTACAA----- 518
Db 550 TGGGCTGAAGATTTGATTTTGAAGGGCCAAATTCAAAGGTACACAGACAATCTTA 609
QY 519 -----GGATTACTACTTTCACACTACC 541
Db 610 TCAGGGTGGCTCTTTTATACATAACAGACTCGTTTACACTACTACTCCGGAACAC 669
QY 542 AATCGCCCGCTTCTGTGTACATGACACGCTTTC----- 579
Db 670 AGGCTGCGAGATTCTGTGTACACAGATCATGTATGATGTGTGACACT 729
QY 580 -----ATGAAGACTGTGGAAGTCC 601
Db 730 AATCATGGAGCAAAACGAAGATGGGCTGACACTTATGCAAGCTGGGAAGATGGCT 789
QY 602 ACTTTGGTGGAGTGGAGGCTACATATATACAGCAGAGGCTGAGATGCTCGTCTTC 661
Db 790 ATTGAGACAGGCTGGCGCTACCTGATCAAGACCCAGCTGAGGAGCGGCTGGCTTC 849
QY 662 CTAGTGGCTATGCGAGTTCGATATCCCTGTATCTGATCGGCGCAAGTACTATACGCCG 721
Db 850 CTTGCGGTTACGAAAATACGACATCCCACTGCTGCTCAAGTTCTACAAACAGTG 909
QY 722 ATGATACCTGCTGGCTGAGCGAGGCTGAGACAGGACGCTGGGGAGATGTCATCATG 781
Db 910 ATGGAATCTCCAGACCACTGTGGAGAGAACACAGTCTTGGGGCGAGCTATCATG 969

QY 782 TCAACGGAGCCATGCGCTTTCCTTAACGTCCAGCCCGCAAGTACGCTTTCGATTC 841
Db 970 TCAACGGTACGCCCTGCGCATTTCTCAACGTGAGCTCGAAGATATGCGCTTCATTC 1029
QY 842 TCAAGCTGCGCTGTCTGCTGCTTGGCTCTCTACTCTGTCAGGACAGCTCTCCCAAG 901
Db 1030 TCAAGTGGCTGTCTTCTGGAAGTCTTGGCTTATTTTCTGCAAGCAACAGCCACTGCTA 1089
QY 902 TCAGATTCCTTCCCAAGCATTTGCTGTGATGCTGCTGCTTCCCAAGCCCGCTTCA 961
Db 1090 CTAGACTCTTCTTCCAGGTCATTTGCTGTGATGAGGCTTACTACAGCCCGGCTCA 1149
QY 962 CTTTAACTCTTACCTTGTGCTGTTGGAGCGCTTACAGATCATTTATTTGACTTCAAC 1021
Db 1150 CTTCAAGATTTTACGTTGAGGAGAGAGAGAGCGGCTACAGATTTATTCGACTTTGGCGCT 1209
QY 1022 TTGCTGGCCAGACTCTTGAACCTGCGCAACGTTGCTGAGACCAACGATGCTGGCAG 1081
Db 1210 ATGCAAGGCGAGAGATGATTTGCGTAACTTGGCAAAAGCCAAATGGGGTCCAGCATG 1269
QY 1082 ATGAGTACGCTGCACTCTGAGGATGATGCGCTTGCCTGAGCTGTGACACTGTTGAG 1141
Db 1270 ACATTTATCAACACTGACCAAGGTCATGCTTCCATGTCAAGCAAGCATGCTG 1329
QY 1142 ACAACAGCCAGGTCCTCCACTCTCCGTGACGTTTCCTCTCTCAAGAAAGGCC 1201
Db 1330 ATAACTGGTGTACCCGACAGCATATCTCAAGATCAAGTTCCCGCCGACCA--AAACCG 1386
QY 1202 CCGCGCAAGACACTTCAAGTTTGAACGAGACAGGACACTGATGATCAACGATGTTG 1261
Db 1387 GCATGACCAACCACTTCCCTTCCATGCGACCAACAGCGAGGGGCAACAGGCAATG 1446
QY 1262 GCTTTGCCATGTCAATGAGCTGTCTGCGCAAGCCAGCTCGGACCGTGTGAGTCT 1321
Db 1447 GGTTCGACAGCTCCAGAACGATATCTGCGCAAGTACCAGGCGGCACTGTGACGCT 1506
QY 1322 GGGAGCTGAGAACTCTCTGAGAGCTGAGGCGCACCCGTCACATTCACCTTGTGACT 1381
Db 1507 GGGAACTCGAAGAAAGCTCGGCGGCTGTGCGACCCCATCCAGGTCACCTGTGACT 1566
QY 1382 TCAAGATCTTCAAGCACTGCTG-----GTCTGTGCGGAGTCAATGCTGAGTCTG 1435
Db 1567 TCGGATCTGTGCGAGCTTACGCTGAGCAAAAGCACTGCGGCTCATGCTTACGAGTCCG 1626
QY 1436 CTGTGCTTAAGATGTCGTGTGTGGGAGGAGGAGGAGACCTGACATGAGGCGCACT 1495
Db 1627 CCGGTCTCAAGAGAGTCTGTGTGCTGCGGCGCAGAGAGGCTGCTGTGAGAGCACT 1686
QY 1496 ACCAACCTGAGCTGAGCTTACATGTGAGCTGTTCACAACCTTTCACGAGATTAACG 1555
Db 1687 ACGCCCTCGGGAGCGAGTCAATGTTTCCACTGCGCACAACTGATCCAGAAAGCAAG 1746
QY 1556 ACATGATGCTGATTTCAACGTCACCGCCATGAGAGAGAGGATATCTTCA---GGAGG 1612
Db 1747 ACATGATGCGCGCTTGTGAGCTGATCAAGCTTCCAGAACTTGTGCTTCAACAGAGAGCG 1806
QY 1613 ACTTGAGAGACCCCATGAAGCCCAAGTGGCGCGCTTCTTACAAACCCAGCAAGCTTCC 1672
Db 1807 ATTTCCAGACCCCGGAAGATTTCTGCTGTGTGCAAGACCTTTCACCGGCTGACTTGA 1866
QY 1673 ATGCTGCGCTGAAACCTTCTGCGCGAGTCCATCACTGCGAGGTGAGAGCTGCGCG 1732
Db 1867 CCGCGGATCGGGATATCTTCTCAGAAAGCATCATGAGGCTAGAGTGAAGAGTGGCGCC 1926
QY 1733 ACAGAGAGCCGTAACAACCCCTGATGATGATCTGCG 1768
Db 1927 TGAACAGCCGTAACAGCAAGTGGCAAGTCAAGTCAAG 1962

RESULT 8
US-09-401-476-1
; Sequence 1, Application US/09401476

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? Patent No. 6168936
? GENERAL INFORMATION:
? APPLICANT: Wang, Huaming
? TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
? FILE REFERENCE: GC584
? CURRENT APPLICATION NUMBER: US/09/401,476
? CURRENT FILING DATE: 1999-09-22
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO.1
? LENGTH: 1958
? TYPE: DNA
? ORGANISM: Stachybotrys chararum
? US-09-401-476-1

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Query Match	25.7%	Score 460.4;	DB 4;	Length 1958;
Best Local Similarity	55.3%	Pred. No. 5.3e-117;		
Matches 996; Conservative	0;	Mismatches 521;	Indels 163;	Gaps 6

Oy	241	ATCTTTACCAACCTGTGACCCGGCAAGGACATTGGTACTATGAGATCGAATCAAGCCA	300
Db	257	ACCGTCCCAACCCCAACACTGGAGAGACATCTTTCTACAGATGAGATGTAGGCC	316
Oy	301	TTTGAGCAAGGANTTTACCCACCTTGGCGCCGACCTCGTGCGGACATGGCAATG	360
Db	317	TTTCTCCCAACGATCTACCTTGATCTGGAGCCGGCCACACATGGTTGGATACGATGGCATG	376
Oy	361	AGCCCTGCTCTACTTTCATGTTTCCACAGAGAAACAGACTGTAGTTAGTTTCATCAAC	420
Db	377	TCCCAAGAGACTTACATCATTGTTCTCGTGGGACATGAGATGTTGTCCGCTTGGTGAAC	436
Oy	421	A-----ATGCCACCGTGGAGAACTGGGTGCATCTGCACGGCTCCCATCGCGTCCCT	474
Db	437	AGCGAGAGAACACTCTCCCAACACGGTCCACTTCGACGGCTCTTCTCTGAGACTCC	496
Oy	475	TTTCATGTTGGGCTGGAAGATGAGCTTCCCGGGGACATACAAGATTACTACTTCC	534
Db	497	TTTATGTGTGGCTGAGGACACTACCCAGCCGGGAGATACAAAGATTACTACTACCC	556
Oy	535	AACACCAATCCGGCCGCTTCTGTGGTACATGACACACGCTTTCATGAAGACTCTGAG	594
Db	557	AACGAGAGAGCTGGCCGACATGTTGGTACATGACATGACATGCTTCATACGCGCAG	616
Oy	595	AATGCTACTTTGGTACAGCTGGCGCCCTCATATTATCAAGACAGAGCTGAGGATCTTC	654
Db	617	AACGCTACATGGGTGAGGCTGTGCTCTCATGATATCCAGAGCCCGGTGAGGATGCTCTG	676
Oy	655	GGTTCCTGTGGCTATGGCGGAGTTCGATATCCCTCATCTCTACGCGCAAGTACTAT	714
Db	677	AACCTCCCAAGCGGCTACGGCGGAGTTGATATCCCTTGTTCTGACATCCCAAGGATAC	736
Oy	715	AACGCCAGTGTACCCGTGACCTTTCAGACCGAGGAGGACCAAGAGCTTGGGGAATATGC	774
Db	737	AAGCAACAGCGCACTCTCTTCCACCAATGGAGAGGTTTCCAGCTTGGGGGTACGTT	796
Oy	775	ATTCATGT-----	782
Db	797	ATTCAAGTGTAGTTGAGCCCATGTGAGATGCTTGAGATCTAGAAATATGATGATAGA	856
Oy	783	-----CAAGGAAACGCCATGGCTTTCCTTAAG	811
Db	857	AATTTGTCATGCTCTAACCAGTGTATCAAGAGAACGTTAGGCTTGGCTATAGCTCAAGC	916
Oy	812	TCCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCGTGTCTGGTGGTCC	871
Db	917	TGCAGCGCGGCAAGTACCGTTTCCGCTTCTCAAGCGTCCGCTCTCACAGCTTTCGCTC	976
Oy	872	TCATACCTGTCAGGACCACTCTCCCAACGTCAGAATTCCTTCCAAAGTCAATGGCTCTG	931
Db	977	TGTATCTTGTACTCTGAGAGATTTCAGAGACGACATTCCTTCCAGGTCATTTCCGCTG	1036
Oy	932	ATGCTGGTCTCTTCAAGCGCCCGTTCAGACCTCTAACCCTTACCTTGGTGTGCGGAC	991

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Db 1037 ACGGTGGCTGCTGAGAGGCCCGTTGGTACACTCAACCTCTGTACATCTCTATATGCCCCAGC 1093b
Oy 992 GTTACGAGATCATTTATTGTAACCTTGACCAACCTTTTGCGGACAGACTCTTGACCTGCGCAACG 1051b
Db 1097 GCTGGGAGAGTGTATTGATGACTTCTCCACCTTGCGCTGGCCAGTTCATCGATTATCCGCAACG 1156b
Oy 1052 TTGCTGAGACCAACGATGTGGCGGACGAGGATGTAGTACCTTGCCACTCTCGAGGTGATGC 1111b
Db 1157 TTCTCTGGGTGAGACGGCTCTGGGTGTGAGGCTGAGTTTATTAACACTGCAAGGTCTATGC 1216b
Oy 1112 GCTTCTGCTGAGGCTCTGGGCACTGTTGAG---GACAACAAGCCAGGTCCTCCACTCTCC 1168b
Db 1217 GATTGCTGTGTATGAAAGTCTTGAAGTTCGCCGACACTTCTGAGTGGCTCGCAACCTCC 1276b
Oy 1169 GTGACGTTCTCTTCC-----TCCTTACAAGAGAGGCCCGCCGCAACG 1213b
Db 1277 GAGATGTTTCTTTCGCCGAGGGGGGCAACTGGGAGACCCCGCAACCCCACTGATGACGAGA 1336b
Oy 1214 ACTTCAGTTTGAACGCAACGACACTACCTGATCAAGATGTTGGCTTTTGCCATG 1273b
Db 1337 CTTTACACTTGGCGCGTGAATGAGACAGTGCACATCAACGAGATTTACCTTCTCGATG 1366b
Oy 1274 TCATAGAGCGTGTCTTGCGCCAAACCCGAGCTGGGACCGTTGAGTCTTGAGGCTCGAGA 1333b
Db 1397 TCGAAGAACCGTCTGCTCCGAATGTGCCCGCACACTTGTAGATCTGGCGCATGGAGA 1456b
Oy 1334 ACTCCTCTGAGGCTTGAGGACCAACCCGCTCACATTTACCTTGTAGCTTCAAGATCTCA 1393b
Db 1457 ACAACTCCAAAGTGTGGACATCACCCCTGTTACATTTACTCTGTGACTTCCGAGTCTTT 1516b
Oy 1394 AGCGAAGTGGTGTCTGCGGCAAGCTATGCGCTTACAGATCTCTGATCTTAAAGATGTG 1453b
Db 1517 CTGCTTCCACTGCGCCGTHG---AGTGGAGCTTATGAGCGCTGTGATCAAGGATGTTG 1573b
Oy 1454 TCTGTGTGGGAGGGGTGAGAACCTGACCATGAGAGGCCCACTACCAACCCGTGAC----- 1508b
Db 1574 TCTGTGTGGCTGTGCTGAGGTTGTCTATGTGAGGCCCACTACGCTCTTCCCGTAA 1633b
Oy 1509 -----TGAGGCTTACAT 1520b
Db 1634 TTTCGCGCTTTTACCTAACTGTTTTCACCTACATGCTACATCTACAAAGTGGTCTACAT 1693b
Oy 1521 GTGCGACTGTCAACCTCATTTACGAGAGATTAACGACATGATGGCTGTATTTCAACGTAC 1580b
Db 1694 GTTTCACATGCGACCACTGTATCCAGAGGACCAACGACATGATGGCTGTTCAATGTAC 1753b
Oy 1581 CGCCATGAGAGAAAGGATATCTTCAAGAGACTTTCAGAGACCCCAATGAACCCCAAGTG 1640b
Db 1754 TGTTCCTGGGTACTATGTGCTAACACTACACCGGTTTCAATTTGACCCCAATGAGACCTCTG 1813b
Oy 1641 GCGGCGCGTTCCTTACAAACGCAACGCACTTCCATGTGCTGCGGTGGAAACTTCTCGCGCA 1700b
Db 1814 GAGGCCCCGCTTCTCTCTCGGAAGATTTCCGAATGCTTGGGTACCTTCAGCGACT 1873b
Oy 1701 GTCCATCACTGCCGAGTTCGAGAGAGCTGGCCGAGCAAGAGCCGTTCAACCGCTTCGATGA 1760b
Db 1874 TGCCATCACTAGACCGCATTCAGAGAGATGGGTAGCTTCAACCCCTTACGCCCAAGGCTGATGA 1933b

RESULT 9
US-09-401-476-3
: Sequence 3, Application US/09401476
: Patent No. 6168936
: GENERAL INFORMATION:
: APPLICANT: Wang, Huaming
: TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
: FILE REFERENCE: GC584
: CURRENT APPLICATION NUMBER: US/09/401,476
: CURRENT FILING DATE: 1999-09-22
: NUMBER OF SEQ. ID NOS.: 8
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 2095

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; TYPE: DNA
; ORGANISM: Stachybotrys chararum
us-09-401-476-3

Query Match      25.7%; Score 460.4; DB 4; Length 2095;
Best Local Similarity 59.3%; Pred. No. 5.4e-117;
Matches 996; Conservative 0; Mismatches 521; Indels 163; Gaps 6;

Oy 241 ATCATACCAACACCTGTGACCCGCAAGACATTTGGTACTATGATGATCGATCAAGCCA 300
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Db 321 ACCGTCGCCAACCCCAACACTGAGAGGACATCTGTACTACGATGATGATGAGGCC 380

Oy 301 TTTCAGCAAAAGATTTACCCCACTTGGCCCTGCCACTCTGCTGGCTACGATGCGATG 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 381 TTCTCCCAACACATCTACCTGATCTGGAGCCGCCAACATGTTGGATGATCATGCAAG 440

Oy 361 ACCCGTGGCTACCTTCAATGTTCACAGACAGACAGACTGTGTTGGTTTCATCAAC 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 TCCCAAGACACTACATCTCTGTTCTGCTGGCACTGAGAGTGTGTCCGCTTCGGAAC 500

Oy 421 A-----ATGCCACCGTGGAGAACTCGGTCATCTGCACGGCTCCCATCGGCTGCCCT 474
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 501 ACCGGAGAACACCTCTCCCAACAGCGTCACATTGGACGGCTCTTCTCTGAGCTGCC 560

Oy 475 TTCGATGCTGGGCTGAGATGTGACCTTCCCTGGCGAGTACAGAGATTACTTCTCC 534
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 561 TTGTAGGTTGGGCTGAGAGAACTACCCAGCCTGGCGATACAGAGATTACTACACCC 620

Oy 535 AACCTACCAATCGCCGCGCTTCTGTGTACCAATGACACAGCTTTCATGAAGACTGCTAG 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 621 AACAGGACGAGCTGCCGCGCTGCTTGTGTACCATGACATGACATGCTATGCAACGCCGAG 680

Oy 595 AATGCCCTACTTTGGTACGAGCTGGCGCTACATTAACAAGACAGAGCTGAGATGCTCTC 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 681 AACGCTACATGGGTGACGCTGTGTCTACATGATCAAGACACCGGCTGAGATGCCCTG 740

Oy 655 GGTCTTCCATAGTGGCTATGGCGAGTTCCGATATCCCTGATCCTGACGGCCAAAGTACTAT 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 741 AACCTCCCAAGCGGCTACGAGATTTGATATCCCTGTGTGACTCCCAAGCAATATC 800

Oy 715 AACGCGATGTATACCTGCTGTGACCGAGGTGAGACACGAGCTGTGGGAGATGTC 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 801 AACGAGACGAGCACTCTTCTTCACCAATGGAGAGGTTTCCAGCTTCTGGGGTGACGTT 860

Oy 775 ATCCATGT----- 782
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Db 861 ATTCAAGTGTAAAGTTGAGCCCATTTGAGATGCTTCAATCTAGAAGTATCATGATGA 920

Oy 783 -----CAACGAGACGCAATGCGCTTTCCTTAAG 811
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 921 AATTGTGATGCTCTAACCAAGTGTATCAAGAACGATGAGCTTGGCTATGCTCAACG 980

Oy 812 TCCAGCCCGCAAGTACCTTTCGATTCCTCAACGCTGCCGTGTGCTGTGGCTCC 871
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 981 TGCAGCCCGCAAGTACCTTTCGATTCCTCAACGCTGCCGTGTGCTGTGGCTCC 1040

Oy 872 TCTACCTGCTCAGGACCACTCTCCCAACGTCAGAAATTCCTTCCAAAGTATTTCCCTG 931
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1041 TGTATCTGCTACCTCTGAGATTCAGAGACCAAGACTTCCCTCCAGGTCATTTGCCGCTG 1100

Oy 932 ATGCTGCTCTCTCTCAAGCCCGCTTCAGACCTTAACCTTAACCTTGTGTTGCCGAGC 991
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1101 ACGGTGTGCTGTGAGGCGCTGTTGACACTGTGACACTCTGTATGACATCTTATGAGCAGAC 1160

Oy 992 GTTACAGATCATTAATGACTTCACCAACTTGTGTCGACAGACTTTCGACGCGCAAG 1051
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Db 1161 GCTGGAGGTTGTTATGACACTTCTCCACTTTCGCTGGCCAGTCAATGATTCGCAACC 1220

Oy 1052 TTGCTGAGAACCAAGTATGTCGGGACGAGATGATGATGACCTGCACTTCGAGGTATGC 1111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1221 TTCTGTGCTGTACGCTTCGCGGTGAGGCTGAGTTGATTAACACTGACAAAGGTATGC 1280

Oy 1112 GCTTGTGCTGTACGCTTCGGCACTGTTGAG---GACAACAGCCAGGTCCCTCCACTCTCC 1168
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Db 1281 GATTGTGCTGTGATGATGAGTCTTTGAGTGCCTCCGACACTTCTGAGGTGCTGCACTTC 1340

Oy 1169 GTGACGTTCTTTTCCC-----TCTCACAGGAAGGCCCGCCGCAACAGC 1213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1341 GAGATGTTCTTTTCCCAGGCGGCGCACTGAGACCCCGCAAAACCCCACTGATGACGAGA 1400

Oy 1214 ACTTCAATTTGACGACGACAAAGACACTTACCTGATCAAGATGTTGGCTTGGCGATG 1273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1401 CTTCACCTTGGCGCGCTGTATATGACAGTGCATACAGCGATGATCTTCTCGGATG 1460

Oy 1274 TCAATGAGGTGTCTCCGCGCAAGCCGAGCTGGACCGCTGAGGTGAGTCTGGAGCTCGAGA 1333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1461 TCGAAGACCGTGTGCTCCGCAATGTGCCCGCGACACTGTTGATGATCTGCGACTTGAGA 1520

Oy 1334 ACTCCTTGGAGGCTGAGACCAACCCCGTCACTTACCTTGTGACTTCAATGATCTCA 1393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1521 ACACTTCAACGCTTGGAGACTACCTGTTCAATTCACCTGTTGACTTTCGAGTCCATTT 1580

Oy 1394 AGCGAATGTGTGTGTGGCCAGTCAATGCCCTACGAGTCTGTGTGTTAAGATGTGC 1453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1581 CTGTTTCCACTGCCCCGTGG---AGTCAGACCTTATGAGGCTGCTGTCAAGGATGTTG 1637

Oy 1454 TCTGATGGGCGAGGGGTGAGACCTGACCATGAGGCGCCACTACCAACCCGTGAGC----- 1508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1638 TCTGCTGCTGCTGTGTGAGTTGTTATGTTGAGGCCCACTACCTCTTCCCGTAAAG 1697

Oy 1509 -----TGAGCTTACAT 1520
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Db 1698 TTCTGCGCTTTTACCACTGTTTTCATGCTATGCTAACATCTACAGGCTGTCTACAT 1757

Oy 1521 GTGCACTGTCAACACCTTATTCAGAGAGATTAACGACATGATGCTATTTACAGTCAAC 1580
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Db 1758 GTTGCACTGCGCAACCTGATTCACAGAGACCCACATGATGAGTGTTCCTCAAGTCAAC 1817

Oy 1581 GCGCATGGAAGAGGAGTATCTTCAGAGAGACTTCGAGACCCCATGAACCCCAAGTG 1640
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Db 1818 TGTTCCTGCTGTATGCTTACACTACCGAGTTCAATGACCCCATGAGACTCTCTG 1877

Oy 1641 GCGCGCGCTTCTTACCAACCGCAAGACTTCCATCTCGCGCTGGAACCTTCTCCGCGGA 1700
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1878 GAGGCGCGCGCTTCTCTCTCGGAGAGTTGAGATGCTCGGGGTGACTTCAAGGAGCT 1937

Oy 1701 GTTCATCTACTGCCAGTCTCAGAGAGCTGCCGAGACGAGACCGCTTACACCCCTGATGA 1760
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Db 1938 TCCATCTACTGACCGCATTCAGAGATGCTTCAACCCCTACGCCACGCTGATGA 1997

RESULT 10
us-09-468-578-8
; Sequence 8, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wand, Huming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Amersporium atrum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(858)
; OTHER INFORMATION: n = A,T,C or G
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US-09-468-578-8

Query Match	10.5%;	Score 188.6;	DB 4;	Length 858;
Best Local Similarity	60.2%;	Pred. NO. 2.1e-42;		
Matches 434; Conservative	0;	Mismatches 254;	Indels 33;	Gaps 6

QY	586	ACTGCTAGAAATCCCTACTCTTGGCTCAGGGCTGGCGGCTACTATTATCAAGACAGACTGAG	645
Db	2	ACGGCCGAGAACGCTTACTTTGGTCAAGCTGGCTTTTACATTCTGCACGACCCCGCTGAA	61
QY	646	GATGCTCTCGGCTTCTCTAATGAGCTATGGCGATTCGATATCCCTGATCTGTGACGGCC	705
Db	62	GATGCAATGGCTGGCT-----TGTGGCAAGTATGATGTACCTCTGTGCACTGTCTCC	115
QY	706	AAGTACTATPACGCCGATGTACCTTGCCTTGCACCGAGGGTGAAGACAGGACTGTGG	765
Db	116	AAGCAGTACAAACAGCAGCAGGTACCTCTTTCGACCCCAAGAACGAAACGATTCAGTTC	175
QY	766	GGAGATGTCATCATGTGCAACGAGACGACATGGCCCTTCTTAAAGTCCAGCCCGCCGAG	825
Db	176	GGGAGTGTATTCACGTGCAACGAGACGACCATGGCCCTTATTAAGGTGAGGCTGTGCAAG	235
QY	826	TACCGTTTCGATTTCCCTCAACGCTGGCGGTGTCGCTGTGGCTCTCTACTCTGTGAG	885
Db	236	TACCGTTCGGCTTCTCTCAATGCTGTATCAGCCGGC-----CTTCAAGCTCACT	286
QY	886	ACCAAGCTTCCCAACGTCAAGATTCCTTTCAAGTCAATTCGCTGTGATGCTGGTCCCT	945
Db	287	TTTGAGAGCTGATGGCAAAAGTACACTTTCCTGTCATCGGTGCGGATCTGTGCTTGG	346
QY	946	CAGGCCCGGCTGAGACCTCTAACCTCTACCTTGTGCTGTGCGGACGCTTACGAAATCAT	1005
Db	347	ACCAAGCTGTGTAGACAAAGCAACCTTGTGATCTCTATGGCCGACGCTGGAGGATGATT	406
QY	1006	ATTGACTTTCACCAACTTGTGCTGGCGAGACTCTTGTGACCTGCGCAAGTGTGCTGAGACAA	1065
Db	407	TTTGTACTTACGCAATTTTTCGGGAAGAACGTACCCCTCAAAAGAGGTGC-----C	457
QY	1066	GATGTGGGCGACGAGATGATGCTGTGCACCTCTTCGAGGTGATGCGCTTGTGTGCAG	1125
Db	458	GATGTGGGCGACGAGATGATGCTGTGCACCTCTTCGAGGTGATGCGCTTGTGTGCAG	517
QY	1126	TCTGGGCACTGT-----GAGGACAAACAGCAGGTCCCTCCACACTCTCCGTGACTTCT	1179
Db	518	AAGGATTTACGAGCCAGGCTGTATATGGCAACCTTCCGCGTCTGTGGCACTGTCTCC	577
QY	1180	TTTCCCTCTACAGAGAAAGGCCCGGCGACAGCACTTCAAGTT--TGAACGCGACGACGG	1238
Db	578	TTTCCCTCTAAGAAAG--GGCGGAGTGCACAGAGCTTAAATTTGGCGACGAGCCGAGTG	635
QY	1239	ACACTACCTGATCAACGATGTGGCTTTGCGATGTGCAATGACGCTGTGCGCCAAAGC	1298
Db	636	CCAGTGACATGTTAATGGCTTGACCTTGCCTGATGTCAACAAACCGCATCTGGTAAGCC	695
QY	1299	C 1299	
Db	696	C 696	

RESULT 11
 US-08-232-463-14
 : Sequence 14, Application US/08232463
 : Patent No. 5670367
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: DORNER, F.
 : APPLICANT: SCHEIFLINGER, F.
 : APPLICANT: FALKNER, F. G.
 : TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 : NUMBER OF SEQUENCES: 52
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: Foley & Lardner
 : STREET: 1800 Diagonal Road, Suite 500
 : CITY: Alexandria

STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT99pt-F15
US-08-232-463-14

Query Match	3.0%;	Score 54.6;	DB 1;	Length 7218;
Best Local Similarity	5.2%;	Pred. No. 4.1e-05;		
Matches	21;	Conservative 218;	Mismatches 162;	Indels 0;
			Gaps	0;

[illegible]

RESULT 12
5183745-1/C
; Patent NO. 5183745
; APPLICANT: DACHIN, ANTOINE; GLASER, PHILIPPE; KRIN, EVELYN;
; BARU, OCTAVIEN; LADANT, DANIEL; ULLMAN, AGNES

TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
BIOLOGICAL USES
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,541
FILING DATE: 25-OCT-1989
SEQ ID NO:1:
LENGTH: 4649

Query Match 2.6%; Score 45.8; DB 6; Length 4649;
Best Local Similarity 48.0%; Pred. No.0.0088;
Matches 131; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 934 GCTGCTCTCCTTCAGACCCCGCTTCAGACCTCTACCTCTACCTCTGCTTGGCCAGCGT 993
Db 3372 GCCGCGCGCGCGGATGACCGTGTGTTGGCCCTCGCCGACACAGGAGTGTGTTCCGGC 3313
Qy 994 TACGAGATCATTTATTGACTTTCACCACTTTGCTGGCCAGACTCTTGACCTGGCAGACGT 1053
Db 3312 GCCGCCATTCAGACCTGTGTCGCCCGCCAGCCCGCGCTAGGAAGTGTGTCGTCATTGCC 3253
Qy 1054 GCTGAGACCAACGATGTGGCGAGAGATGATAGCTCGCAGCTCTGAGGTATGGCC 1113
Db 3252 GGTGATTCGAATGTGTCGCCGCCCGCGATGATGTGCTGCACATGCTGAGCGTTCGAC 3193
Qy 1114 TTGCTGTCAGCTCTGCGACTGTGTAGAGACACAGCAGTCCCTCAGCTCTCCGTGAC 1173
Db 3192 CTCACCACTTGGCCGACAGCGGCCGCTCGACATGGCGATTGTGACATTTCCGTGG 3133
Qy 1174 GTTCTTTCCCTCTCACAAGAGAGCCCGCC 1206
Db 3132 CTGGCGTAGGCGGTTGTGTGGTAGCCAGCC 3100

RESULT 13
US-08-669-785-1/c
Sequence 1, Application US/08669785
Patent No. 6309648
GENERAL INFORMATION:
APPLICANT: Betsou, Fotini
APPLICANT: Sebo, Peter
APPLICANT: Guiso, Nicole
TITLE OF INVENTION: Protective Epitopes Of Adenyl
TITLE OF INVENTION: Cyclase-Haemolysin(AC-Hly), Their Application To
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,785
FILING DATE: 27-JUN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0072-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6441 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 979..6096
OTHER INFORMATION: /note= "AMINO ACID SEQUENCE
OTHER INFORMATION: CORRESPONDING TO THE NUCLEOTIDE SEQUENCE OF THE GENE
OTHER INFORMATION: CODING FOR THE B. Pertussis AC-Hly"
US-08-669-785-1

Query Match 2.6%; Score 45.8; DB 4; Length 6441;
Best Local Similarity 48.0%; Pred. No.0.01;
Matches 131; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 934 GCTGCTCTCCTTCAGACCCCGCTTCAGACCTCTACCTCTACCTCTGCTTGGCCAGCGT 993
Db 4167 GCCGCGCGCGCGGATGACCGTGTGTTGGCCCTCGCCGACACAGGAGTGTGTTCCGGC 4108
Qy 994 TACGAGATCATTTATTGACTTTCACCACTTTGCTGGCCAGACTCTTGACCTGGCAGACGT 1053
Db 4107 GCCGCCATTCAGACCTGTGTCGCCCGCCAGCCCGCGCTAGGAAGTGTGTCGCAATTGCC 4048
Qy 1054 GCTGAGACCAACGATGTGGCGAGAGATGATAGCTCGCAGCTCTGAGGTATGGCC 1113
Db 4047 GGTGATTCGAATGTGTCGCCGCCCGCGATGATGTGCTGCACATGCTGAGCGTTCGAC 3988
Qy 1114 TTGCTGTCAGCTCTGCGACTGTGTAGAGACACAGCAGTCCCTCAGCTCTCCGTGAC 1173
Db 3987 CTCACCACTTGGCCGACAGCGGCCGCTCGACATGGCGATTGTGACATTTCCGTGG 3928
Qy 1174 GTTCTTTCCCTCTCACAAGAGAGCCCGCC 1206
Db 3927 CTGGCGTAGGCGGTTGTGTGGTAGCCAGCC 3895

RESULT 14
5183745-5/c
Patent No. 5183745
APPLICANT: DANCHIN, ANTOINE;GLASER, PHILIPPE;KRIN, EVELYN;
BARU, OCTAVIEN;LADANT, DANIEL;ULMAN, AGNES
TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
BIOLOGICAL USES
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,541
FILING DATE: 25-OCT-1989
SEQ ID NO:5:
LENGTH: 6443
5183745-5

Query Match 2.6%; Score 45.8; DB 6; Length 6443;
Best Local Similarity 48.0%; Pred. No.0.01;
Matches 131; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 934 GCTGCTCTCCTTCAGACCCCGCTTCAGACCTCTACCTCTACCTCTGCTTGGCCAGCGT 993
Db 4169 GCCGCGCGCGCGGATGACCGTGTGTTGGCCCTCGCCGACACAGGAGTGTGTTCCGGC 4110
Qy 994 TACGAGATCATTTATTGACTTTCACCACTTTGCTGGCCAGACTCTTGACCTGGCAGACGT 1053
Db 4109 GCCGCCATTCAGACCTGTGTCGCCCGCCAGCCCGCGCTAGGAAGTGTGTCGCAATTGCC 4050
Qy 1054 GCTGAGACCAACGATGTGGCGAGAGATGATAGCTCGCAGCTCTGAGGTATGGCC 1113
Db 4049 GGTGATTCGAATGTGTCGCCCGCCCGCGATGATGTGCTGCACATGCTCGAGCGTTCGAC 3990
Qy 1114 TTGCTGTCAGCTCTGCGACTGTGTAGAGACACAGCAGGTCCTCAGCTCTCCGTGAC 1173
Db 3989 CTCACCACTTGGCCGACAGCGGCCGCTCGACATGGCGGATTGTGACATTTCCGTGG 3930
Qy 1174 GTTCTTTCCCTCTCACAAGAGAGCCCGCC 1206

Db 3929 CTTGCCGTAGCGCGTGTCTGCGTAGCCACGCC 3897

RESULT 15

US-08-669-785-3/c

; Sequence 3, Application US/08669785
; Patent No. 6309648

GENERAL INFORMATION:

APPLICANT: Betsou, Fotini

APPLICANT: Sebo, Peter

APPLICANT: Guiso, Nicole

TITLE OF INVENTION: Protective Epitopes Of Adeny1

TITLE OF INVENTION: Cyclase-Haemolysin(AC-Hly), Their Application To

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flanagan, Henderson, Farbow, Garrett & Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent, Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/669,785

APPLICATION NUMBER: US/08/669,785

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 02356.0072-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4400

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 5118 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..5115

OTHER INFORMATION: CORRESPONDING TO THE NUCLEOTIDE SEQUENCE OF THE GENE

OTHER INFORMATION: CODING FOR THE B. Bronchiseptica AC-Hly"

US-08-669-785-3

Query Match

Best Local Similarity 2.5%; Score 45.6; DB 4; Length 5118;

Matches 126; Conservative 48.5%; Pred. No. 0.01; Mismatches 134; Indels 0; Gaps 0;

QY 947 AAGCCCCGTTACGACCTCTTACCTCTGTTGCCGAGCGTTAGAGATCATTA 1006

Db 3173 ACGACCGTGTGTGTCCTCGCCGCGACAGTGTGTCGTCGCCGCCGCGCATCCAGC 3114

QY 1007 TTGACTTACCACTTGTGTCGCGGAGACTCTTGACCTGCGCAAGTGTGAGACCAAG 1066

Db 3113 CTGTGTGTCGCCGCCGCCGCGGAGAGTGTGTCGCGCATTCGCCGTATGCAATCG 3054

QY 1067 ATGTGCGGAGAGATGATACCTCTGACCTCTGAGGTGATGCGTTGCGTCAGCT 1126

Db 3053 TTGCGGCGCCGCGCATGATGTCGACATGCTGAGCGTTCGACCTCCACCAAGTGC 2994

QY 1127 CTGACACTGTGAGGACACAGCCAGTCCCTCCACTCTCGTGACGTTCCCTTCCTC 1186

Db 2993 CCGACACGCGCCAGCTGACATGCGGATTTGAGACATTTCTCGCTTGCCTGAGCG 2934

QY 1187 CTCACAGAGAGCCCCGCC 1206
| | | | |
Db 2933 GTTTCTGTGGTAGCCACGCC 2914

Search completed: February 13, 2003, 05:10:52
Job time : 93.3199 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 20:54:16 : Search time 80.9029 Seconds
(without alignments)
11275.230 Million cell updates/sec

Title: US-09-218-702-1

Perfect score: 1791
Sequence: 1 gcatatgctgtctcaagc.....atcttggaatcgaggaagtaa 1791

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1791	100.0	1791	10	US-10-080-210-5
3	1791	100.0	1791	12	US-10-080-233-1
4	1474	82.3	3677	10	US-09-338-723A-1
5	1474	82.3	3677	12	US-10-080-210-1
6	1474	82.3	3677	12	US-10-080-233-5
7	1470	82.1	2067	12	US-09-338-723A-3
8	503.4	28.1	2905	10	US-10-080-210-3
9	502.8	28.1	2063	12	US-10-080-210-6
10	460.4	25.7	1958	9	US-09-842-185-1
11	460.4	25.7	2055	9	US-09-942-185-3
12	188.6	10.5	858	12	US-10-080-210-8
13	188.6	10.5	1533	9	US-09-738-626-1053
14	79.8	4.5	6442	9	US-09-950-335A-11
15	45.8	2.6	6442	9	US-09-974-300-2204
16	44.6	2.5	1470	10	US-09-822-830A-368
17	42.6	2.4	1082	10	US-09-790-399-7
18	41.8	2.3	390	10	US-09-938-842A-186
19	40.8	2.3	1707	9	US-09-938-842A-186

20	39.2	2.2	1467	10	US-09-981-900B-6	Sequence 6, Appl1
21	37.8	2.1	1872	10	US-09-452-599-17	Sequence 17, Appl
22	37.6	2.1	1512	9	US-10-124-800-31	Sequence 31, Appl
23	37.6	2.1	4509	9	US-10-124-800-51	Sequence 5, Appl1
24	37.6	2.1	4512	9	US-10-124-800-27	Sequence 27, Appl
25	37.4	2.1	615	9	US-10-125-815-4	Sequence 4, Appl1
26	35.8	2.0	1642	10	US-09-765-231A-25	Sequence 25, Appl
27	35.6	2.0	651	9	US-09-738-626-2385	Sequence 2385, Ap
28	35.6	2.0	2148	9	US-09-738-626-1384	Sequence 1384, Ap
29	35.4	2.0	698	9	US-09-764-668-156	Sequence 156, Ap
30	35.2	2.0	1002	9	US-09-738-626-1755	Sequence 1755, Ap
31	35.2	2.0	2748	9	US-09-738-626-2853	Sequence 2853, Ap
32	35	2.0	951	9	US-09-975-719-432	Sequence 432, Ap
33	35	2.0	1050	9	US-09-975-719-428	Sequence 428, Ap
34	35	2.0	1104	10	US-09-815-242-7676	Sequence 7676, Ap
35	35	2.0	42235	9	US-09-975-719-1	Sequence 1, Appl1
36	34.8	1.9	1185	10	US-09-887-576-784	Sequence 784, App
37	34.8	1.9	6442	9	US-09-950-335A-11	Sequence 11, Appl
38	34.6	1.9	2787	10	US-09-815-242-6320	Sequence 6320, Ap
39	34.4	1.9	927	9	US-10-029-180-97	Sequence 97, Appl
40	34.4	1.9	1494	9	US-09-738-626-1237	Sequence 1237, Ap
41	34.2	1.9	522	10	US-09-880-107-1314	Sequence 1314, Ap
42	34.2	1.9	2419	10	US-09-939-408A-12	Sequence 12, Appl
43	34.2	1.9	2741	10	US-09-939-408A-28	Sequence 28, Appl
44	34	1.9	1191	10	US-09-949-562-1	Sequence 1, Appl1
45	34	1.9	3945	10	US-09-747-835A-30	Sequence 30, Appl

ALIGNMENTS

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RESULT 1
US-09-338-723A-5
; Sequence 5, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Humming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338, 723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220, 871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-338-723A-5

Query Match      100.0%: Score 1791; DB 10; Length 1791;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTCAATATGCTGTTCAAGTATGCACTGACACCTCCGGGCTCCTGTGAGTC 60
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Db 1 GTCAATATGCTGTTCAAGTATGCACTGACACCTCCGGGCTCCTGTGAGTC 60
    |||||||

OY 61 CTCGCGATCCCGATGAGCAGCCGAGCCACCCATTGAGGCTGTTGCCGAGTGAAG 120
    |||||||
Db 61 CTCGCGATCCCGATGAGCAGCCGAGCCACCCATTGAGGCTGTTGCCGAGTGAAG 120
    |||||||

OY 121 ACTAGGCTTTCGCTGACTCCCTCCTTGTGTCAGCAGGCGATGACGACTGGAGTCACTT 180
    |||||||
Db 121 ACTAGGCTTTCGCTGACTCCCTCCTTGTGTCAGCAGGCGATGACGACTGGAGTCACTT 180
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OY 181 CCATACAACTGCTTTCAGGAATGCGCCCTGCCATTCCACTGTCACAGCCCAAGATG 240
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Db 181 CCATACAACTGCTTTCAGGAATGCGCCCTGCCATTCCACTGTCACAGCCCAAGATG 240
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OY 241 ATCATTAACAACCTGTTCACCGGCAAGACATTGTGTAATGATGAGATCAAGCA 300
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Db 241 ATCATTAACAACCTGTTCACCGGCAAGACATTGTGTAATGATGAGATCAAGCA 300
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Db 301 TTTCAGCAAAAGATTATACCCACCTTGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 AACCCCTGCTCTACTTTTCATGTTTCCAGAGAGAACAGACTGTAGTTAGTTGATCAAC 420
Db 361 AACCCCTGCTCTACTTTTCATGTTTCCAGAGAGAACAGACTGTAGTTAGTTGATCAAC 420
QY 421 AATGCCACCGTGGAGAACCTCGGCTCATTCGACAGGCTCCCCACCGGCTGCCCTTCGAT 480
Db 421 AATGCCACCGTGGAGAACCTCGGCTCATTCGACAGGCTCCCCACCGGCTGCCCTTCGAT 480
QY 481 GGTGGGCTGAAGATGTGACTTCCCTGGCGAGTACAGAGATTACTTATCTTCCCACTAC 540
Db 481 GGTGGGCTGAAGATGTGACTTCCCTGGCGAGTACAGAGATTACTTATCTTCCCACTAC 540
QY 541 CAATCCGCGCCCTTCTGTGTGATCATGACACGCTTTGATGAAGACTGCTGAAGATGCC 600
Db 541 CAATCCGCGCCCTTCTGTGTGATCATGACACGCTTTGATGAAGACTGCTGAAGATGCC 600
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Db 721 GATGTACCTCGCTGTCGACCGAGGCTGAGAGACAGAGACCTGTGGGAGATGTATCAT 780
QY 781 GTCAAGGAG 840
Db 781 GTCAAGGAG 840
QY 841 CTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 CTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
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Db 1201 CCGCGCGACAAAGCACTTCAAGTTTGAACGAGCAAGCAAGCAAGCAAGCAAGCAAG 1260
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QY 1381 TTCAAGATCCTCAAGGCAACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
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QY 1681 GCTGGAACCTTCTCCCGCGAGTCCATCAGTCCGAGTGCAGAGAGGCTGGCCGAGAG 1740
Db 1681 GCTGGAACCTTCTCCCGCGAGTCCATCAGTCCGAGTGCAGAGAGGCTGGCCGAGAG 1740
QY 1741 CCGTACAAACCGCCTGATGATGATCTGAGAGATCTTGAATCGAGAGTAA 1791
Db 1741 CCGTACAAACCGCCTGATGATGATCTGAGAGATCTTGAATCGAGAGTAA 1791

RESULT 2
US-10-080-210-5
; Sequence 5, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bode, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA
US-10-080-210-5

Query Match 100.0%; Score 1791; DB 12; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCATATGTGCTGTTCAAGTATGAGCAATGGGCAACGCTCCGGGCTCCTGTCTGAGTC 60
Db 1 GTCATATGTGCTGTTCAAGTATGAGCAATGGGCAACGCTCCGGGCTCCTGTCTGAGTC 60
QY 61 CTCGGCATCCCGATGAGACACCGGACAGCCCATTTGAGGCTGTTGATCCCGAAGTGAAG 120
Db 61 CTCGGCATCCCGATGAGACACCGGACAGCCCATTTGAGGCTGTTGATCCCGAAGTGAAG 120
QY 121 ACTGAGTCTTTCGCTGACTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 ACTGAGTCTTTCGCTGACTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 CCATACACTTGTCTTTCAGAGATGCCCCGCAATTCACCTGTCAAGCAAGCCCAAGATG 240
Db 181 CCATACACTTGTCTTTCAGAGATGCCCCGCAATTCACCTGTCAAGCAAGCCCAAGATG 240

Db 181 CCATACACTGCTTTACAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATG 240
QY 241 ATCATTTACCAACCTGTGACCGGCAAGGACATTTGGTACTATGAGATGCAGATCAAGCA 300
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Db 301 TTTGAGCAAAAGGATTTTACCCCACTTGGCCCTTGCCACTCTGCTGGCTACGATGCGCATG 360
QY 361 AGCCCTGGTCTTACTTTCAATGTTCAGAGAGACAGACGTGTAGTTGATTCATCAAC 420
Db 361 AGCCCTGGTCTTACTTTCAATGTTCAGAGAGACAGACGTGTAGTTGATTCATCAAC 420
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Db 421 AATGCCACCGTGGAGAACGTCGCTCATCTGCAGGCGTCCCATCGGCTGCCCTTTGCAT 480
QY 481 GGTGGGCTGAAGATGTGACCTTCCCTGGGAGTACAAAGATTAATCTTTCCCACTAC 540
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QY 541 CAATCGGCGGCTCTGCTGGTACCATGACGACGCTTTGATGAAGCTGTGAGATGCG 600
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Db 601 TACTTTGGTCAAGCTGTGGCCCTACATTTATCAAGAGAGGCTGAGGATCTCTCGGCTTT 660
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Db 1021 TTTGCTGGCCAGACTCTTGACCTGCGCAACGTTGCTGAGACCAACGATGTCGCGACGAG 1080
QY 1081 GATGAGTACGCTGCGACACTGAGAGTATGCGCTTCTGCTGATGCTGTGGCACTGTTGAG 1140
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QY 1681 GCTGGAACCTTCCGCGCAGTTCATCACTGCCGAGTGCAGAGCTGGCCGAGCAGAG 1740
Db 1681 GCTGGAACCTTCCGCGCAGTTCATCACTGCCGAGTGCAGAGCTGGCCGAGCAGAG 1740
QY 1741 CCGTACAAACCGCCTCGATGAGATCTCGAGATCTTGAAGTGAAGAGATTA 1791
Db 1741 CCGTACAAACCGCCTCGATGAGATCTCGAGATCTTGAAGTGAAGAGATTA 1791

RESULT 3
US-10-080-233-1
; Sequence 1, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1e1 Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Stachybotrys sp.
US-10-080-233-1

Query Match 100.0%; Score 1791; DB 12; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCATATAGCTCTTCAAGTATGACATGCACTGCGACAGAGCTCTCGGAGCTCTGCTGGAGTC 60
Db 1 GTCATATAGCTCTTCAAGTATGACATGCGAAGCTGCGAGAGCTCTGCTGGAGTC 60
QY 61 CTGGGATCCGATGAGACACCGGACGCCACCCCATTTGAGAGCTGTTGATCCGAAGTGAAG 120
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Db 121 ACTGAGGTCCTTGGTACTCCCTCTTGGCTGAGAGAGCGATGACAGCTGGAGTCTACCT 180
QY 181 CCATACAACTTCTTTACAGGAATGCGCTCGCAATTCACACCTGTCAACAGCAGCCAAAGTG 240
Db 181 CCATACAACTTCTTTACAGGAATGCGCTCGCAATTCACACCTGTCAACAGCAGCCAAAGTG 240
QY 241 ATCATTTACCAACCTGTGACCGGCAAGGACATTTGGTACTATGAGATGCAGATCAAGCA 300

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Db AGCCCTGGTCTACTTTCATTTGCCAGAGAACAGACTGTAGTTAGGTTCAATCAAC 420
Oy AATGCCACCTGGAGAACTCGGTGCATCTGCAGGCTCCCATGCGCGCCCTTTCAT 480
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Oy CTCAACGCTGCGGTCTGCTGCTTGGCTCTCTACTCTGTCAGACAGCTCTCCCAAC 900
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Db GTGAGAAATCTCTTCCAAATGATGCTGTGATGCTGTCTCTTCAAGCCCGCTTCA 960
Oy ACCCTTAACCTTACTTGTCTGTGCCAGGCTTACGAGATCATTTATGACTTCCAC 1020
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Oy GATGAGTACGCTGCGACCTCTGAGTGAATGCGCTTGTGCTGAGCTTGGCACTGTT 1140
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Db GACACACGAGCTGCGCTTCCCTGCACTCTCCGTGACGTTCTCTTCCCTCAAGAG 1200
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Db GCGTTTGGCGATGTCAATGAGCGGTCTCGGCCAAAGCCGAGCTGGGACCGTTGAG 1320
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Oy 1381 TTCAAGATCTTCAAGCGAATGCTGTGTCGTGGCCAGTGCATGCCCTACGATCTGCTG 1440
Db 1381 TTCAAGATCTTCAAGCGAATGCTGTGTCGTGGCCAGTGCATGCCCTACGATCTGCTG 1440
Oy 1441 CTTAAGATGTCGTCTGTGGTGGGAGGAGTGAACCCCTGACATCTGAGGCCACTACCA 1500
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Db 1741 CCGTCAACCGCGCTGATGAGATCTCGAGAGATCTTGAATCGAGAGTAA 1791

RESULT 4
US-09-338-723A-1
; Sequence 1, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Humming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-338-723A-1

Query Match 82.3%; Score 1474; DB 10; Length 3677;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
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Qy 261 CGGCAAGGACATTTGGTACTATAGATCGAGATCAAGCATTTCAGCAAA-----311
Db 1398 CGGCAAGGACATTTGGTACTATAGATCGAGATCAAGCATTTCAGCAAAAGGTTGAGTTT 1457
Qy 312 -----GATTTACCACCTT 326
Db 1458 GCTCAAAAACCTTGGTATTAATCATATTGTAACCTTTCACCTTTCACCTTACCCACCTT 1517
Qy 327 GCGCCCTGCACACTCTGTGGGTACGATGGATGGACCCCTGGCTCACTTCAATGTTCC 386
Db 1518 GCGCCCTGCACACTCTGTGGGTACGATGGATGGACCCCTGGCTCACTTCAATGTTCC 1577
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Db 1878 ATCAACGACGAGGCTGAGAGATGCTCGGCTTCCAGTGGCTATGGGAGATTCGATATC 1937
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Db 1938 CCTGTGATCCTGACGCGCAAGTACTATAAGCGGATGGTATCCCTGGCTTCGACGAGGCT 1997
Qy 748 GAGGACACGAGACTGTGGGAGATGTCAATGTCATACGACAGCCATGGCTTCCCT 807
Db 1998 GAGGACACGAGACTGTGGGAGATGTCAATGTCATACGACAGCCATGGCTTCCCT 2057
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Qy 868 CTCTCTACTCTGTGACGACACAGCTCTCCCAAGTCAAGTTCCTTCCAACTCATTTGCC 927
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Qy 1054 GCTGAGACCAACGATGTGGGACAGAGATGATGACGCTCGACACTCTCGAGGTGATGGCC 1113
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Db 2478 GTTCCCTTCCCTCTCCACAGGAAGGCCCGCCGACCAACGACTTCAAGTTTGAAGCAAC 2537
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Db 2778 ACCGTGACCATGGAGGCCACTACCAACCCCTGGAGCTGGAGCTTACATGTCGACTGTAC 2837
Qy 1534 AACCTCATTCACGAGGATTAACGATGATGGCTGTAATTAACAGTCAACGCCATGAGAGAG 1593
Db 2838 AACCTCATTCACGAGGATTAACGATGATGGCTGTAATTAACAGTCAACGCCATGAGAGAG 2897
Qy 1594 AAGGATATCTTCAGAGGACTTCGAGAGCCCATGAAACCCCAAGTGGCGCCGCTTCT 1653
Db 2898 AAGGATATCTTCAGAGGACTTCGAGAGCCCATGAAACCCCAAGTGGCGCCGCTTCT 2957
Qy 1654 TACAACCGCAAGACTTCATGCTCGCGCTGGAAACTTCGCGCGAGACATCACTGCGC 1713
Db 2958 TACAACCGCAAGACTTCATGCTCGCGCTGGAAACTTCGCGCGAGACATCACTGCGC 3017
Qy 1714 CGAGTGCAGAGCTGGCCGAGCAGAGAGCCGTACAAACCGCTCGATGAGATTCCTGGAGAT 1773
Db 3018 CGAGTGCAGAGCTGGCCGAGCAGAGAGCCGTACAAACCGCTCGATGAGATTCCTGGAGAT 3077
Qy 1774 CTTGCAATCGAGAGTAA 1791
Db 3078 CTTGCAATCGAGAGTAA 3095

RESULT 5
US-10-080-210-1
; Sequence 1, Application US/10080210
; Patent No. US2002014242A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO. 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-10-080-210-1
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Query Match		82.3%;	Score 1474;	DB 12;	Length 3677;
Best Local Similarity		87.0%;	Fred. No. 0;		
Matches 1791;		Conservative	0;	Mismatches	0; Indels 267; Gaps 5;
Qy	1	GCATATATGCTGTTCAGTCATGACGACGCGAGCGCTCCGGGCTCCTGCTGGAGTC	60		
Db	1038	CTCATATATGCTTTTAAGTCATGCGAAGCTGCGACAGACCTCCGGGCTCCTGTCTGGAGTC	1097		
Qy	61	CTGGGCAATCCCGATGAGACACCGGCGAGCCACCCATTGAGGCTGTGTATCCCGAAGTGAAG	120		
Db	1098	CTGGCAATCCCGATGAGACACCGGCGAGCCACCCATTGAGGCTGTGTATCCCGAAGTGAAG	1157		
Qy	121	ACTGAGGCTTGGCTGACTCCTCCTTGTGTGACGACGCGGATGACGACTGGGATGCCT	180		
Db	1158	ACTGAGGCTTGGCTGACTCCTCCTTGTGTGACGACGCGGATGACGACTGGGATGCCT	1217		
Qy	181	CCATACCACTTCTTAC-----	198		
Db	1218	CCATACCACTTCTTACAGGTGAGACACCTTCCACCTGTTTCCCTCGATTAAC	1277		
Qy	199	-----AGGAATGCCCTGGCAATTCACCTGTCAAGCACGCCAGAT-----	239		
Db	1278	TCTTATAGGAATGCCCTGGCAATTCACCTGTCAAGCACGCCAGATGTATGTTTGTAT	1337		
Qy	240	-----GATCATTACCAACCCGTGCAC	260		
Db	1338	TTTCTACGAAGCACTCGGCCCCGACATAATGTATCTTAGGATCATTTACCAACCCGTGCAC	1397		
Qy	261	CGGCAAGGACATTTGGTACTATGAGATGAGATCAAGGCATTTCAGCAAG-----	311		
Db	1398	CGGCAAGGACATTTGGTACTATGAGATGAGATCAAGGCATTTCAGCAAGGGGTAGTTT	1457		
Qy	312	-----GATTTACCCGACCTT	326		
Db	1458	GCTCAGAAACCTTGTGTATTAATCAATGTATGACTGACCCCTTTCAGATTTACCCGACCTT	1517		
Qy	327	GGGCGCTGCACTCTGCTGCGGCTAGATGGCATGAGCCCTGCTCTACTTTCAATGTTCC	386		
Db	1518	GGGCGCTGCACTCTGCTGCGGCTAGATGGCATGAGCCCTGCTCTACTTTCAATGTTCC	1577		
Qy	387	CAGAGGAACAGAGACTGTAGTAGTTCATCAACATGCGACCGTGGAGAACCTGCGTCA	446		
Db	1578	CAGAGGAACAGAGACTGTAGTAGTTCATCAACATGCGACCGTGGAGAACCTGCGTCA	1637		
Qy	447	TCTGCAAGGCTCCCATGCGCTGCCCCCTTTCGATGTTGGGCTGAAGATGACCTTCCC	506		
Db	1638	TCTGCAAGGCTCCCATGCGCTGCCCCCTTTCGATGTTGGGCTGAAGATGACCTTCCC	1697		
Qy	507	TGGCGAGTACAGAGATTAATTAATTCATCCCACTACCAATCCGCCCTTCTGTGGTACA	566		
Db	1698	TGGCGAGTACAGAGATTAATTAATTCATCCCACTACCAATCCGCCCTTCTGTGGTACA	1757		
Qy	567	TGACCACGCTTTCATGA-----	583		
Db	1758	TGACCACGCTTTCATGAGATGCTAGCAGAGCCTTATCTTCTTGGCTACCTTTGGCTA	1817		
Qy	584	-----AGACTGCTGAGATGCTACTTGTGTCAGGCTGGCGCCCTACATTT	627		
Db	1818	ACCAACTTCTTTCGTAGACTGCTGAGAAATGCTTACTTGTGTCAGGCTGGCGCCCTACATTT	1877		
Qy	628	ATCAACGACGAGGCTGAGATGCTCTCGGTCTTCTTAAGGGCTAATGGGAGTTTGCATATC	687		
Db	1878	ATCAACGACGAGGCTGAGATGCTCTCGGTCTTCTTAAGGGCTAATGGGAGTTTGCATATC	1937		
Qy	688	CCTCTGATCTACGAGCAAGTACTATAACGCCGATGATGACCTCGTTTGCACCGAGGT	747		
Db	1938	CCTCTGATCTACGAGCAAGTACTATAACGCCGATGATGACCTCGTTTGCACCGAGGT	1997		
Qy	748	GAGGACGAGGACCTTGGGGAGATGTCAATGTCAAGGACAGCCATGCGCTTTCCTT	807		
Db	1998	GAGGACGAGGACCTTGGGGAGATGTCAATGTCAAGGACAGCCATGCGCTTTCCTT	2057		
Qy	808	AACGTCCAGCCCCGCAAGTACCGCTTCCGATTCTCAACGCTGCCGTGTCTGCTGCTTGG	867		

Db	2058	AACGTCCAGCCCCGCAAGTACCGCTTCCGATTCTCAACGCTGCCGTGTCTGCTGCTTGG	2117		
Qy	868	CTCTCTACCTCTGTCAGGACACAGCTCTCCCAACGTACAGAAATCTTTTCCAAGTCAATTC	927		
Db	2118	CTCTCTACCTCTGTCAGGACACAGCTCTCCCAACGTACAGAAATCTTTTCCAAGTCAATTC	2177		
Qy	928	TCTGATGCTGTCTCTTCAAGCCCCCGTTTACAGCTCTTAACCTCTACCTTGTGTGCC	987		
Db	2178	TCTGATGCTGTCTCTTCAAGCCCCCGTTTACAGCTCTTAACCTCTACCTTGTGTGCC	2237		
Qy	988	GAGCGTTACGAAATCATTAAT-----	1008		
Db	2238	GAGCGTTACGAAATCATTAATGATGCCCTCCCTCTCACGAATGAGTCAAGAACTCTA	2297		
Qy	1009	-----GACTTCCCAACTTGTGTGCGCACAGCTTGTGACCTGGCAAGCTT	1053		
Db	2298	AGACTAACACTTGTAGACTTTCACCAACTTGTGTGCGCACAGCTTGTGACCTGGCAAGCTT	2357		
Qy	1054	GCTGAGACCAACGATGTGCGCGAGAGATGATACGCTCGCATCTCGAGGTGATGGCC	1113		
Db	2358	GCTGAGACCAACGATGTGCGCGAGAGATGATACGCTCGCATCTCGAGGTGATGGCC	2417		
Qy	1114	TTGCTGCTACGCTGTGGCATGTGAGGACACACGACGATCCCTCCACATCTCGGTGAC	1173		
Db	2418	TTGCTGCTACGCTGTGGCATGTGAGGACACACGACGATCCCTCCACATCTCGGTGAC	2477		
Qy	1174	GTTCCCTTCCCTCTCACAGGAAGGCCCGCGCAGACATTCGAAGTTTGAAGCGAC	1233		
Db	2478	GTTCCCTTCCCTCTCACAGGAAGGCCCGCGCAGACATTCGAAGTTTGAAGCGAC	2537		
Qy	1234	AAGGACACTATCTGATCAAGATGTGGCTTGGCCATGTCAATGAGCGTCTCTGGCC	1293		
Db	2538	AAGGACACTATCTGATCAAGATGTGGCTTGGCCATGTCAATGAGCGTCTCTGGCC	2597		
Qy	1294	AAGCCGAGCTCGGACCGTGTGAGGCTGGGAGCTCGGAATCTCTGAGAGCTGGAGC	1353		
Db	2598	AAGCCGAGCTCGGACCGTGTGAGGCTGGGAGCTCGGAATCTCTGAGAGCTGGAGC	2657		
Qy	1354	CACCCGCTCACATTCACCTGTGTACTTCAAGATCTCAACGACGAACGTGTTGTTGGC	1413		
Db	2658	CACCCGCTCACATTCACCTGTGTACTTCAAGATCTCAACGACGAACGTGTTGTTGGC	2717		
Qy	1414	CAGTCAATGCCCTTACGAGTCTGCTGTCTTAAGGATGTCTGTGTTGGGACGGGTGAG	1473		
Db	2718	CAGTCAATGCCCTTACGAGTCTGCTGTCTTAAGGATGTCTGTGTTGGGACGGGTGAG	2777		
Qy	1474	ACCCTGACCATGAGAGGCCACTACCAACCTGAGTGTGAGCTTACATGTGGACGTGAC	1533		
Db	2778	ACCCTGACCATGAGAGGCCACTACCAACCTGAGTGTGAGCTTACATGTGGACGTGAC	2837		
Qy	1534	AACCTCATTCACGAGGATTAACGACATGATGGCTGTATTCAACGTCACGCCCATGAGAG	1593		
Db	2838	AACCTCATTCACGAGGATTAACGACATGATGGCTGTATTCAACGTCACGCCCATGAGAG	2897		
Qy	1594	AAGGATATCTTTCAGAGGACTTTCAGAGACCCCATGAACCCCAAGTGGCGCGCTTCTT	1653		
Db	2898	AAGGATATCTTTCAGAGGACTTTCAGAGACCCCATGAACCCCAAGTGGCGCGCTTCTT	2957		
Qy	1654	TACAACCGCAACGACTTTCATGCTGCGGTGGAACCTTCTCGCGGATTCATCACTGCC	1713		
Db	2958	TACAACCGCAACGACTTTCATGCTGCGGTGGAACCTTCTCGCGGATTCATCACTGCC	3017		
Qy	1714	CGAGTGCAGGAGCTGGCGGAGAGAGCGTCAACACCCCTTCGATGAGATCTTGAGAGAT	1773		
Db	3018	CGAGTGCAGGAGCTGGCGGAGAGAGCGTCAACACCCCTTCGATGAGATCTTGAGAGAT	3077		
Qy	1774	CTTGAATTCGAGAGTAA	1791		
Db	3078	CTTGAATTCGAGAGTAA	3095		

RESULT 6

US-10-080-233-3
: Sequence 3, Application US/10080233
: Patent No. US20020151450A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Huming
: TITLE OF INVENTION: No. US20020151450A1 Phenol Oxidizing Enzymes
: FILE REFERENCE: GCS67
: CURRENT APPLICATION NUMBER: US/10/080,233
: CURRENT FILING DATE: 2002-02-19
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 3677
: TYPE: DNA
: ORGANISM: Stachybotrys chartarum
US-10-080-233-3

Query Match 82.3%; Score 1474; DB 12; Length 3677;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

QY 1 GTCAATATGCTGTTCAAGTCATGCGCACTGCGAGCGAGCTCGGGCTCCTGTGTGAGTC 60
DB 1038 GTCAATATGCTGTTCAAGTCATGCGCACTGCGAGCGAGCTCGGGCTCCTGTGTGAGTC 1097
QY 61 CTCGGCATCCCGATGGACACCGCGACGACCCCATTTGAGGCTGTTGATCCCGAAGTGAG 120
DB 1098 CTCGGCATCCCGATGGACACCGCGACGACCCCATTTGAGGCTGTTGATCCCGAAGTGAG 1157
QY 121 ACTGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 1158 ACTGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1217
QY 181 CCATACAACTTGTGTTAC----- 198
DB 1218 CCATACAACTTGTGTTACAGGTGAGACACCTGTCCACCTGTTTCCCTGATACATAAC 1277
QY 199 -----AGGAATGCCCTGCAATTTCCAGCTGTGACAGAGCCCAAGAT----- 239
DB 1278 TCTTATAGGAATGCCCTGCAATTTCCAGCTGTGACAGAGCCCAAGATGTAATGCTTTGAT 1337
QY 240 -----GATCATTTACCAACCCCTGTAC 260
DB 1338 TTTCTAGGAAGCACTCGGCGCCGACTAATGTAATCTAGAGATCATTTACCAACCCCTGTAC 1397
QY 261 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAG----- 311
DB 1398 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAGGGGTGAGTTT 1457
QY 312 -----GATTTTACCCCACTT 326
DB 1458 GCTCAGAAACCTTTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1517
QY 327 GGGCCCTGCGACTCTGCTGCGGCTAGCATGAGATGAGCCCTGTCTTACTTTCAATGTTC 386
DB 1518 GGGCCCTGCGACTCTGCTGCGGCTAGCATGAGATGAGCCCTGTCTTACTTTCAATGTTC 1577
QY 387 CAGAGGAACAGAGACTGTAGTTAGTTTCAACAATGCCACCGGTGAGAGACTGTGTCCA 446
DB 1578 CAGAGGAACAGAGACTGTAGTTAGTTTCAACAATGCCACCGGTGAGAGACTGTGTCCA 1637
QY 447 TCTGCAGGCTCCCATGCGGTGCGCCCTTTGATGGTGGGAGAGATGATGACCTTCCC 506
DB 1638 TCTGCAGGCTCCCATGCGGTGCGCCCTTTGATGGTGGGAGAGATGATGACCTTCCC 1697
QY 507 TGGCGAGTACAAGGATTTACTATTTCCCAACTACAAATCGCGCCGCTTCTGTGTACCA 566
DB 1698 TGGCGAGTACAAGGATTTACTATTTCCCAACTACAAATCGCGCCGCTTCTGTGTACCA 1757
QY 567 TGACCAAGCTTTTCATGA----- 583
DB 1758 TGACCAAGCTTTTCATGAAGGATGCTACAGAGCTTATCTTCTTGTGCTACCTTTGGCTA 1817

QY 584 -----AGACTGCTGAGAAATGCTTACTTTGGTCAAGGCTGGGCTCAATTT 627
DB 1818 ACCAACTTCTTTCTGTAAGCTGTGAGAAATGCTTACTTTGGTCAAGGCTGGGCTCAATTT 1877
QY 628 ATCAAGGAGAGGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 687
DB 1878 ATCAAGGAGAGGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1937
QY 688 CCTGTGATCTGACGGCAAGTACTATTAACGGCGATGTAACCTGGCTTGCAGCCGAGGT 747
DB 1938 CCTGTGATCTGACGGCAAGTACTATTAACGGCGATGTAACCTGGCTTGCAGCCGAGGT 1997
QY 748 GAGGACGAGGACTGTGGGAGATGTCATGTCATGTCAGGAGACGACGACCTTCCCTT 807
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QY 808 AACGTCAGGCGCCGCAAGTACCTTTCCGATTCCTCAAGCTTCCGCTGCTGCTTGG 867
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QY 868 CTCCTTACCTGCTCAGAGACACCTCTCCACGTCAGAAATTCCTTTCCAGTCAATGCC 927
DB 2118 CTCCTTACCTGCTCAGAGACACCTCTCCACGTCAGAAATTCCTTTCCAGTCAATGCC 2177
QY 928 TCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987
DB 2178 TCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2237
QY 988 GAGCGTTAGAGATCAATTT----- 1008
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QY 1009 -----GACTTCACCAACTTTGCTGCGCAGACTCTTGAACCTGCGCAACGTT 1053
DB 2298 AGACTAACACTTGTAGACTTACCACTTGTGCTGCGCAGACTCTTGAACCTGCGCAACGTT 2357
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DB 2418 TTGCTGTCAGCTCTGCGCACTGTTGAGGACAAACGACAGTCCCTTCCACTGCTGCGTAC 2477
QY 1174 GTTCTCTTCCCTCTCACAAGAGAGCCCGCGCAGACGACTTCAAGTTTGACGACAC 1233
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QY 1234 AAGGACACTACCTGATCAACGATGTTGGCTTGGCGAGTGCATTAAGGAGTGCCTGGGC 1293
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DB 2658 CACCCGTCACATTCATCTTGTGACTTCAAGATCTTCAAGGCAACTGTGTGCTGCGC 2717
QY 1414 CAGGTCATGCGCTAGAGTCTGCTGCTTGAAGATGCTGCTGCTTGGGAGGAGGTGAG 1473
DB 2718 CAGGTCATGCGCTAGAGTCTGCTGCTTGAAGATGCTGCTGCTTGGGAGGAGGTGAG 2777
QY 1474 ACCCTGACCATGAGGCGCCACTACCAACCTGTGACTGAGGCTTACATGTGGCACTGTAC 1533
DB 2778 ACCCTGACCATGAGGCGCCACTACCAACCTGTGACTGAGGCTTACATGTGGCACTGTAC 2837
QY 1534 AACCTATTACAGAGATTAACGATGATGCTGTATTTCAAGCTACCGCCATGAGAGAG 1593
DB 2838 AACCTATTACAGAGATTAACGATGATGCTGTATTTCAAGCTACCGCCATGAGAGAG 2897
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Db 2898 AAGGATATCTTCAGAGACTTCGAGAACCCCATGAACCCCAAGTGGCGGCCCTTCT 2957
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Db 2958 TACAACCCGAAGACTTTCATGCTCGCGTGAAGAACTTTCGCGGAGTCCATCACTGCC 3017
Qy 1714 CGAGTGCAGAGAGCTGGCGGAGAGAGCCGTTACACCCGCTCGATGAATCTGAGAGT 1773
Db 3018 CGAGTGCAGAGAGCTGGCGGAGAGAGCCGTTACACCCGCTCGATGAATCTGAGAGT 3077
Qy 1774 CTGGAATCGAGAGTAA 1791
Db 3078 CTTGGAATCGAGAGTAA 3095

RESULT 7
US-10-080-233-5
; Sequence 5, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1el Phenol oxidizing Enzymes
; FILE REFERENCE: GCS67
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid
US-10-080-233-5

Query Match 82.1%; Score 1470; DB 12; Length 2067;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 187; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
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Db 487 CCCTGCCACTCTCGTGGCTACGATGGCATGAGCCCTGGTCTCACTTTCATATGTTCCAG 546
Qy 390 AGGAACAGAGACTGTAGTTAGTTCATACAAATGCGCACCGTGGAGAACTGGTTCATCT 449
Db 547 AGGAACAGAGACTGTAGTTAGTTCATACAAATGCGCACCGTGGAGAACTGGTTCATCT 606
Qy 450 GCAGGGCTCCCATGGCGTGGCCCTTTGATGTTGGGCTGGAATGATGAGACTTCCCTGG 509
Db 607 GCAGGGCTCCCATGGCGTGGCCCTTTGATGTTGGGCTGGAATGATGAGACTTCCCTGG 666
Qy 510 CGAGTACAGAGATTACTACTTTCACCACTACCAATCCGCGCCCTTCTGTGTGATACATGA 569
Db 667 CGAGTACAGAGATTACTACTTTCACCACTACCAATCCGCGCCCTTCTGTGTGATACATGA 726
Qy 570 CCAGCCTTTCATGA----- 583
Db 727 CCAGCCTTTCATGAAGGATATGCTACAGACCTTATCTTCTTGGCTACCTTGGCTAAC 786
Qy 584 -----AGACTGTGAGAAATGCTACTTGGTGGAGGCTGGCGCTACATATTC 630
Db 787 AACTTCTTTCGTAGACTGTGAGAAATGCTACTTGGTGGAGGCTGGCGCTACATATTC 846
Qy 631 AACGACAGAGCTGAGAGATCTCGGTCTTCTAGTGGCTATGCGAGTTCGATATCCCT 690
Db 847 AACGACAGAGCTGAGAGATGCTCGGTCTTCTAGTGGCTATGCGAGTTCGATATCCCT 906
Qy 691 CTGATCTGAGGGCCCAAGTACTATTAACGCCGATGGTATCCCTGCTTCGACGAGGCTGAG 750
Db 907 CTGATCTGAGGGCCCAAGTACTATTAACGCCGATGGTATCCCTGCTTCGACGAGGCTGAG 966
Qy 751 GACGAGGACCTGGGGAGATGTCATTCATGCAACGGGACGACCATGGGCTTTCCTTAAC 810
Db 967 GACGAGGACCTGGGGAGATGTCATTCATGCAACGGGACGACCATGGGCTTTCCTTAAC 1026
Qy 811 GTCCAGCCCGCAAGTATACGTTTCGATTCCTCAACGCTGCGGTCTGCTGCTTGGCTC 870
Db 1027 GTCCAGCCCGCAAGTATACGTTTCGATTCCTCAACGCTGCGGTCTGCTGCTTGGCTC 1086
Qy 871 CTCTACCTCTGTCAGAGACCAAGCTCTCCCAAGCTGACAGATTCCTTTCAGTCACTTGCCTCT 930
Db 1087 CTCTACCTCTGTCAGAGACCAAGCTCTCCCAAGCTGACAGATTCCTTTCAGTCACTTGCCTCT 1146
Qy 931 GATGCTGGTCTGCTCAACCCCGTTCAGACCTGTAACCTCTACCTTCTGTTGCGGAG 990
Db 1147 GATGCTGGTCTGCTCAACCCCGTTCAGACCTGTAACCTCTACCTTCTGTTGCGGAG 1206
Qy 991 CCTTACGAGATCAATAT----- 1008
Db 1207 CGTTAGGATCATTAATGTTATGCCCTCCCTCTCAGCATGAGTCAAGAACTTAAGA 1266
Qy 1009 -----GACTTCAACCACTTGTCTGGCGAGACTCTTGTAGCTGGCAACGTTGCT 1056
Db 1267 CTAAACCTGTGAGACTTCAACCACTTGTCTGGCGAGACTCTTGTAGCTGGCAACGTTGCT 1326
Qy 1057 GAGACCAAGAGTGTGGGCGAGCGAGATGATGAGTACGCTGCGACTCTCGAGGTGATGGCTTC 1116
Db 1327 GAGACCAAGAGTGTGGGCGAGCGAGATGATGAGTACGCTGCGACTCTCGAGGTGATGGCTTC 1386
Qy 1117 GTGTGAGTCTGTGGCACTGTGAGCAACAGCAGAGTCCCTCCACTCTCGTGAAGTT 1176
Db 1387 GTGTGAGTCTGTGGCACTGTGAGCAACAGCAGAGTCCCTCCACTCTCGTGAAGTT 1446
Qy 1177 CCTTTCCTCTCACAAGAGAGCCCGCGAGACACTTCAAGTTTAAAGCGACAAAC 1236
Db 1447 CCTTTCCTCTCACAAGAGAGCCCGCGAGACACTTCAAGTTTAAAGCGACAAAC 1506
Qy 1237 GGAACACTACGATCAACAGATGTGGCTTGGCGGATGTAATGAGGCTGCTGGGCAAG 1296
Db 1507 GGAACACTACGATCAACAGATGTGGCTTGGCGGATGTAATGAGGCTGCTGGGCAAG 1566
Qy 1297 CCCGAGCTCGGACCGTTGAGGTCTGGAGCTCGAAGACTCCTTGTGAGGCTGAGCCAC 1356
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Db 1567 CCCGAGCTCGCCACCCGCTTGAGGCTCGGAGCTCGAGAACCTCCCTCTGGAGCTGAGCCAC 1626
Qy 1357 CCCGTCACATTCACCTTGTTGACTTCAAGATCTCAACGCAAGCTGGTGGTGGCCAG 1416
Db 1627 CCCGTCACATTCACCTTGTTGACTTCAAGATCTCAACGCAAGCTGGTGGTGGCCAG 1686
Qy 1417 GTCATGCCCTACGAGCTGCTGCTGCTTAAGATGTCGTGCTGGTGGGAGGGGTGAGAC 1476
Db 1687 GTCATGCCCTACGAGCTGCTGCTGCTTAAGATGTCGTGCTGGTGGGAGGGGTGAGAC 1746
Qy 1477 CTGACCATCGAGGCCCACTACCAACCCCTGGACTGAGCTTACATGTGGCATCTCAAC 1536
Db 1747 CTGACCATCGAGGCCCACTACCAACCCCTGGACTGAGCTTACATGTGGCATCTCAAC 1806
Qy 1537 CTGATTCAGAGGATACGACATGATGGCTGTATTCACGTCACGCCCTGGAGGAGAG 1596
Db 1807 CTGATTCAGAGGATACGACATGATGGCTGTATTCACGTCACGCCCTGGAGGAGAG 1866
Qy 1597 GGATATCTTCAGAGGAGCTTCGAGGAGCCCATGAACCCCAATGGCGCGCTTCTTAC 1656
Db 1867 GGATATCTTCAGAGGAGCTTCGAGGAGCCCATGAACCCCAATGGCGCGCTTCTTAC 1926
Qy 1657 AACCCCAAGACTTCCATGCTCTGCGCTGGAAACTTCTCCGCGAGTCATCACTGCCGA 1716
Db 1927 AACCCCAAGACTTCCATGCTCTGCGCTGGAAACTTCTCCGCGAGTCATCACTGCCGA 1986
Qy 1717 GTGAGAGGCTGGCGGAGGAGGCGGTACACGCCCTCGATGATCTCTGGAGATCTT 1776
Db 1987 GTGAGAGGCTGGCGGAGGAGGCGGTACACGCCCTCGATGATCTCTGGAGATCTT 2046
Qy 1777 GGAATCGAGAGTA 1790
Db 2047 GGAATCGAGAGTA 2060

RESULT 8
US-09-338-723A-3
: Sequence 3, Application US/09338723A
: Patent No. US20020019038A1
: GENERAL INFORMATION:
: APPLICANT: Humming, Wang
: TITLE OF INVENTION: Phenol Oxidizing Enzymes
: FILE REFERENCE: GC561-2
: CURRENT APPLICATION NUMBER: US/09/338, 723A
: PRIOR FILING DATE: 1999-06-23
: PRIOR APPLICATION NUMBER: 09/220, 871
: PRIORITY DATE: 1998-12-23
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 2905
: TYPE: DNA
: ORGANISM: Bipolaris splicifera

Query Match 28.1%; Score 503.4; DB 10; Length 2905;
Best Local Similarity 60.6%; Pred. No. 1,4e+13;
Matches 998; Conservative 0; Mismatches 511; Indels 138; Gaps 5;

Qy 245 TTACCAACCTGTGCACGGCAAGACATTTGGTACTATGATCGAGTCAAGCCATTTTC 304
Db 423 TCACGAATCTGTGCACAAAGAGATATGTTACTACGATTTGTCATCAAAACCTTCA 482
Qy 305 AGCAAGAATTTACCCCACTTGGCCCTGCCACTCTGCTGGCTACGATGGCATGAGCC 364
Db 483 CCCAGACAGTGTATCAAGCCCTGCGCTCTGTTAGTAGTATACGCGCATCTCC 542
Qy 365 CTGCTCTACTTTCAATGTTCCAGAGAACAGAGACTAGTATGTTAGTTCATCAACATG 424
Db 543 CAGGTCTCAGCATCATATATGCGGAGAGACAGAGCTGTTTACGGTTTATTAACCAAG 602
Qy 425 CCACGCTGAGAACTGGTTCATCTGACGCGCTCCCATGCGGTGCCCTTTGATGTT 484

Db 603 GTATCGCGAAAGCTTCATCATCTTCACAGGCTCCCGCTCCGTCGCTTTGAGGAT 662
Qy 485 GGGCTGAAGATGTGACCTTCCCTGGCGAGTACAA----- 518
Db 663 GGGCTGATGATATGATCATGAAGGGGAATACAAAGTAGATAGCTGTGATTTCTACGC 722
Qy 519 -----GGATTACTACTTCCCACTA 539
Db 723 ATCAGGAAGCCTTATCATACTACAGAGACTTCTTCTCAGACTTACTACCCGACAA 782
Qy 540 CCAATCCGCGCGCTTCTGTGTATCCATGACACGCTTTCA----- 580
Db 783 CCAAGCTGCCAGATTTTGTGTACACGATCATGTATGATGTTGAAGTCTTACGC 842
Qy 581 -----TGAAGACTGCTGAGATG 598
Db 843 ACTTTTCATGATGTAAGAAAGAGATTAAGCTAACATCTGTGGAGAGCCGCAAAAAG 902
Qy 599 CCTACTTTGTGAGGCTGGCGCTACATATACAGAGAGGCTGAGATGCTCTCGCTC 658
Db 903 CCTATTTTGGGCAAGCGCGCTTACTGATACAGACCGCGCTGAGATGCTCTCGCGC 962
Qy 659 TTCTAGTGTATGGCGAGTTGATATCCCTGTATCTGACGCGCAAGTACTATAACG 718
Db 963 TTCTAGTGTATGGCGAGAAATACAGACATTCGCTGGTCTCGATTCAAGTACTACAG 1022
Qy 719 CCGATGTATCCCTGGCTTGACCGAGGTGAGAGACGAGACTGTGGGAGATGTATC 778
Db 1023 CCGATGGAATCTTAAAGACATGTGGGAGAAAGAGTGTGGGCGCATCATC 1082
Qy 779 ATGCAACGAGACCATGCGCTTCTTAAGCTTACGTCAGCGCCGCAAGTACGTTCCGAT 838
Db 1083 ATGTCACGCTGACCGCTTGTGATGATGTTGAGAGCTGGAAGATGTCTTTCAT 1142
Qy 839 TCCTCAAGCTGCGCTGTCTGCTTGGCTCTCTACCTGTCAGAGACGCTCTCCA 898
Db 1143 TCCTCAAGCGCGCTGTCTTGAAGACTTGGCTTACTTCTCAAGCAAGACACATG 1202
Qy 899 AGCTGAGATTCCTTCCAGTCATCTGCTGATGCTGTCTCTTCAAGCCCCGTTTC 958
Db 1203 CCAGTGTGCTCTTCCAGGTGATTCCTGTGAGAGGCTACTCACACCGGTTTC 1262
Qy 959 AGACCTGTAACTTCACTTACCTGCTGTGCGAGCGTTAGAGATTAATTATGCTACCA 1018
Db 1263 AAACCTCAGATATGATATGTGTCAGCGCGAGAACGCTAGAGATTTGTTCATTTCCGCC 1322
Qy 1019 ACTTGTGCGCGAGACTTGTACCTGCGCAAGTGTGAGACCAAGATGTGCGCGAG 1078
Db 1323 CCTATGCGCGCAAAAGTGTGATGTGCGCAACTTGGCAAAAGGCCAATGGTATCGGTACCG 1382
Qy 1079 AGGATGAGTACGCTGCGACTCTCGAGGTGATGCGCTGTGCTCAGCTCTGCGACTTTG 1138
Db 1383 AGGAGACTACGCAAAACACTGACAGGTGATGCTGTTCCAGCTCAGACCCAAACAGTGC 1442
Qy 1139 AGCAACAGCCAGGATCCCTCCACTTCCGAGAGTTCCTTCCCTCCCAAGAGAG 1198
Db 1443 TCGATTAATCCGTGGTACCGGACAGCTATCTCAATCAAGTTCCTCCCGGAGCA---AAA 1499
Qy 1199 GCGCGCGAGCAAGCACTTCAAGTTTGAACGCGCAAGCGACATCTGATCAACGATG 1258
Db 1500 CCGACATAGACCATCACTTCCGTTTCCATCGTACCAAGGCGAGTGGCGATCCGCGCA 1559
Qy 1259 TTGGCTTTGGCGATGTCATATGAGCTGTCTGCGCAAGCCGAGCTGGCACCTTTGAGG 1318
Db 1560 TCGGGTTTGGCAAGCTGCGAAGCCGTGTTTGGCCAAAGTACCGCGGTATCTGCGAGC 1619
Qy 1319 TCTGGAGCTCGAAGATCTCTGGAGCTGAGAGCCCGCTCCACATTCATCTTGTG 1378
Db 1620 TTTGGGAATTAAGAACAGCTCGCGCGCTGTCAACCCCTTCCAGCTCCACTAGTAG 1679
Qy 1379 ACTTCAAGATCTCAAGCAACTGG-----TGATCGTGGCCAGGCTATGCCCTACGAGT 1432
Db 1680 ACTTCCGAGTGTGTCGCGCTACGCGCAAGAGGACATCTGCGCGCTCATAGCCCTATGAGG 1739


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QY 1613 ACTTCGAGACCCCATGAAACCCCAAGTGGCGCGCTTCCTTACAAACCGCAAGCACTTCC 1672
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1807 AATTCCAGACCCCGGAAGATTTCTGCTGTGCGAAGACCCCTTACACCGCGGTGACTTGA 1866
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1673 ATGCTCGCGCTGGAAACTTCTCCCGGAGTCCATCATCTGCCGAGTGAAGAGCTGGCCG 1732
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1867 CGGCGCGATCGGCTATCTTCTCAGAAAGCATCATCAGGCTAGAGTAAGCAGATTGGCGC 1926
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1733 AGCAGAGCCCGTACAAACCGCTCGATGAGATCTGG 1768
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1927 TGGAAACGCCGTACAGCAACTGGCAGACAGTTCACGG 1962
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-09-942-185-1
: Sequence 1, Application US/09942185
: Patent No. US20020165113A1
: GENERAL INFORMATION:
: APPLICANT: Aehle, Wolfgang
: APPLICANT: Convents, Daniel
: APPLICANT: Doornink, Monique
: APPLICANT: van Gastel, Frans
: APPLICANT: Rodrigues, Ana
: APPLICANT: Topozada, Amr
: APPLICANT: De Vries, Cornelis Hendrikus
: TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1el Phenol ox
: FILE REFERENCE: C7567
: CURRENT APPLICATION NUMBER: US/09/942,185
: NUMBER OF FILING DATE: 2001-08-29
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 1958
: TYPE: DNA
: ORGANISM: Stachybotrys chartarum
US-09-942-185-1

Query Match 25.7%; Score 460.4; DB 9; Length 1958;
Best Local Similarity 59.3%; Pred. No. 2,2e-121;
Matches 996; Conservative 0; Mismatches 521; Indels 163; Gaps 6;

QY 241 ATCATTTACCAACCTGTGACCGGCAAGACATTTGGTACTATGAGATCGAGATCAAGCCA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 257 ACCGTCGCCAACCCCACTGAGAGAGCAATCTTACTAGAGATGAGATGAGCC 316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TTTCAGCAAGATTTACCCCACTTGGCCCTTGGCACTCTGCTGGGTACATGTCATG 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 317 TTCTCCCAACAGATCTACCTGATCTGGAGCCGCCAACATGGTGGATACGATGGCATG 376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 AGCCCTGCTCCTTTTCAATGTTCACAGAGACAGAGACTGTAGTAGTTCAATCAAC 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 TCCCAAGACCTACCATCATCTGCTTCTGCTGAGCACTGAGAGTGTGTCCGCTTGTGAAC 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 A-----ATGCCACCGTGGAGAACTCGGTCAATGCAAGCGCTCCCATCGCGTGCCT 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 437 AGCGAGAGAAACACTCTCCCAAGCAGCGCTTGCACAGGCTCTTCTGCTGAGCTGCC 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 475 TTTCGATGGTGGGCGAAGATGTGACCTTCCCTGGCGAGTACAGAGATTACTTTC 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 497 TTTGATGTGGGTGGAGACACTACCCAGCCTGGCGAGTACAGAGATTACTACTACCCC 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 535 AACCTCAATCGCGCGCTCTGTGTACATGACCAACGCTTCATGAGACTGCTGAG 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 557 AACAGGACAGCTGCGCGCTGCTTGTGTACATGACCATGACATGCTCATCTCACCGCGAG 616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 595 AATGCTACTTTGTGAGGCTGGCGCTACATATCAAGAGAGAGAGAGAGTCTCTC 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 617 AACGCTCATGAGTCAAGCTGTGTCTATCATGATCAAGAGACCGCGCTGAGAGTGCCTG 676
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 655 GGTCTTCTAGTGGCTATGAGGAGTTGCATATCCCTCTGATCTGACGGCCAACTACT 714
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 677 AACCTCCCAAGCGCTACGCGAGTTGTATATCCCTTGTGTTCTGACTGCCAAGCGATAC 736
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 715 AACGCCATGTGTACCTGCTGCTTCGACGAGGGTGAAGACCAAGCACTGTGGGAGATGTC 774
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 737 AACGAGAGGACACTCTTCTTCCACCAATGAGAGGTTTCCAGCTTCTGGGGGTAGACTT 796
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 775 ATTCATGT----- 782
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 797 AATCAAGGTATAGTTGAGCCCATTTGAGATGCTTCAGATCTTAGAAGATATCATATGA 856
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 783 -----CAACGAGACCGCATGGCTTTCCTTAAC 811
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 857 AATTGTGATGCTCTAACCAAGTCTATACAGAAAGGCTAGAGCTTGGCTTATGCTCAACG 916
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 812 TCAGACCCCGCAAGTACCGTTTCCGATTCTCAACGCTGCGGTGTCTGCTGGCTTC 871
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 917 TGCACCCGCGCAAGTACGCGTTCCGCTTCCCAACGCTGCGGTCTCAAGCTTCTTCCGCTC 976
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 872 TCTACCTGTGAGGACCAAGCTCTCCCAAGCTCAGATTCCTTCCAGTCAATGCTCTG 931
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 977 TGTATCTTGTACCTCTGAGGATTCAGAGACCAAGCTTCCCTCCAGGTCAATGCGCGCTG 1036
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 932 ATGCTGCTCTCTTCAACGCCCGCTTCAAGCCTTAACCTTAACCTTGTGTCGCGAGC 991
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1037 ACGGTGCTCTGTGAGGGCCCTGTTGAACACTGACACTCTGTATCTATATGCGCGAGC 1096
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 992 GTTACAGATCATTTATGACTTACCACTTGTGCTGCGCAGACTTGGACCTGCGCAAG 1051
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1097 GCTGGAGAGTGTATATGACACTTCTACACTTCTGCTGGCAGTCCATGATATCCGCAAC 1156
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1052 TTGCTGAGAACCAAGATGTGCGGACAGAGATGAGTACGCTCGACTCGAGTGTATGC 1111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1157 TTCTGCTGTGACGCTCTGCGGTGTGAGCTGAGTGTGATTAACACTGACAAAGGATGAC 1216
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1112 GCTTCGTGTGAGCTCTGCGCACTGTTGAG---GACAACGACGCTGCCCTCCACTCTC 1168
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1217 GATTCGTGTGTGATGATGATCTTGTAGTGCCTGACACTTCTGAGTGTGCTGACACTCTC 1276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1169 GTGACGTTCTTTC-----TCTCACAAGAAAGGCCCGCCGCAAGC 1213
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1277 GAGATGTTCTTTCGCCGAGGGCGGCAACTGGGACCCGCAACCCCACTGATGAGGAGA 1336
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1214 ACTTCAAGTTTGAACGCAAGCAAGCACTTATCAAGAGTGTGGCTTTCGCGATG 1273
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1337 CTTCACCTTGGCCGCTGCTATGAGCAAGTGAACATCAACGAGTTCCTTCTGCGATG 1396
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1274 TCAATGAGGTGTCTCTGGGCAAGCCGAGCTGGCAAGCTGGAGTTCGGAGCTGAGA 1333
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1397 TCGAAGACCGTCTGCTCCGCAATGTGCCCCGAGACACTGTGTGAGATCTGGCGACTTGA 1456
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1334 ACTCCTTGAAGGCTGAGAGCAACCCCGTCAACATTCACCTTGTGACTTCAAGATCTCA 1393
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1457 ACAACTCCAAAGGTTGAGATCAACCTGTTTCAATTCACCTGTTACCTTCCGAGTCTTT 1516
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1394 AGCGAATGTGTGTGTGGCCAGGTATGCTTACGAGTGTGTGTGTTAAGATGTG 1453
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1517 CTGCTTCCACTGCCCCGTG---AGTGAAGCTTATGAGAGCTGTGCTCAAGGATGTG 1573
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1454 TGTGTTGGGCGAGGGGTGAGAACCTTGACCATGAGAGGCCACATCAACCAACCTGAGC----- 1508
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1574 TCTGCTGCTGTGCTGTGAGGTTGTATGTTGAGGCCCACTACCTCTTCCCTGTAAG 1633
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1509 -----TGGAGCTTACAT 1520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1634 TTCTGCGCTTTTACCTAATGTTTCACTCATGCTAACATCTACAAGTGGGTCTACAT 1693
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1521 GTGCACTGTACAACTCATTTACGAGAGATTAAGCATGATGCTGTATTTCAACGTCAC 1580
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1694 GTTGCACGTGCCCAACATGATCCAGAGAGACCAAGCATGATGAGTGTGCTTCAATGTAC 1753
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1581 CGCCATGAGAGGAAGGATATCTTCAGAGAGACTTTCAGAGACCCCAATGAACCCCAAGTG 1640
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1754 TGTCTCGGTGACTATGCTACACTACACCGATTCATTTGACCCCATGAGACCTCTCTG 1813
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 1641 GCAGCCGCTTCTTACACCGCAACGATTCATGCTCGCGCTGGAACCTTCTCCGCCA 1700
    || || || || || || || || || || || || || || || || || || || || ||
Db 1814 GAGGCCCGCCCTTCTCTCGAGAGATTGCGAATGGCTGGGAGCTTCAAGCGAGCT 1873
QY 1701 GTCCATCACTGCGCGAGTGCAGAGCTGGCCGAGACGACCGCTGACACCGCTGATGA 1760
    || || || || || || || || || || || || || || || || || || || || ||
Db 1874 TGCATCACTGACCGGATTCAGAGATGGCTTACACCCCTTACGCCAGGCTGATGA 1933

RESULT 12
US-09-942-185-3
; Sequence 3, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Convens, Daniel
; APPLICANT: Doornik, Monique
; APPLICANT: van Gastel, Frans
; APPLICANT: Rodrigues, Ana
; APPLICANT: Topozada, Amr
; APPLICANT: De Vries, Cornelis Hendrikus
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Defergent Compositions Comprising No. US20020165113A1el Phenol Ox
; FILE REFERENCE: C7567
; CURRENT APPLICATION NUMBER: US/09/942,185
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-942-185-3

Query Match 25.7%: Score 460.4; DB 9; Length 2095;
Best Local Similarity 59.3%: Pred. No. 2.3e-121;
Matches 996; Conservative 0; Mismatches 521; Indels 163; Gaps 6;

QY 241 ATCATTACCAACCCCTGTCACCGGCAAGACATTTGGTACTATGATCGAGATCAACCA 300
    || || || || || || || || || || || || || || || || || || || || ||
Db 321 ACCGTCCCAACCCCAACACGAGAGACATCTTGTACTACGAGATGGAGTACGCC 380
QY 301 TTTCAGCAAGATTTTACCCACCTTGGCCCGCCACTCTGTGGCTACGATGGCATG 360
    || || || || || || || || || || || || || || || || || || || || ||
Db 381 TTCTCCACACAGATCTACCTGATCTGAGACCGGCAACATGGTTGGATACGATGCAATG 440
QY 361 AGCCCTGTCTACTTTCATGTTCCAGAGAAACAGACTGTAGTTAGTTTCATCAAC 420
    || || || || || || || || || || || || || || || || || || || || ||
Db 441 TCCCGAGACATCACTATCATCTGTTCTGTGGACATGAGAGTGTGTCGGCTTCGTGAAC 500
QY 421 A-----ATGCCACCGTGGAGAACTGTGTCATCTGCACGGCTCCCATCGCTGCCCT 474
    || || || || || || || || || || || || || || || || || || || || ||
Db 501 ACGGAGAAACACCTCTCCCAACAGCTTCACATTCGACGGCTCTTCTCTGACGCTCC 560
QY 475 TTGCATGTTGGGCTGAAGATGATGACCTTCCCTGGGAGAGACAAAGATTACTACTTCC 534
    || || || || || || || || || || || || || || || || || || || || ||
Db 561 TTGATGTTGGGCTGAGACACTACCTCCAGCTGGGAGATACAGAGATTACTACTACCC 620
QY 535 AACCTAACATTCGCGCCGCTTGTGTGATGACATGACACGCTTTCATGAAGATGCTGAG 594
    || || || || || || || || || || || || || || || || || || || || ||
Db 621 AACAGCAGAGCTGCCGATGCTTGTGTGATGACATGACATGACATGTCATCAACGCCGAG 680
QY 595 AATGGCTACTTTGTGAGGCTGGCGCTACATTTATCAAGACGAGGCTGAGATGCTCTC 654
    || || || || || || || || || || || || || || || || || || || || ||
Db 681 AAGGCTTACTATGGGTGAGGCTGTGTCTACATGATCAGAGACCGGCTGAGGTGCTG 740
QY 655 GGTCTCTAGTAGGCTATGCGATGATGATCCCTGATCCCTGAGCGGCAAGTACTAT 714
    || || || || || || || || || || || || || || || || || || || || ||
Db 741 AACTCTCCAGGAGGCTAGCGGAGATTGATATCCCTTGTGCTGCAAGCATATAC 800
QY 715 AACGCCGATGATCCCTGCTGCTGACCGAGGCTGAGACACGAGACCTGTGGGAGATGTC 774
    || || || || || || || || || || || || || || || || || || || || ||
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Db 801 AACGACAGCGACCTCTTCTCCACCAATGAGAGGTTTCCAGTTTGGGGTGACGTT 860
QY 775 ATCCATGT----- 782
Db 861 ATTCAAGTGTAAATTGAGCCCATGAGATGCTTCAGATCTAGAGATATCATGATATGA 920
QY 783 -----CAAGGACAGCCATGAGCTTTCCTTAAG 811
    || || || || || || || || || || || || || || || || || || || || ||
Db 921 AATTGTGATGCTCTAACCAAGTCTATCACAGAACGCTTGGCTATGCTCAAG 980
QY 812 TCCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCGTGTCTGTGGCTCC 871
    || || || || || || || || || || || || || || || || || || || || ||
Db 981 TGCAGCGCGCAGATACCGCTTCCGCTTCAACGCTGCGCTCAAGCTTTCGCTC 1040
QY 872 TCTACCTCGTCAGGACGAGCTCTCCACAGTCAGAATTCCTTCCAAATGCTGCTC 931
    || || || || || || || || || || || || || || || || || || || || ||
Db 1041 TGTATCTTGTACTCTTGAGATTCAGAGACAGACGCTTCCCTTCAGGTCATGCGCTG 1100
QY 932 ATGCTGATCTCTTCAAGCCCGCTTCAGACCTCTAACCTCTACCTTGGTGGCGAG 991
    || || || || || || || || || || || || || || || || || || || || ||
Db 1101 ACGGTGCTCTGTGAGGCGCCCTGTGACACTGACACTCTGTACATCTCTATGCGGAGC 1160
QY 992 GTTACGAGATCAATTATGACTTCCACCACTTTCGTGGCCAGACTCTTGAACCTGCGCAAG 1051
    || || || || || || || || || || || || || || || || || || || || ||
Db 1161 GCTGGGAGGTTGTTATGACTTCTCCACCTGCTGGCCAGCTCATGATATCGCAAC 1220
QY 1052 TTCTGAGACCAACGATGTCGCGAGAGATGATACGCTGCGACTCTCGAGGTATGC 1111
    || || || || || || || || || || || || || || || || || || || || ||
Db 1221 TTCTGCTGTGAGGCTGCTGCTGCTGAGGCTGAGTTGATTAACCTGACGAAAGTCTATGC 1280
QY 1112 GCTTGCAGCTCTGCGACCTGCGACGTTGAG---GACAACAGCGAGTCCCTGACCTCC 1168
    || || || || || || || || || || || || || || || || || || || || ||
Db 1281 GATTGCTGTTGATGAAGTCTTGAAGTCCGCGACACTTCTGAGTGCTGCGCAACTCC 1340
QY 1169 GTGAGCTTCTTCCC-----TCTCACAAGAGAGCCCGCGCACAAAC 1213
    || || || || || || || || || || || || || || || || || || || || ||
Db 1341 GAGATGTTCTCTTCCCGAGGCGGCACTGAGACCCCGCAAMCCCACTGATGAGAGA 1400
QY 1214 ACTTCAAGTTTGAACGACGACGACACTACTGTATCAACGATGTTGGCTTGGCGATG 1273
    || || || || || || || || || || || || || || || || || || || || ||
Db 1401 CTTTCACTTCCGCGCTGTGTAATGAGACAGTGAACAATCAACGAGATTACTCTTCGAGATG 1460
QY 1274 TCAATGAGCGTGTCTGCGCAACCGGAGCTGCGACCGTGTGAGTCTGGAGCTGAGAG 1333
    || || || || || || || || || || || || || || || || || || || || ||
Db 1461 TCGAGAACCTGCTGCTCCGCAATGTCCCGGACACTGTTGATCTGCGCACTTGAAG 1520
QY 1334 ACTCTCTGAGAGCTGAGACGACCCGCTCCACATTCACCTTGTGACTTCAGATCTCA 1393
    || || || || || || || || || || || || || || || || || || || || ||
Db 1521 ACAATCTCAACGAGTTGGAGCTACCCGTTTCACTTCACTCCGTTGACTTCGAGTCTT 1580
QY 1394 AGCGAATGCTGCTGTGCGCAGGCTATGCGCTACAGATCTGCTGTTTAAAGATGTCG 1453
    || || || || || || || || || || || || || || || || || || || || ||
Db 1581 CTGCTTCCACTGCGCCGTGG---AGTGAAGCTTATAGAGCTGTGCTTCAAGAGATGTTG 1637
QY 1454 TCTGTTGGGCAAGGCTGAGACCTGACCATGAGAGCCCACTCAACCAACCTGAGAC----- 1508
    || || || || || || || || || || || || || || || || || || || || ||
Db 1638 TCTGCTGCTGCTGCTGAGGTTGCTATGTTGAGGCCCACTACGCTCTTTCGCCTAAG 1697
QY 1509 -----TGAGACTTACAT 1520
    || || || || || || || || || || || || || || || || || || || || ||
Db 1698 TTCTGCTTTTACTCAATGATGTTTTCACATGATGATCAATCAAGATGATGATCAAT 1757
QY 1521 GTGGCACTGTCAACACCTATTTACAGAGATTAACGATGATGCTGTATTCAACGCTCAC 1580
    || || || || || || || || || || || || || || || || || || || || ||
Db 1758 GTTGCACCTGCAACACCTATTCACGAGAGACGACGATGATGAGCTGTTTCAATGTCAC 1817
QY 1581 CGCATGAGAGAGAAAGATATCTTCAGAGAGACTTCGAGAGACCCCAACCCCAAGT 1640
    || || || || || || || || || || || || || || || || || || || || ||
Db 1818 TGTTCGCTGAGCTATGCTACACTACACGAGTTTCAATGACCCCATGAGAGCTTCTG 1877
QY 1641 GCAGCCGCTTCTTACACCGCAACGATTCATGCTCGCGCTGGAACCTTCTCCGCCA 1700
    || || || || || || || || || || || || || || || || || || || || ||
Db 1878 GAGGCCCGCCCTTCTCTCGAGAGATTGCGAATGGCTGGGAGCTTCAAGCGAGCT 1937
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QY 646 GATGCTCTGCTCTTCTAGTGGCTATGGAGATTGCTGATCTGACGGC 705
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Db 544 GACAACTGTGATCTGCGAGCGGATGCTGAGATATTCGGCTTATATGAT 603

QY 706 AAGTACTATAAGCCGCGATGACCTGCTGACCGAGGTGAGAACGACTGTGG 765
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Db 604 CACCGCTTCTTGAAGACCGTTCTTGTATGAGAGAACCTCCCGATCTTGGGCTGTG 663

QY 766 GGAGATGATCATGTCAACGAGCATGCGCTTCTTACGTCGACCGCCCAAG 825
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QY 826 TACCGTTTCCGATTCTCTCAACGCTGCC 852
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RESULT 15
US-09-950-335A-11/c
; Sequence 11, Application US/09950335A
; Publication No. US20020193330A1
; GENERAL INFORMATION:
; APPLICANT: HONE, DAVID M.
; TITLE OF INVENTION: GENETICALLY ENGINEERED CO-EXPRESSION DNA VACCINES, CONSTRUCTION M
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 4115-128
; CURRENT APPLICATION NUMBER: US/09/950,335A
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6442
; TYPE: DNA
; ORGANISM: Bordetella pertussis
US-09-950-335A-11
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Query Match 2.6%; Score 45.8; DB 9; Length 6442;
Best Local Similarity 48.0%; Pred. No. 0.0091;
Matches 131; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
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QY 934 GCTGCTCTCTTCAAGCCCCGTTGAGACCTTAACCTTACCTTGTGGCGAGCGT 993
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Db 4169 GCCGGCGCGCGGATGACCGGTGTTGGCCCTGCGCCGCAACGAGGCTGCTGGCGG 4110

QY 994 TAGAGATCATATATGACTTCAACCACTTGTGCGGCAACTCTTGACCTGGCAACGTT 1053
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Db 4109 GCCGCCATCAACCTGTCTGTCGCCGACCCGCGCTAGGAAGTTGCTGCGCATTTGCC 4050

QY 1054 GCTGAGACCAAGATGTGCGAGAGATGATGAGTCACTCTCGACCTTCGAGGTGATGCGC 1113
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Db 4049 GGTGATCGAATGTGTCGGCCCCCGCGGATGATGTCTGCACATGCTCGAGCGTTCGAC 3990

QY 1114 TTGCTGTCAGCTGTGCGACTGTTGAGACAACAGCAGTCCCTCCACTCTCCGTGAC 1173
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Db 3989 CTCCACCACTTCCCGACGAGCGGACGCTCGACATGCGGTAATGACATTTCTCGTGGC 3930

QY 1174 GTTCCTTTCCCTCTCTCACAGGAGGCCCCGCC 1206
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Db 3929 CTTGCGGTAGGCGGTTGCTGGGTACCGACGCC 3897
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Search completed: February 13, 2003, 05:15:01
Job time : 105.903 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 18:21:11 ; Search time 2415.3 Seconds
(without alignments)
12009.347 Million cell updates/sec

Title: US-09-218-702-1

Perfect score: 1791

Sequence: 1 gtcaatagctgtcaagtc.....atcttgatcgagagatga 1791

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
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9: gb_est1:*
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11: gb_hlc:*
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17: gb_gss:*
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24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112.4	6.3	600	10	BE188240 M7ATIG in
2	112.4	6.3	700	10	BE187716 BE188099
3	78.8	4.4	664	10	BE188099 CF377-R
4	51.8	2.9	580	13	BU159802 BU159802
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	9	46.2	2.6	608	14	B0094667
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	20	43.6	2.4	646	13	BM635882
	21	43.6	2.4	662	13	BM626865
	22	43.6	2.4	670	13	BM637091
	23	43.6	2.4	682	13	BM652511
	24	43.6	2.4	694	13	BM637162
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	26	43	2.4	337	9	AA788842
	27	43	2.4	409	9	AA731500
	28	43	2.4	426	9	AA807669
	29	43	2.4	442	9	AA807287
	30	43	2.4	451	9	AI189014
	31	43	2.4	463	10	AA576243
	32	43	2.4	500	9	AI126707
	33	43	2.4	507	9	AA977691
	34	43	2.4	538	10	BE379236
	35	43	2.4	571	10	AA007209
	36	43	2.4	646	14	BM794003
	37	43	2.4	777	12	BG744974
C	38	42.6	2.4	435	10	AA575077
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	41	42.6	2.4	486	9	AA825413
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	43	42.6	2.4	497	9	AI187025
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ALIGNMENTS

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BE216983 EST0376 T
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BF059036 7K26d11.x
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BF115462 7n83d03.x
AI432408 t973c04.x
BG321313 Zm04_04d0
AZ302933 GSSBR187
BF258684 HVSMEF001
AI333417 wp67e12.x
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W15474 zc19b12.s1
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BF446871 7n94g10.x
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AI606012 wk93c05.x
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AA411507 zv27h02.s
AI200611 qf87e08.x

RESULT 1
LOCUS BE188240 600 bp mRNA linear EST 25-SEP-2000
DEFINITION M7ATIG in vitro expressed cDNAs Cladosporium fulvum CDNA similar to
ACCESSION BE188240
VERSION BE188240.1 GI:8667479
KEYWORDS
SOURCE
ORGANISM Cladosporium fulvum.
Cladosporium fulvum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetochytriumycetes incertae sedis; Mycosphaerellaceae; mitosporic
Mycosphaerellaceae; Cladosporium.
REFERENCE
1 (bases 1 to 600)
AUTHORS Clark,A.J., Rasmussen,S.W. and Oliver,R.P.
TITLE In vitro expressed genes of Cladosporium fulvum
JOURNAL Unpublished (2000)
COMMENT Contact: R.P. Oliver
Necrotrophic Phytopathology Research Centre
Murdoch University
SABC, Perth 6150, Western Australia
Tel: +61-8-9360-7404
Fax: +61-8-9360-6303
Email: roliver@central.murdoch.edu.au
High quality sequence stop: 600
POLYA-No.
location/Qualifiers
1..600
/organism="Cladosporium fulvum"

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/strain="Race 4"
/db_xref="taxon:5499"
/clone.lib="In vitro expressed cDNAs"
/tissue.type="Mycelium"
/note="Vector: Lambda bluescript: A mixture of mycelial
cultures grown in liquid B5 for 48 hours and transferred
for 24 hours to media lacking carbon, nitrogen or
supplemented with hydrogen peroxide"
BASE COUNT      131 a      176 c      162 g      128 t      3 others
ORIGIN

Query Match      6.3%; Score 112.4; DB 10; Length 600;
Best Local Similarity 55.9%; Pred. No. 1.8e-17;
Matches 313; Conservative 0; Mismatches 238; Indels 9; Gaps 5;

OY 1062 CAACGATGTCGGGAGGAGGATGATGACCGCTGCACATCGAGGTGATGCGCTGCTGCT 1121
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DB 42 CAACAGGGGGGACAAACACGNGTNCATACACCGACAGGTGATGAGTTGCTGCT 101
OY 1122 CAG--CTCTGGCACTGTTGAGGACAAACAGCCAGGTCCCTCCACTCTCCGTGACGTTCC 1178
    |||||
DB 102 TGGAGACAGCGTCACCGAGGTCCAAACAAACAGTACCATCACTGACGCTGCCAT 161
OY 1179 TTTCCTCTCTACACAGGAAGCCCCCGACAAAGCACTTCAAGTTGAAACGACAAACG 1238
    |||||
DB 162 CGACTGGCCAGCGACGACGACACTATTGACAAAGACCTTCAACTTCCAGATGGCGCGC 221
OY 1239 ACACACTGCTGA---TCAGAGATGTTGGCTTGGCGATGTCATGATGAGCGTCTGCGCAA 1295
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DB 222 GGAAGTGTGAGACCGGTCAATAGCGCTGATTTACAGCGACCCGAACTCCGCTGCTGCTAG 281
OY 1296 GCCGAGCTCGGACCGGTGAGGTCTGGAGCTCGAGAACTCCTCTGGAAGGCTGAGCCA 1355
    |||||
DB 282 GCCGCCAACAAAGGACACTGTGAGGCTTGGCGCTCGTGACACTGGGCGTCCGCTGCCA 341
OY 1356 CCCCCTCCACTTACACAGGAAGCCCCCGACAAAGCACTTCAAGTTGAAACGACAAACG 1415
    |||||
DB 342 CCCAGTACATATCCATCTGTCAACATGCAAGGTCTCTGCGACTGTGGTGCCCGCTG 401
OY 1416 GGTCAATGCCCTACGAGTGTGCTGCTTAAAGATGTCGTCGTGGTGGGACGGGGTGAAG 1475
    |||||
DB 402 CCTCATGCGCATACGAAAGCTGTGCTGTAAGACGTCGTTATCTGCTGCTGCGCAGAT 461
OY 1476 CTTGACCATTCGAGGCCCATACCAACCTGAGCTGAGCTTACATGTGGACATGTACAA 1535
    |||||
DB 462 TGTGACAGTGTGCTCTTTTACGCTCTTGAACGG-CTTGACATGTTTCATTGTCAC-A 519
OY 1536 CCTCATTCACGAGGATACGACATGATG-CTGTATTCAACGTCACCGCATGGAGAGAA 1594
    |||||
DB 520 CCTGTACACGAAGATCACACCATGATGGCCGCTTCAACACGACACCCCTTGAACGCTG 579
OY 1595 AGGATATCTTCAGAGGAC 1614
    |||||
DB 580 GGCTACGACTTCAACAGCAC 599

RESULT 2
BE187716 700 bp mRNA linear EST 25-SEP-2000
LOCUS BE187716
DEFINITION Billrubin in vitro expressed cDNAs Cladosporium fulvum cDNA similar to
ACCESSION BE187716
VERSION BE187716.1 GI:8666955
KEYWORDS EST.
SOURCE Cladosporium fulvum.
ORGANISM Cladosporium fulvum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothyrionmycelis incertae sedis; Mycosphaerellaceae; mitosporic
Mycosphaerellaceae; Cladosporium.
REFERENCE 1 (bases 1 to 700)
AUTHORS Clark,A.J., Rasmussen,S.W. and Oliver,R.P.
TITLE In vitro expressed genes of Cladosporium fulvum
JOURNAL Unpublished (2000)
```

```
COMMENT
Contact: R.P.Oliver
Neurotrophic Phytopathology Research Centre
Murdoch University
SABC, Perth 6150, Western Australia
Tel: +61-8-9360-7404
Fax: +61-8-9360-6303
Email: roliver@central.murdoch.edu.au
High quality sequence stop: 700
POLYA-No.

FEATURES
source
location/Qualifiers
1..700
/organism="Cladosporium fulvum"
/strain="Race 4"
/db_xref="taxon:5499"
/clone.lib="In vitro expressed cDNAs"
/tissue.type="Mycelium"
/note="Vector: Lambda bluescript: A mixture of mycelial
cultures grown in liquid B5 for 48 hours and transferred
for 24 hours to media lacking carbon, nitrogen or
supplemented with hydrogen peroxide"
BASE COUNT      158 a      206 c      183 g      146 t      7 others
ORIGIN

Query Match      6.3%; Score 112.4; DB 10; Length 700;
Best Local Similarity 55.9%; Pred. No. 2e-17;
Matches 313; Conservative 0; Mismatches 238; Indels 9; Gaps 5;

OY 1062 CAACGATGTCGGGAGGAGGATGATGACCGCTGCACATCGAGGTGATGCGCTGCTGCT 1121
    |||||
DB 42 CAACAGGGGGGACAAACACGNGTNCATACACCGACAGGTGATGAGTTGCTGCT 101
OY 1122 CAG--CTCTGGCACTGTTGAGGACAAACAGCCAGGTCCCTCCACTCTCCGTGACGTTCC 1178
    |||||
DB 102 TGGAGACAGCGTACCGAGGTCCAAACAAACAGTACCATCACTGACGCTGCCAT 161
OY 1179 TTTCCTCTCTACACAGGAAGCCCCCGACAAAGCACTTCAAGTTGAAACGACAAACG 1238
    |||||
DB 162 CGACTGGCCAGCGACGACGACACTATTGACAAAGACCTTCAACTTCCAGATGGCGCGC 221
OY 1239 ACACACTGCTGA---TCAGAGATGTTGGCTTGGCGATGTCATGATGAGCGTCTGCGCAA 1295
    |||||
DB 222 GGAAGTGTGAGACCGGTCAATAGCGCTGATTTACAGCGACCCGAACTCCGCTGCTGCTAG 281
OY 1296 GCCGAGCTCGGACCGGTGAGGTCTGGAGCTCGAAGAACTCCTCTGGAAGGCTGAGCCA 1355
    |||||
DB 282 GCCGCCAACAAAGGACACTGTGAGGCTTGGCGCTCGTGACACTGGGCGTCCGCTGCCA 341
OY 1356 CCCCCTCCACTTACACAGGAAGCCCCCGACAAAGCACTTCAAGTTGAAACGACAAACG 1415
    |||||
DB 342 CCCAGTACATATCCATCTGTCAACATGCAAGGTCTCTGCGACTGTGGTGCCCGCTG 401
OY 1416 GGTCAATGCCCTACGAGTGTGCTGCTTAAAGATGTCGTCGTGGTGGGACGGGGTGAAG 1475
    |||||
DB 402 CCTCATGCGCATACGAAAGCTGTGCTGTAAGACGTCGTTATCTGCTGCTGCGCAGAT 461
OY 1476 CTTGACCATTCGAGGCCCATACCAACCTGAGCTGAGCTTACATGTGGACATGTACAA 1535
    |||||
DB 462 TGTGACAGTGTGCTCTTTTACGCTCTTGAACGG-CTTGACATGTTTCATTGTCAC-A 519
OY 1536 CCTCATTCACGAGGATACGACATGATG-CTGTATTCAACGTCACCGCATGGAGAGAA 1594
    |||||
DB 520 CCTGTACACGAAGATCACACCATGATGGCCGCTTCAACACGACACCCCTTGAACGCTG 579
OY 1595 AGGATATCTTCAGAGGAC 1614
    |||||
DB 580 GGCTACGACTTCAACAGCAC 599

RESULT 3
BE188099 664 bp mRNA linear EST 25-SEP-2000
LOCUS BE188099
DEFINITION CFC377-R In vitro expressed cDNAs Cladosporium fulvum cDNA similar
to Billrubin in vitro expressed precursor, mRNA sequence.
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ACCESSION	BE188099	GI:8667338
VERSION	BE188099.1	GI:8667338
KEYWORDS	EST.	
SOURCE	Cladosporium fulvum.	
ORGANISM	Cladosporium fulvum	
REFERENCE	Eukaryota: Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et	
AUTHORS	Clark, A.J., Rasmussen, S.W. and Oliver, R.P.	
TITLE	Unpublished (2000)	
JOURNAL	Contact: R.P. Oliver	
COMMENT	Necrotrophic Phytopathology Research Centre	
	Murdoch University	
	SABC, Perth 6150, Western Australia	
	Tel: +61-8-9360-7404	
	Fax: +61-8-9360-6303	
	Email: roliver@central.murdoch.edu.au	
	High quality sequence stop: 664	
	POLYA-NO.	
FEATURES	Location/Qualifiers	
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	/organism="Cladosporium fulvum"	
	/strain="Race 4"	
	/db_xref="taxon:5499"	
	/clone_lib="In vitro expressed cDNAs"	
	/tissue_type="Mycelium"	
	/note="Vector: Lambda bluescript; A mixture of mycelial	
	cultures grown in liquid B5 for 48 hours and transferred	
	for 24 hours to media lacking carbon, nitrogen or	
	supplemented with hydrogen peroxide"	
BASE COUNT	149 a 174 c 174 g 140 t	27 others
ORIGIN		
Query Match	4.4%	Score 78.8; DB 10; Length 664;
Best Local Similarity	58.1%	Pred. No. 6e-09;
Matches 176; Conservative	0; Mismatches 120; Indels 7; Gaps 2.	
QY 758	ACCTGTGGGAGATGTCAATCATGTCAACGAGACCATGGCCTTCCCTTAACGTCACG	817
DB 32	ACTTCTTGGGGATACGATTCGAGTGAAGTCCGACCATGCCATATCTGAACGTCGAC	91
QY 818	CCCGCACTACCGTTTCCGATTCCTCAACGCGTGCCTGTGCTGGCTCTCTAC	877
DB 92	CTCGCAATGACGATTCAGACTCTT-----TGATATGCTCTAAGCAGATCTTACGACA	145
QY 878	TGCTGACGACCAAGCTCTCCCAACGTCACAATTCCTTCCAACTCATTTGCTGTGCTG	937
DB 146	TCTACATTTGATGATGAGAACCAACCAATTCATTCAGAGTCAATGGCTCAGACTCG	205
QY 938	GTCCTTCACAGCCCGGCTTCAGAGCTCTAACCCCTTACCTGCTGTGGCGAGGCTTACG	997
DB 206	GCTATTTGGCGGCTTCGCGCGCAAGAGAGTGTATTTTCATTTGGAGAGCCCT-TG	264
QY 998	AGATCATATTTGACTTCCACCACTTTGCTGGCGCAAGCTTGTACCTGGCAAGCTTGGTG	1057
DB 265	AGATCATATTTGACTTTCATTTGCTTTGCTGGCGCAAGATATATTTCTATTTTCANCGGTCAAC	324
QY 1058	AGA 1060	
DB 325	AGA 327	
RESULT 4		
LOCUS	BU159802/c	
DEFINITION	BU159802 full length cDNA library, chloronemat and young	
ACCESSION	BU159802	
VERSION	BU159802.1	
KEYWORDS	EST.	

SOURCE	ORGANISM
REFERENCE AUTHORS	Physcomitrella patens subsp. patens. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella. 1 (bases 1 to 580) Fujita,T., Shin-I,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T. , Carinci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe ,M.
TITLE	Comparison of the moss Physcomitrella patens genome with flowering plants genome
JOURNAL	Unpublished (2002)
COMMENT	Contact: Tadasu Shin-i National Institute of Genetics 111 Yata, Mishima, Shizuoka 411-8540, Japan Tel.: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified IPS phage vector (Mo bi Tec, Germany). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. cDNA instert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonemata were blended by the POLYTIRON, and then cultivated on the BCDAY medium for 13-14 days under the continuous light.
FEATURES	location/Qualifiers 1..580 /organism="Physcomitrella patens subsp. patens" /db_xref="taxon:145481" /clone_1pb="full length cDNA library, chloronemata and young gametophores" /tissue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"
BASE COUNT	124 a 138 c 170 g 148 t
ORIGIN	
Query Match	2.9% Score 51.8; DB 13; Length 580;
Best Local Similarity	56.9%; Pred. No. 0.037; Indels 0; Gaps 0;
Matches	95; Conservative 0; Mismatches 72;
Db	753 CCAGACCTGTGGGAGATGTCATCATGCATCAAGCAGACGCCATTGCTTAAGT 812 415 CCCGAGATTTTCGGCGACGTATCTCTGTGAACGGCAAAGCATGGCTTACTGCTCT 416
OY	813 CCAGCCCGCAAGTACGCTTGTCGATTCCTCAACGCTGCCGTCTGCTTGGCTCTT 872 Db 415 CAAGCTCGCAAGTACGCTTCCGTCGTGTGAATGGTGGCAATGTTGGAGCT 356
OY	873 CTACCTGTCAGGACCAGCTCTCCCAAGCTCAGATTCTTTCCAAG 919 Db 355 TTCTCTGAGACCCACAACCGCGCTTCATTCATAATGGTACGACG 309
RESULT 5	BP258534
LOCUS	BP258534
DEFINITION	BP258534 599 bp mRNA linear EST 22-OCT-2001 HVSMEF0015P21f Hordeum vulgare seedling root EST library HYCDNA000701 (Etioiated and unstressed) Hordeum vulgare cDNA clone HVSMEF0015P21f, mRNA sequence.
ACCESSION	BP258534
VERSION	BP258534.2 GI:13119477
KEYWORDS	EST.
SOURCE	Hordeum vulgare.
ORGANISM	Hordeum vulgare
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae , Triticeae; Hordeum. 1 (bases 1 to 599) Wing,R., Close,T.J., Kleinhofis,A., Wise,R., Begum,D., Fritsch,D., Yu

FEATURES		Class: shotgun.	
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	/note="Vector: Lambda DASH II; sequenced using Li-Cor sequencer"		
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ORIGIN			
Query Match	2.7%; Score 47.6; DB 17; Length 1128;		
Best Local Similarity	43.5%; Pred. No. 0.66;		
Matches 215; Conservative	0; Mismatches 279; Indels 0; Gaps 0;		
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DB	841 GGGCCGACAATCCGCGTGTGGAAGGCGATGACGTTAAACTATCTATPACAAACGCCCTG 782		
QY	427 ACCGTGGAACCTCGGTCCATCTGACAGCGCTCCCATCGCGCCCTTTCGATGGTTGG 486		
DB	781 GCGGAATATGCTCCATGACGTTCTGTGTTACTGTGTGTCGCGGGCCCTGATGGGTGGC 722		
QY	487 GCTAAGATGTGACCTTCCCTGGGAGTACAAAGATTACTCTTTCACCAACTCAATCC 546		
DB	721 CCGGCGCTATGATGTCCCGAACCGGACGCTGGCGCGCGGTGTCGATTCGTGAGAGC 662		
QY	547 GCCCGCTTTCGTGTGTACCATATGACACCGCTTTCATGAAAGACTGTGAGATGCTACTTTT 606		
DB	661 GCCGCGACGCTGTGTATATACGCTAACACGCGCTTAACCGCACCGCAGGTGTATAC 602		
QY	607 GGTACGCTGCGCGCTTACATTATCAACGACGAGCGCTGAGATGCTCTGCTTCTCTAGT 666		
DB	601 GGGCTGGAGGAATGTGGCTGTGTGCAACGACATCACTAAACGCTGCCATTTCCGAAC 542		
QY	667 GGCTATGGCGAGTTCGATATCCCTCTGATCTCTGACGCCCAAGTACTATTAACGCCGATGGT 726		
DB	541 CATPACGCGGTGATGATGATTTCCCTCATTTATCCAGATTAACGGCGCTGATTAATTTGGG 482		
QY	727 ACCCGGCTTGTGACGAGGAGTGAGACGACGACCTGTGGGAGATGTCATTCATGCTCAAC 786		
DB	481 ACGCGGAGTACAGGGAACCGGGAACCGGTGGTTTGTGCGGATACCGTCTGTGTGAAC 422		
QY	787 GGACAGCCATGAGCCCTTCTCTTAACGTCCAGCCCGCAAGTACCGTTCGATTCCTCAAC 846		
DB	421 GGGCGGCAAAACCCCTATGTGGAATGTGTCCCGCGCTGGGTTCGGTTACGTTTGTGAAC 362		
QY	847 GCTGCCGTGTCTCG 860		
DB	361 GCCTTCGAACCTCGCG 348		
RESULT 8			
LOCUS	BE216983		
DEFINITION	BE216983 848 bp mRNA linear EST 03-JUL-2000		
LOCATION	EST0376 Triticum aestivum Lambda Zap Triticum aestivum cDNA clone		
ACCESSION	JAL5A06.T3 5', mRNA sequence.		
VERSION	BE216983		
KEYWORDS	BE216983.1 GI:8904523		
SOURCE	EST.		
ORGANISM	bread wheat.		
	Triticum aestivum		
	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:		
	Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; Pooidaeae		
	; Triticeae; Triticum.		
	1 (bases 1 to 848)		
REFERENCE	Anderson,J.M., Williams,C.E. and Goodwin,S.B.		
AUTHORS	Analysis of an EST database reveals a probable CF2 resistance gene		
TITLE	homolog in wheat		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Anderson, J.M.		

Crop Production & Pest Control Research Unit
USDA-ARS
1150 Lilly Hall, West Lafayette, IN 47907, USA
Tel.: 765-494-5565
Fax: 765-496-2926
Email: janderson@purdue.edu
Seq primer: T3
High quality sequence stop: 848.
Location/Qualifiers
1. 848

FEATURES
Source
/organism="Triticum aestivum"
/strain="P29"
/db_xref="taxon:4565"
/clone_id="Triticum aestivum Lambda Zap"
/tissue_type="leaf"
/dev_stage="9 day old seedlings"

BASE COUNT
ORIGIN
139 a 312 c 263 g 134 t

Query Match
Best Local Similarity 48.3%; Pred. No. 0.61;
Matches 190; Conservative 0; Mismatches 176; Indels 27; Gaps 1;

OY 519 GGATTACTACTCTTTCCCAACTACCAATCCGCCGCTTCGTGTGGTAACCATGACCAGCCTTT 578
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 16 GCGCTACGAGTGATCCGGAACAGCACGCCTCCCGGTAACTCTGTGTACCAAGCACAGCCAT 75
OY 579 CATGAAGAAGCTGTGAGTAATGCTTACTTTGTGTGACGCTGGCGCTCATATTACACGACGA 638
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 76 GGGCTTCACCCCGGCAACATCTCTGTGGGCTCTCGGCGGTACCGGTACCGTGTGGCGGACCC 135
OY 639 GCGTAGAGATGCTCTCGGCTCTTCTAAGTGGCATGGGAGTTGCATTCCTCTGTATCT 698
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 136 GGCACACGAGGGGCCCCCTCGGCTCTCCCTCCGCGCGGAGATTGACACGGAACCTGTCTCT 195
OY 699 GACGGCCAAGTATATAACCCGATGTACCTGCTTGTGACGAGGAGGTGAGAACAG-- 756
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 196 CTTGACCGCGGACTTCAGGAGGAGCGGCGGCTTTCATGAACGCCACGCGCACACACACC 255
OY 757 -----GACCTGGGGGAATGTCAATGCATTCATCAACGGACA 791
DB 236 GCAGCTGCACCCGCGAGTGGACACCCGAGTACTTGGGCCCCGTCGTGCGGCAACGGGCAA 315
OY 792 GCCATGGGCTTTCTTAACGTCCACAGCCCAGCAAGTACGTTTCGATTCCTCAACAGCTGC 851
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 316 GGCCTGGGCTTCGTCGCGGCGTGGCGGCGGCGGAGTACGCGTTCCGCATCTCAACGCCAG 375
OY 852 CGTGTCTGTGCTTGGGCTCTCTACTCTGTACG 884
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 376 CAACGCGCGCTTCTTCGCGCTCTCTCTCGCG 408

RESULT 9
LOCUS B0094667
DEFINITION BO094667 608 bp mRNA linear EST 08-Apr-2002
VERSION san50c09.y1 Gm-cl052 glycine max cdna clone SOYBAN CLONE ID:
KEYWORDS Gm-cl052-3185.5' similar to TR:Q9ZMQ5 Q9ZMQ5 UDP-GLYCOSE:FLAVONOID
GLYCOSYLTRANSFERASE.; mRNA sequence.

ACCESSION B0094667
VERSION B0094667.1 GI:20075884
SOURCE soybean.
ORGANISM Glycine max
Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
Shenmaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvelli,V., Rhana,
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Stepien,M., Theisling,B., Allen,M., Bowers
.Y., Person,B., Swallier,T., Gibbons,M., Pape,D., Harvey,N., Schurk

TITLE
JOURNAL
COMMENT

R. R. Rittner, E. S. Kohn, S. Shin, T. Jackson, Y. Cardenas, M. McCann, R. R. Waterston, R. and Wilson, R. Public Soybean EST Project
Unpublished (1999)
Contact: Snomemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact: cu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gtbco
High quality sequence stop: 423.

FEATURES

1. .608
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOTBEAN CLONE ID: Gm-cl052-3185"
/clone_1ib="Gm-cl052"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="1 week old"
/lab_host="DH10B"
/note="vector: bluescript II SK+, Site_1: EcoRI, Site_2:
XhoI; The Harosoy NIL was constructed and seed was
provided by Dr. J. Specht, University of Nebraska
(Shoemaker and Specht, 1995). The cDNA library was
constructed from mRNA isolated from whole seedlings of 1
week old greenhouse grown plants. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site and a 3'
anchor. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by XhoI digestion. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the bluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(GibcoBRL). The library was constructed in cooperation
with Dr. Paul Keim's laboratory at Northern Arizona
University."

BASE COUNT	131 a	241 c	105 g	131 t
ORIGIN				

Query Match	2.68;	Score 46.2;	DB 14;	Length 608;
Best Local Similarity	51.28;	Pred. No. 0.98;		
Matches 108; Conservative	0;	Mismatches 103;	Indels 0;	Gaps 0;

QY	820	CGCAAGTACGGTTTCCGATTCCTCAAGCGTGCCTGTCTGGTGGCTCTCTACTTC	879
Db	45	CACATGATCCCTCTCTCTGCGCATGGCCACACTCTTCTCCACTGGCGGCCACAGTACC	104
QY	880	GTCAGAGCAGCTCTCCCAACGTCAGATTCTTCCAGTCATATGGCTCTGATGCGGT	939
Db	105	ATCATCAACAGCCCCCTCCAGGCCCAATCTCTCGAAATCCCTCCCTCCACACCTCTC	164
QY	940	CTCCTTCAAGCCCCCGTTCAAGACCTTAACTCTACCTGCTGTGGCGAGCGTTACGAG	999
Db	165	CTCCGCCCTCCACACCGTTTCAGTGTCCCTCCCAATAGGTGGGTCTTCCGAGCGGATGAA	224
QY	1000	ATCATATATGACTTCACCAACTTGGCTGGCC	1030
Db	225	AACATCTCCGCCGTCCTCCGATTTGGACAGCC	255

RESULT 10	LOCUS	DEFINITION	ACCESSION
BF059036	463 bp	NCI-CGAP_OV18 Homo sapiens CDNA clone IMAGE:3476621 3'	BF059036
		Similar to TR:Q03928 Q03928 BRAHMA RELATED PROTEIN 1 ; mRNA	
		Sequence.	
		BF059036	

VERSION
KEYWORDS
SOURCE
ORGANISM

VERSION	BF059036.1	GI:10812932
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
	1 (bases 1 to 463)	
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap	
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
TITLE		

JOURNAL
COMMENT

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaps@emall.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michel R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed By: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN, send email to: info@image.lnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 341.

FEATURES
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TM6E:3476421"
/clone_lib="NCI_CGAP_Ov18"
/tissue_type="fibrothecoma"
/lab_host="DH10 (phage-resistant)"
/notes="Organ: ovary; Vector: pTRT3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - 0190(dT) primer (5'
TGTTCACCAATCTCAAGTCGAGCGCGCGCAGCACTTTTCTTTTCTTTT
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTRT3 vector. Library
went through one round of normalization, and was
constructed by Benito Soares and M. Fatima Bonaldo.
"

```

BASE COUNT	133 a	127 c	128 g	75 t
ORIGIN				

Query Match	2.58;	Score 44.6;	DB 12;	Length 463;
Best Local Similarity	45.98;	Pred. No. 2.1;		
Matches 152;	Conservative 0;	Mismatches 179;	Indels 0;	Gaps 0;

OY	1461	GGGGAGGGGTGAACCCCTGCATCTCAGAGGCCCTCAACAACCTGGACTGAGTGGCTTTAAT	1520
Dd	88	GGACAGCAGTGGACGTCACTCAGCAGAGGTCTTCATCCAGCTGCGCCTCGCGAAAGAGACT	147
OY	1521	GTGGCACTGTCAACAACCTCATTTACAGAGATAACGACATGATGCTGTATTCAACGTCAC	1580
Dd	148	GCCCCATTACTACGAGGTCTATCGCAAAGCCCGTGAGCTTCAAGAAGATTAAGAGCCGAT	207
OY	1581	CGCCATGAGAGAGAAAGGATATTCTTAGAGAGCACTTCGAGAACCCCATFAMCCCACAATG	1640
Dd	208	TGCGAACCAACGATACCAGCCTCAACAGCACTAAGAAAGAGAGTCATCTCTCTGTGGCA	267
OY	1641	GCGCGCCGTTCTTACAAACCGCAACGACTTCCATGCTCGCGCTGGAACTTCTCCGCCGA	1700
Dd	268	GAACGCACAGACCTTCAMAACCTGGAGGGCTCCCTGATCTATTGAAGACTCCATCGTTCGA	327
OY	1701	GTCCATACTGCCCCGATGAGAGAGCTGGCGAGCAGAGACCCGATACCCGCTCGATGA	1760
Dd	328	GTGCGTCTTACCAACGCGTGGCGGAGAAAATTCGAAAGAGAGATGACAGTGAATGGAGTA	387
OY	1761	GATCCTGGAAGATCTTGGAAATCGAGAGATRA	1791
Dd	388	GAGTGAAGAGAGAAAGAGGCGAGGAGGANA	418

RESULT 11

AI394530 481 bp mRNA linear EST 30-MAR-1999
 LOCUS tff7b06.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2105267 3'
 DEFINITION similar to SR:SNR3_HUMAN P51532 POSSIBLE GLOBAL TRANSCRIPTION
 ACTIVATOR SNR2L3 ; mRNA sequence.
 ACCESSION AI394530
 VERSION AI394530.1 GI:4224077
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 481)
 NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/Brn23), Tumor Gene Index
 UNPUBLISHED (1998)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bbrp/image/image.html
 Insert Length: 905 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 452.
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 Location/Qualifiers
 1..481
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 /db_xref="taxon:9606"
 /clone="IMAGE:2105267"
 /clone_lib="NCI-CGAP_Brn23"
 /tissue_type="glioblastoma (pooled)"
 /lab_host="DH10B"
 /note="Organ: Brain; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGGCATATCTTTTTTTTTTTTTTTTTTTT
 T 3'] : double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT73 vector.
 Library is normalized, and was constructed by Bento
 Soares and M.Fatima Bonaldo."
 BASE COUNT 138 a 128 c 141 g 74 t
 ORIGIN
 Query Match 2.5%; Score 44.6; DB 9; Length 481;
 Best Local Similarity 45.9%; Pred. No. 2.1;
 Matches 152; Conservative 0; Mismatches 179; Indels 0; Gaps 0;
 Oy 1461 GGGCAGGGGTGAGACCTGACATGAGGCCCAACCACTGACGAGCTTACAT 1520
 Db 70 GAGCAGCAGGTGAGCTCAGCTCAGCAGGTCTTCATCCAGCTGCCGAAAGAGCT 129
 Oy 1521 GTGGCACTGTCAACAATCATTTACAGAGATTAAGCATGATGGCTGTATTCAAGCTAC 1580
 Db 130 GCGCAGTACTAGAGCTCATTCGCAAGCCCTGGACATTCAGAAAGATTAAGAGCGCAT 189
 Oy 1581 CGGCATGGAGGAAGGATATCTTCAGAGAGACTTCAGAGACCCCATGAACCCCAAGTG 1640
 Db 190 TCGCAACCAAGTACCGCAGCCTCAACGACCTATAGAGAGAGCTCATCTCTGTGCA 249
 Oy 1641 GCGCGCGCTTCTTCAACCGCAAGCAAGCACTTCGCGCTGGAAACTTTCTCGCCCA 1700
 Db 230 GAGCAGCAGACCTTCAAGCTTGAGAGGCTCTCTGATCTATGAAGACTTCATGCTTGA 309
 Oy 1701 GTTCATCACTGCCGAGTGCAAGAGCTGGCGAGCAGAGAGCCGTACAAACCGCTGATGA 1760

Bf115462 475 bp mRNA linear EST 24-OCT-2000
 LOCUS 7n83d03.x1 NCI CGAP Ov18 Homo sapiens cDNA clone IMAGE:3571229 3'
 DEFINITION similar to FR:Q63928 Q63928 BRAHMA RELATED PROTEIN 1 ; mRNA
 sequence.
 ACCESSION Bf115462
 VERSION Bf115462.1 GI:10984864
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 475)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 UNPUBLISHED (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
 Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 334.
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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:3571229"
 /clone_lib="NCI-CGAP_Ov18"
 /tissue_type="fibrotheoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Ovary; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGGCATATCTTTTTTTTTTTTTTTTTTTT 3'] :
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 133 a 132 c 136 g 74 t
 ORIGIN
 Query Match 2.5%; Score 44.2; DB 12; Length 475;
 Best Local Similarity 45.9%; Pred. No. 2.7;
 Matches 151; Conservative 0; Mismatches 178; Indels 0; Gaps 0;
 Oy 1463 GCAGGGGTAGACCTGACCATTCAGAGCCCACTACCAACCTTGAGACTGACCTTACAT 1522
 Db 93 GCAGAGTGTAGAGCTCAGCTCAGCAGAGCTTCATCAGCTGCCCTGCGAAAGAGACTGC 152
 Oy 1523 GGCAGCTGACAAACCTTCACAGAGATTAAGCAATGATGGCTGTATTCAACGTCACCG 1582
 Db 153 CCGAGTACTAGAGCTCATTCGCAAGCCCGTGGACTTCAAGAAGATTAAGAGCGCATTC 212
 Oy 1583 CCATGGAGAGAGAGGATATCTTCAGAGAGACTTCGAGAGACCCCATGAACCCCAAGTGC 1642
 Db 213 GCACCAAGATAGACCGCAGACCTTCAACGACCTTAGAGAGAGCGTCAATGCTCTGTGCA 272

QY	1643	GGGCGCTTCTTACAAACCCAGCAGCTTCATGCTCGCGCTGGAACCTTCTCCGCCAGT	1702
Db	273	AGCAGACAGACTTCAACCTCGAGGAGCTCCCTGATCTATGAAACATCCATCTGCTTGCACT	332
QY	1703	CCATCTACTCCCGAGTGCAGGAGCTGCGCCAGCAGAGAGCCGTACACCGCCCTCGATGAGA	1762
Db	333	CGGTCTTACACGAGCGTGGCGGCGAAAAATTCGAGAGAGATGACAGTGAAGCCGATGAGA	392
QY	1763	TCCGTGAGGATCTTGGATCGAGGAGTAA	1791
Db	393	GTGAGGAGAGGAGAGGCGCAGAGAGAA	421
RESULT 13			
LOCUS	A1432408	541 bp	mRNA linear EST 30-MAR-1999
DEFINITION	tg73c04.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2114406		
ACCESSION	A1432408		
VERSION	A1432408.1	GI:4281458	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 541)		
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-tr@mail.nih.gov		
	This clone is available royalty-free through LLNL; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	Insert Length: 861 Std Error: 0.00		
	Seq primer: -400p from Gibco		
	High quality sequence stop: 499.		
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	/clone="IMAGE:2114406"		
	/clone_jib="Soares_NHMPu_S1"		
	/tissue_type="Pooled human melanocyte, fetal heart, and		
	pregnant uterus"		
	/lab_host="DH10B"		
	/note="Organ: mixed (see below); Vector: p7773D-Pac		
	(Pharmacia) with a modified polylinker; Site 1: Not I;		
	Site 2: Eco RI; Equal amounts of plasmid DNA from three		
	normalized libraries (melanocyte 2NBHb, pregnant uterus		
	NBHPu, and fetal heart NBHN19W) were mixed, and ss circles		
	were made in vitro. Following HAP purification, this DNA		
	was used as tracer in a subtractive hybridization		
	reaction. The driver was PCR-amplified cDNAs from pools of		
	5,000 clones made from the same 3 libraries. The pools		
	consisted of 1 M.A.G.E. clones 260232-265223,		
	340488-345479, and 484488-489479."		
BASE COUNT	148 a 150 c 167 g 76 t		
ORIGIN			
Query Match	2.5%: Score 44.2; DB 9; Length 541;		
Best Local Similarity	45.9%: Pred No. 2.9; Indels 0; Gaps 0;		
Matches 151; Conservative 0; Mismatches 178; Indels 0; Gaps 0;			
QY	1463	GCAGGGGTAGACCCGTGACCATCGAGCCGACCTACCAACCTCGAGCTGAGCTTACATGT	1522
Db	93	GCAGCAGTGAGAGCTGAGCAGCAGAGAGCTTCATCCAGCTGCCGCGGAAGAGGCTGC	152
QY	1523	GGCAGCTGTACAACTCATTTACAGAGAGATACAGCATGATGCGCTGATTTCAACGTACCG	1582
Db	153	CCGAGTACACGAGCTATCCGACCCGCTGAGCTTCAAGAAAGTAAAGAGCCATTC	212

OY	1583	CCATGAGAGAGAAGGGATTCTTCACGAGAGACTTGAGAGACCCTTGAACCCCAAGTGGC	1642
Db	213	GCMAACCAAAAGTAACCGCAGGCCCTAACACGACCTTAGAAGAAGCATGTCTCTGTGCCAGA	272
OY	1643	GCGCGCTTCTTACAACCGCACGACCTTCGATGCTGGCGCTGGAACCTTTCCGCCGAGT	1702
Db	273	ACGCACAGACCTTCAACCTTGAGAGGCTTCTCTGATCTATTGAAGACTCCATCGCTTGCGAGT	332
OY	1703	CCATCACTGCCCGATGAGAGAGACTGGCCGAGCAGAGACCCTTACAACCGCCTCGATGAGA	1762
Db	333	C GGCTTTCACCGAGCGCGGCGGAGAAAATTCAGAAAGAGAGATGACAGTGAAGCGGAGGA	392
OY	1763	TCTTGAGAGATCTTGGAATCGAGAGCTAA	1791
Db	393	GTGAGAGAGAGAGAAAGGCGGAGGAGGA	421
RESULT 14			
BG321313			
LOCUS	BG321313	700 bp	mRNA linear EST 27-FEB-2001
DEFINITION	Zm04_04d06_R Zm04_AAF-C_ECORC_cold-stressed_maize_seedlings Zea mays		
ACCESSION	CDNA clone Zm04_04d06 mRNA sequence.		
VERSION	BG321313		
KEYWORDS	BG321313.1 GI:13150991		
SOURCE	EST.		
ORGANISM	Zea mays.		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea. Singh,J.A., Wakui,K., Couroux,P., De Moors,A., Harris,L.J., Hattori, J.I., Oneil,T., Robert,L.S., Spritt,D. and Tinker,N.A. Expressed Sequence Tags from Cold-Stressed Maize Seedlings Unpublished (2001) Contact: Singh,J.A. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA OC6, Canada Tel.: (613) 759-1662 Fax: (613) 759-1701 Email: singhj@agr.ca.		
TITLE	JOURNAL COMMENT		
FEATURES			
source			
	Location/Qualifiers		
	1..700		
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	/cultivar="CO328"		
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	/clone_lib="Zm04_AAF-C_EORC_cold_stressed_maize_seedlings"		
	/tissue_type="Leaf, crown"		
	/note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI;		
	Site_2: Xho I; Lower temperature 50 C / hour from 22 to		
	12oc; bring to 50 in 1 hour from 12oc. leave at 5oc 2 days		
	, photoperiod 16 hours. Light intensity was 125 uE-l.		
	Library prepared by in vivo mass excision from amplified		
	library."		
BASE COUNT	103 a 283 c 158 g 102 t 54 others		
ORIGIN			
Query Match	2.5%; Score 44.2; DB 12; Length 700;		
Best Local Similarity	43.0%; Pred. No. 3.5;		
Matches 133; Conservative 15; Mismatches 161; Indels 0; Gaps 0;			
OY	863	GCTTGAGCTCTTACCTGCTGTCAGGACGAGCTTCCCACAGTCAGATCTCTTCCAAGTC	921
Db	192	GCACGCCCTCTTACAGCGCTGCTKTKMACCGCCGCHCTTGGCCBGC CGGAGTGCTG	251
OY	922	ATTGCGCTGTGATGCTGCTCTTCAAGCCCCGCTTCAGAGCTTCAACCTTACTTCT	981
Db	252	ATTCGCGCGCGCTGCTATGCTATGCATGCAATGCAATCAGTTCGCTTCCTCTCCCTCCGCGC	311

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 21:13:53 : Search time 61 seconds
(without alignments)
1297.555 Million cell updates/sec

Title: US-09-218-702-2

Perfect score: 3189

Sequence: 1 MLFKSMQAAASGLSLGVIG.....AEQEPYRLDFLEDLGIEE 594

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3189	100.0	594	AA145222	Stachybotrys chart
2	3189	100.0	594	AA139992	Stachybotrys pheno
3	3189	100.0	594	AA195537	Stachybotrys chart
4	3189	100.0	594	AA195761	Stachybotrys chart
5	3189	100.0	594	AA018210	S chartarum phenol
6	1954.5	61.3	627	AA195538	Bipolarium spicifer
7	1954.5	61.3	627	AA196762	Bipolarium spicifer
8	1954.5	61.3	627	AA018211	B spicifera phenol
9	1929.5	60.5	627	AA195539	Curvularia pallesc
10	1929.5	60.5	627	AA196763	Curvularia pallesc

11	1929.5	60.5	627	23	AA018212	C pallescens pheno
12	1735.5	54.4	583	23	AA097312	Phenol oxidising e
13	1731.5	54.3	583	23	AA097316	Phenol oxidising e
14	1731.5	54.3	583	23	AA097318	Phenol oxidising e
15	1731.5	54.3	583	23	AB075770	Phenol oxidising e
16	1731.5	54.3	583	23	AB075772	Phenol oxidase B v
17	1730.5	54.3	583	23	AA097321	Phenol oxidising e
18	1730.5	54.3	583	23	AA097324	Phenol oxidising e
19	1730.5	54.3	583	23	AA097353	Phenol oxidising e
20	1730.5	54.3	583	23	AB075775	Phenol oxidase B v
21	1730.5	54.3	583	23	AB075778	Phenol oxidase B v
22	1730.5	54.3	583	23	AB075807	Phenol oxidase B v
23	1729.5	54.2	583	23	AA097329	Phenol oxidising e
24	1729.5	54.2	583	23	AA097334	Phenol oxidising e
25	1729.5	54.2	583	23	AA097336	Phenol oxidising e
26	1729.5	54.2	583	23	AB075766	Phenol oxidising e
27	1729.5	54.2	583	23	AB075783	Phenol oxidase B v
28	1729.5	54.2	583	23	AB075788	Phenol oxidase B v
29	1729.5	54.2	583	23	AB075790	Phenol oxidase B v
30	1728.5	54.2	583	23	AA097323	Phenol oxidising e
31	1728.5	54.2	583	23	AA097337	Phenol oxidising e
32	1728.5	54.2	583	23	AA097338	Phenol oxidising e
33	1728.5	54.2	583	23	AA097356	Phenol oxidising e
34	1728.5	54.2	583	23	AA097378	Phenol oxidising e
35	1728.5	54.2	583	23	AB075777	Phenol oxidising e
36	1728.5	54.2	583	23	AB075781	Phenol oxidase B v
37	1728.5	54.2	583	23	AB075791	Phenol oxidase B v
38	1728.5	54.2	583	23	AB075792	Phenol oxidase B v
39	1728.5	54.2	583	23	AB075810	Phenol oxidase B v
40	1728.5	54.2	583	23	AB075832	Phenol oxidase B v
41	1727.5	54.2	583	23	AA097320	Phenol oxidising e
42	1727.5	54.2	583	23	AA097326	Phenol oxidising e
43	1727.5	54.2	583	23	AA097333	Phenol oxidising e
44	1727.5	54.2	583	23	AA097335	Phenol oxidising e
45	1727.5	54.2	583	23	AB075774	Phenol oxidase B v

ALIGNMENTS

RESULT 1
AA145222
ID AA145222 standard: Protein: 594 AA.
XX
AC AA145222:
XX
DT 05-JAN-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidising enzyme.
XX
KW Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
XX detergent; anti-dye transfer; stain removal; bleaching.
XX
OS Stachybotrys chartarum.
XX
PN WO9949010-A2.
XX
PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-EP02042.
XX
PR 24-MAR-1998; 98US-0046969.
XX
PR 22-DEC-1996; 98US-0218702.
PA (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
XX
PI Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;
PI Wang C;
DR WPI; 1999-601211/51.
DR N-PSDB; AA25727.
XX

PT Detergent composition containing phenol oxidase from *Stachybotrys*, used
PT to bleach stains and prevent dye transfer
XX
XX
PS Claim 16; Fig 5; 56pp; English.
XX
CC The present invention describes a detergent composition containing a
CC pulled phenol oxidising enzyme derived from *Stachybotrys*. The present
CC sequence represents *Stachybotrys chartarum* phenol oxidising enzyme. The
CC enzyme can be used to modify the colour of dyes and other coloured
CC compounds (e.g. for use in pulp and paper bleaching also for removing
CC stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
CC transfer during fabric washing.
XX
XX
SQ Sequence 594 AA;
Query Match 100.0%; Score 3189; DB 20; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLFKSMQLAAASGLISGLVIGIPMDTGSHPTEAVDEPKTEVPADSLAAAGDDWDESPY 60
DB 1 MLFKSMQLAAASGLISGLVIGIPMDTGSHPTEAVDEPKTEVPADSLAAAGDDWDESPY 60
QY 61 NLLYRNALPIPPVKPKMIITNPVTGKDIWYEIEIKPQQRITYPLRLPATLVGDGMS 120
DB 61 NLLYRNALPIPPVKPKMIITNPVTGKDIWYEIEIKPQQRITYPLRLPATLVGDGMS 120
QY 121 GPTFVNPRTGETVVFRIINNAATVENSVHLHSGSPRAPFDGMADVTFPGYKXYFPNYS 180
DB 121 GPTFVNPRTGETVVFRIINNAATVENSVHLHSGSPRAPFDGMADVTFPGYKXYFPNYS 180
QY 121 GPTFVNPRTGETVVFRIINNAATVENSVHLHSGSPRAPFDGMADVTFPGYKXYFPNYS 180
DB 121 GPTFVNPRTGETVVFRIINNAATVENSVHLHSGSPRAPFDGMADVTFPGYKXYFPNYS 180
QY 181 ARLLWYHDAFMKTAENAFEGOGAYIINDEADALGLPSYGEFDIPILITAKYYNADG 240
DB 181 ARLLWYHDAFMKTAENAFEGOGAYIINDEADALGLPSYGEFDIPILITAKYYNADG 240
QY 241 TLRSTEGEDQDLMDGVIVHNGQPWPLNVQPRKRYRFLNAAVSRAMLVLTSSPNVR 300
DB 241 TLRSTEGEDQDLMDGVIVHNGQPWPLNVQPRKRYRFLNAAVSRAMLVLTSSPNVR 300
QY 301 IFFOYIASDAGLQAPVOTSNLYLAVEREYIITFTNAGOTLRLRNAETNDVGDEDE 360
DB 301 IFFOYIASDAGLQAPVOTSNLYLAVEREYIITFTNAGOTLRLRNAETNDVGDEDE 360
QY 361 YARTELVMRFEVSSGTVEDNSOVPTSLRDVPPRPKKEGPADNHFKFERNGHYLINDVGF 420
DB 361 YARTELVMRFEVSSGTVEDNSOVPTSLRDVPPRPKKEGPADNHFKFERNGHYLINDVGF 420
QY 421 ADVNERVLAKPELGTVEVWELNENSSGSGMSPVHILVDFKILKRTGGRGQVMPYESAGLK 480
DB 421 ADVNERVLAKPELGTVEVWELNENSSGSGMSPVHILVDFKILKRTGGRGQVMPYESAGLK 480
QY 481 DVVWLGREGTTLTEAHYQPTGTAYMWHCHNLIHEDNDMAVFNVTAMEKGYLOEDFEDP 540
DB 481 DVVWLGREGTTLTEAHYQPTGTAYMWHCHNLIHEDNDMAVFNVTAMEKGYLOEDFEDP 540
QY 541 MNPKRAVYNNRNDFHARAGNFSABESITARVOELAEQEPYNNRLDELLEDLGIEE 594
DB 541 MNPKRAVYNNRNDFHARAGNFSABESITARVOELAEQEPYNNRLDELLEDLGIEE 594
RESULT 2
AA39992
ID AA39992 standard; Protein: 594 AA.
XX
XX
AC AA39992;
XX
XX
DT 16-DEC-1999 (first entry)
XX
XX
DE *Stachybotrys* phenol oxidase protein sequence.
XX
XX
KW Phenol oxidase: enzyme; coloured compound: dye transfer prevention;
XX fabric washing; stain bleaching; anti-dye transfer; detergent.
XX

OS *Stachybotrys chartarum*.
XX
XX
PN W09949020-A2.
XX
XX
PD 30-SEP-1999.
XX
XX
PE 23-MAR-1999; 99WO-US06327.
XX
XX
PR 24-MAR-1998; 98US-0046969.
XX
XX
PR 22-DEC-1998; 98US-0218702.
XX
XX
PR 22-MAR-1999; 99US-0273957.
XX
XX
PA (GENM) GENENCOR INT INC.
XX
XX
PI Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;
XX
XX
DR WPI: 1999-591088/50.
XX
XX
DR N-PSDB: AA227601, AA227602.
XX
XX
PT Novel enzyme for modifying coloured compounds used to prevent
PT dye-transfer
PS
PS Claim 16; Fig 5; 64pp; English.
XX
XX
CC This sequence is the *Stachybotrys chartarum* phenol oxidase enzyme
CC of the invention. The invention is used to modify a coloured compound and
CC prevent dye transfer during fabric washing, or for stain bleaching or
CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC and food industries.
XX
XX
SQ Sequence 594 AA;
Query Match 100.0%; Score 3189; DB 20; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLFKSMQLAAASGLISGLVIGIPMDTGSHPTEAVDEPKTEVPADSLAAAGDDWDESPY 60
DB 1 MLFKSMQLAAASGLISGLVIGIPMDTGSHPTEAVDEPKTEVPADSLAAAGDDWDESPY 60
QY 61 NLLYRNALPIPPVKPKMIITNPVTGKDIWYEIEIKPQQRITYPLRLPATLVGDGMS 120
DB 61 NLLYRNALPIPPVKPKMIITNPVTGKDIWYEIEIKPQQRITYPLRLPATLVGDGMS 120
QY 121 GPTFVNPRTGETVVFRIINNAATVENSVHLHSGSPRAPFDGMADVTFPGYKXYFPNYS 180
DB 121 GPTFVNPRTGETVVFRIINNAATVENSVHLHSGSPRAPFDGMADVTFPGYKXYFPNYS 180
QY 121 GPTFVNPRTGETVVFRIINNAATVENSVHLHSGSPRAPFDGMADVTFPGYKXYFPNYS 180
DB 121 GPTFVNPRTGETVVFRIINNAATVENSVHLHSGSPRAPFDGMADVTFPGYKXYFPNYS 180
QY 181 ARLLWYHDAFMKTAENAFEGOGAYIINDEADALGLPSYGEFDIPILITAKYYNADG 240
DB 181 ARLLWYHDAFMKTAENAFEGOGAYIINDEADALGLPSYGEFDIPILITAKYYNADG 240
QY 241 TLRSTEGEDQDLMDGVIVHNGQPWPLNVQPRKRYRFLNAAVSRAMLVLTSSPNVR 300
DB 241 TLRSTEGEDQDLMDGVIVHNGQPWPLNVQPRKRYRFLNAAVSRAMLVLTSSPNVR 300
QY 301 IFFOYIASDAGLQAPVOTSNLYLAVEREYIITFTNAGOTLRLRNAETNDVGDEDE 360
DB 301 IFFOYIASDAGLQAPVOTSNLYLAVEREYIITFTNAGOTLRLRNAETNDVGDEDE 360
QY 361 YARTELVMRFEVSSGTVEDNSOVPTSLRDVPPRPKKEGPADNHFKFERNGHYLINDVGF 420
DB 361 YARTELVMRFEVSSGTVEDNSOVPTSLRDVPPRPKKEGPADNHFKFERNGHYLINDVGF 420
QY 421 ADVNERVLAKPELGTVEVWELNENSSGSGMSPVHILVDFKILKRTGGRGQVMPYESAGLK 480
DB 421 ADVNERVLAKPELGTVEVWELNENSSGSGMSPVHILVDFKILKRTGGRGQVMPYESAGLK 480
QY 481 DVVWLGREGTTLTEAHYQPTGTAYMWHCHNLIHEDNDMAVFNVTAMEKGYLOEDFEDP 540
DB 481 DVVWLGREGTTLTEAHYQPTGTAYMWHCHNLIHEDNDMAVFNVTAMEKGYLOEDFEDP 540
QY 541 MNPKRAVYNNRNDFHARAGNFSABESITARVOELAEQEPYNNRLDELLEDLGIEE 594
DB 541 MNPKRAVYNNRNDFHARAGNFSABESITARVOELAEQEPYNNRLDELLEDLGIEE 594

Db 541 MNPKRAVPYNNDFHARAGNFSAESITARVOELAEQEPYNNRDLDELIDGIEE 594

RESULT 3

AAV95537
ID AAV95537 standard; Protein: 594 AA.

XX AAV95537;

DT 10-OCT-2000 (first entry)

XX Stachybotrys chartarum phenol oxidizing enzyme.

XX Phenol oxidizing enzyme; detergent; bleaching.

OS Stachybotrys chartarum.

XX WO200039306-A2.

XX 06-JUL-2000.

XX 20-DEC-1999: 99WO-EP10287.

XX 23-DEC-1998: 98US-0220871.

XX 23-JUN-1999: 99US-0338723.

XX (UNIL) UNILEVER NV.

XX (UNIL) UNILEVER PLC.

XX (HIND-) HINDUSTAN LEVER LTD.

XX Bodie EA, Van Der Velden S, De Vries CH, Wang H;

XX WPI: 2000-514528/46.

XX N-PSDB: AAA50018; AAA50019.

XX Detergent composition comprising novel phenol oxidizing enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition

XX Claim 2: Fig 5A-B; 45pp: English.

XX The present sequence is that of a phenol oxidizing enzyme of Stachybotrys chartarum MUC1 38898. A claimed detergent composition comprises a phenol oxidizing enzyme having at least 60% identity to the present sequence, and preferably obtained from a bacterium, yeast or non-Stachybotrys fungus, especially Bipolaris spicifera, Curvularia pallescens or Amersporium atrum (see AAV95538-40). The phenol oxidizing enzyme is capable of modifying the colour associated with dyes or coloured compounds, and can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. It may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidizing enzyme, methods for producing the phenol oxidizing enzyme, and methods for constructing expression hosts are provided.

XX Sequence 594 AA:

Query Match 100.0%; Score 3189; DB 21; Length 594;

Best Local Similarity 100.0%; Pred. No. 2,9e-299; Indels 0; Gaps 0;

Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEKSMQLAASGLISGLVGIPTMTGSHPIEAVDEPVKTEVFADSLAAAGDDMESPEY 60

Db 1 MLEKSMQLAASGLISGLVGIPTMTGSHPIEAVDEPVKTEVFADSLAAAGDDMESPEY 60

QY 61 NLTYNNAIPRPVKKPKMTITNPVTGKDIWYEIEIKPQOQIYTLRPATLVGTGMS 120

Db 61 NLTYNNAIPRPVKKPKMTITNPVTGKDIWYEIEIKPQOQIYTLRPATLVGTGMS 120

QY 121 GPTFNVPGETETVVRFINNATVENSVLHGSFSPRAPFDGMADVFEPGEYKDYFPNQS 180

Db 121 GPTFNVPGETETVVRFINNATVENSVLHGSFSPRAPFDGMADVFEPGEYKDYFPNQS 180

QY 181 ARLLWYHDAFMKTAENAFVGOAGAYIINDEADALGSPGGEFDIPILITAKYNNADG 240

Db 181 ARLLWYHDAFMKTAENAFVGOAGAYIINDEADALGSPGGEFDIPILITAKYNNADG 240

QY 241 TLIRSTEGEDODLMDGVIHVNGQPMPLNVPKRYRFRFLNAAVSRAMLILYRTSSPNR 300

Db 241 TLIRSTEGEDODLMDGVIHVNGQPMPLNVPKRYRFRFLNAAVSRAMLILYRTSSPNR 300

QY 301 IPFOVIASDAGLLOAPVQTSNLYLAVEREYELIIDFTNAGOTLDRNVAETNDGDEDE 360

Db 301 IPFOVIASDAGLLOAPVQTSNLYLAVEREYELIIDFTNAGOTLDRNVAETNDGDEDE 360

QY 361 YARTLEVMRFVSSGTEVDNSQVPTLRDVPKPKKEGPADKHFFERSNGHYLINDVGF 420

Db 361 YARTLEVMRFVSSGTEVDNSQVPTLRDVPKPKKEGPADKHFFERSNGHYLINDVGF 420

QY 421 ADVNERVLAKPELGTVEVWELENSSGWSPVHILVDFKILKRTGGROVVPYESAGLK 480

Db 421 ADVNERVLAKPELGTVEVWELENSSGWSPVHILVDFKILKRTGGROVVPYESAGLK 480

QY 481 DYVWLGRCGETLTIEAHYQPMTCAYMMHCHNLJHEDNDMAVFNVTAMEEKGYLQEDFEDP 540

Db 481 DYVWLGRCGETLTIEAHYQPMTCAYMMHCHNLJHEDNDMAVFNVTAMEEKGYLQEDFEDP 540

QY 541 MNPKRAVPYNNDFHARAGNFSAESITARVOELAEQEPYNNRDLDELIDGIEE 594

Db 541 MNPKRAVPYNNDFHARAGNFSAESITARVOELAEQEPYNNRDLDELIDGIEE 594

RESULT 4

AAV96761
ID AAV96761 standard; Protein: 594 AA.

XX AAV96761;

DT 09-OCT-2000 (first entry)

XX Stachybotrys chartarum phenol oxidizing enzyme.

XX Phenol oxidizing enzyme; colour; dye; modification; detergent; stain; pulp; paper bleaching.

XX Stachybotrys chartarum.

XX WO200037654-A2.

XX 29-JUN-2000.

XX 20-DEC-1999: 99WO-US31009.

XX 23-DEC-1998: 98US-0220871.

XX 23-JUN-1999: 99US-0338723.

XX (GENV) GENENCOR INT INC.

XX Wang H, Bodie EA;

XX WPI: 2000-452191/39.

XX N-PSDB: AAA51313; AAA51314.

XX New phenol oxidizing enzyme for modifying colors associated with dyes or colored compounds, is obtained from fungus and is encoded by a nucleic acid comprising a specific nucleotide sequence

XX Claim 1: Fig 5A-B; 45pp: English.

XX This is the sequence of Stachybotrys chartarum phenol oxidizing enzyme.

XX Phenol oxidizing enzymes encoded by nucleic acid sequences which hybridize to the coding DNA are claimed, as long as the enzyme is capable of modifying the colour associated with dyes or coloured compounds. The

XX of modifying the colour associated with dyes or coloured compounds. The

CC enzymes are useful in detergent compositions and for modifying colors
CC associated with dyes or colored compounds which occur in stains in a
CC sample. The enzymes are also useful for pulp and paper bleaching,
CC anti-dye transfer in detergent and other textile applications.

XX Sequence 594 AA:

Query Match 100.0%; Score 3189; DB 21; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLFKSWQLAASGLISGLVGIPTMTGSHPIEAVDPEVKTEVFADSLAAGDDMESPPY 60
OY 61 NLLYNALPIPPVKOPKMITNPVTGKDIWYEIETKPFQOIRIYPTLRPATLVGDGMS 120
DB 61 NLLYNALPIPPVKOPKMITNPVTGKDIWYEIETKPFQOIRIYPTLRPATLVGDGMS 120
OY 121 GPTFNVPRTGETVVFRIINNAIVENSVLHSGSPRAPFDGMAEDVTFPGEXKYDYPNNQS 180
DB 121 GPTFNVPRTGETVVFRIINNAIVENSVLHSGSPRAPFDGMAEDVTFPGEXKYDYPNNQS 180
OY 121 GPTFNVPRTGETVVFRIINNAIVENSVLHSGSPRAPFDGMAEDVTFPGEXKYDYPNNQS 180
DB 121 GPTFNVPRTGETVVFRIINNAIVENSVLHSGSPRAPFDGMAEDVTFPGEXKYDYPNNQS 180
OY 181 ARLWYHDAHFEMKTAENAYFGQAGAYIINDEAEDALGLPSGGEEDIPILITAKYYNADG 240
DB 181 ARLWYHDAHFEMKTAENAYFGQAGAYIINDEAEDALGLPSGGEEDIPILITAKYYNADG 240
OY 241 TLRTSEGEDDLMGDIYHNGOPWPEFLNVPKRYFRFLNAAVSRAWLLYVRTSSPNVR 300
DB 241 TLRTSEGEDDLMGDIYHNGOPWPEFLNVPKRYFRFLNAAVSRAWLLYVRTSSPNVR 300
OY 301 IPEQVIASDAGLLQAPVQTSNLYLAVEREYELIIDFTNAGOTLDRNVAETNDVGEDE 360
DB 301 IPEQVIASDAGLLQAPVQTSNLYLAVEREYELIIDFTNAGOTLDRNVAETNDVGEDE 360
OY 361 YARTLEVMKRFVYSSGTVEDNSQVPTSLRDVPRPRHKEGPADKHFEKFSNGHYLLINDVGF 420
DB 361 YARTLEVMKRFVYSSGTVEDNSQVPTSLRDVPRPRHKEGPADKHFEKFSNGHYLLINDVGF 420
OY 421 ADVNERVLAKPELGTVEWELENSSGGSHRPHILVDPFKILKRTGGRCQVVPYSAGLK 480
DB 421 ADVNERVLAKPELGTVEWELENSSGGSHRPHILVDPFKILKRTGGRCQVVPYSAGLK 480
OY 481 DVMVLGRGETTLTIEAHYQPMWTGAYMMHCHNLIHEDNDMAAVFNVTAMEBKGYLQEDFEDP 540
DB 481 DVMVLGRGETTLTIEAHYQPMWTGAYMMHCHNLIHEDNDMAAVFNVTAMEBKGYLQEDFEDP 540
OY 541 MNPKRAVPYNNDFHARAGNFSASITARVOELAEQEPYNNRLDEILDGIEE 594
DB 541 MNPKRAVPYNNDFHARAGNFSASITARVOELAEQEPYNNRLDEILDGIEE 594
```

RESULT 5
AA018210

ID AA018210 standard; Protein: 594 AA.

XX AA018210;

DT 13-SEP-2002 (first entry)

XX S chartarum phenol oxidizing enzyme.

XX Phenol oxidizing enzyme; fungus; redox reaction; detergent;

XX paper industry; pulp industry; textile; food industry.

XX Stachybotrys chartarum.

XX US6399329-B1.

XX 04-JUN-2002.

XX 21-DEC-1999; 99US-0468578.

XX

PR 12-DEC-1998; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.
XX
XX (GEMV) GENENCOR INT INC.

XX Wang H, Bodie EA;

XX WPI; 2002-496835/53.

DR N-PSDB; AAL47582, AAL47584.

PT New polynucleotides encoding phenol oxidizing enzymes, useful for
PT preventing the transfer of dyes in solution from one textile to another
PT during detergent washing -

PS Example 5; Fig 4; 37Pp; English.

CC The present invention provides the protein and coding sequences of phenol
CC oxidizing enzymes from Stachybotrys chartarum, Bipolaris spicifera and
CC Curvularia pallescens. These enzymes are useful in the textiles, paper,
CC pulp, detergent and food industries. In particular they are useful for
CC preventing the transfer of dyes in solution from one textile to another
CC during detergent washing (dye transfer inhibition). The present sequence
CC is the S. chartarum phenol oxidizing enzyme.

XX Sequence 594 AA:

Query Match 100.0%; Score 3189; DB 23; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MLFKSWQLAASGLISGLVGIPTMTGSHPIEAVDPEVKTEVFADSLAAGDDMESPPY 60
DB 1 MLFKSWQLAASGLISGLVGIPTMTGSHPIEAVDPEVKTEVFADSLAAGDDMESPPY 60
OY 61 NLLYNALPIPPVKOPKMITNPVTGKDIWYEIETKPFQOIRIYPTLRPATLVGDGMS 120
DB 61 NLLYNALPIPPVKOPKMITNPVTGKDIWYEIETKPFQOIRIYPTLRPATLVGDGMS 120
OY 121 GPTFNVPRTGETVVFRIINNAIVENSVLHSGSPRAPFDGMAEDVTFPGEXKYDYPNNQS 180
DB 121 GPTFNVPRTGETVVFRIINNAIVENSVLHSGSPRAPFDGMAEDVTFPGEXKYDYPNNQS 180
OY 121 GPTFNVPRTGETVVFRIINNAIVENSVLHSGSPRAPFDGMAEDVTFPGEXKYDYPNNQS 180
DB 121 GPTFNVPRTGETVVFRIINNAIVENSVLHSGSPRAPFDGMAEDVTFPGEXKYDYPNNQS 180
OY 181 ARLWYHDAHFEMKTAENAYFGQAGAYIINDEAEDALGLPSGGEEDIPILITAKYYNADG 240
DB 181 ARLWYHDAHFEMKTAENAYFGQAGAYIINDEAEDALGLPSGGEEDIPILITAKYYNADG 240
OY 241 TLRTSEGEDDLMGDIYHNGOPWPEFLNVPKRYFRFLNAAVSRAWLLYVRTSSPNVR 300
DB 241 TLRTSEGEDDLMGDIYHNGOPWPEFLNVPKRYFRFLNAAVSRAWLLYVRTSSPNVR 300
OY 301 IPEQVIASDAGLLQAPVQTSNLYLAVEREYELIIDFTNAGOTLDRNVAETNDVGEDE 360
DB 301 IPEQVIASDAGLLQAPVQTSNLYLAVEREYELIIDFTNAGOTLDRNVAETNDVGEDE 360
OY 361 YARTLEVMKRFVYSSGTVEDNSQVPTSLRDVPRPRHKEGPADKHFEKFSNGHYLLINDVGF 420
DB 361 YARTLEVMKRFVYSSGTVEDNSQVPTSLRDVPRPRHKEGPADKHFEKFSNGHYLLINDVGF 420
OY 421 ADVNERVLAKPELGTVEWELENSSGGSHRPHILVDPFKILKRTGGRCQVVPYSAGLK 480
DB 421 ADVNERVLAKPELGTVEWELENSSGGSHRPHILVDPFKILKRTGGRCQVVPYSAGLK 480
OY 481 DVMVLGRGETTLTIEAHYQPMWTGAYMMHCHNLIHEDNDMAAVFNVTAMEBKGYLQEDFEDP 540
DB 481 DVMVLGRGETTLTIEAHYQPMWTGAYMMHCHNLIHEDNDMAAVFNVTAMEBKGYLQEDFEDP 540
OY 541 MNPKRAVPYNNDFHARAGNFSASITARVOELAEQEPYNNRLDEILDGIEE 594
DB 541 MNPKRAVPYNNDFHARAGNFSASITARVOELAEQEPYNNRLDEILDGIEE 594
```

RESULT 6
AAV95538

CC compositions and for modifying colors associated with dyes or coloured
CC compounds which occur in stains in a sample. The enzymes are also useful
CC for pulp and paper bleaching, anti-dye transfer in detergent and other
CC textile applications.

XX Sequence 627 AA;

Query Match 61.3%; Score 1954.5; DB 21; Length 627;

Best Local Similarity 61.1%; Pred. No. 1e-179; Indels 21; Gaps 8;

Matches 367; Conservative 79; Mismatches 134;

2 LFKSMOLAASGLSGVLGIPMDTGSHPLEAVDPVEKTEVFADSLAAGD----- 53

6 LFSALQVLS---IAKGIYVAL--SERPAKFVDNTPDEKKA--LASTYEDDPADVNNL 58

54 -DMESPYYLLYRNALPVPKQPMIITNPYTGKDIWYEIEIKPFOORITPLRPATL 112

59 KMOSEPEYLLIRPQPLIPPAKEPNK-LTNPTYNKEIWTYELIVKFTQOVPSPSLRPAL 117

113 VGYDMSPGPTNPVPGTETVVRFTINMATVENSVLHGSPPRAPFDGMAEDVTFPGEXKD 172

118 VGYDGSIPGPTIIVPRGTAUVVRFTINMGDRRESSIHLHGSPPRAPFDGMAEDVTFPGEXKD 177

173 YTFPNYQSRLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGIPSGYGEFDIPLILT 232

178 YYYPNNAARFLMYHDHAFMYAENAYFGQAGAYLITDPAEDALGIPSGYGYDIPLVLS 237

233 AKYVADGTLRSTEGEDDLMGVDVIVNGQPMPLNVQPRKTRFRFLNAVSRAMLLYLV 292

238 SKYYNADGTLKTSVGEDKSVMGDIIVHNGQPMPLNVBERKTRFLRLNAVSRNFPALYV 297

293 RTSSPNVRIIPFOVIASDAGLLQAPVOTSNLYLAVAREYTIIDFTNFAQOTDLRNVAFET 352

298 KODNATRLRPFQVIASDAGLLTHPVOTSDMYVAAAEYRIEIVDFAPYAGOTDLRNFAPA 357

353 NVGDEDEYARTLEVMRFVYSSGTVEDNSQVSTLRDVPFRPHKEGPADKHFKERSNGH 412

358 NGIGTDDVDYANNDKVMRFVYSSQTVVDSNVPEQLSQIOFPADKT-DIDHHRFRHTNCE 416

413 YLINDGFADVNERVLAKBELGTVEVWELNSSGGSHPVHILYDFKILKRTGRCG-- 470

417 WRINGGFADVENRVLAKVPRGTVELMELENSGGSHPIVHVLVDFRVARVARGDGTG 476

471 VMPYESAGLKDVYVWVGRGFTLTTEAHQWPTGAYMMHCHNLHEDDMAVENVYAMEK 530

477 VMPYEAGAKDVYVWVGRHETVLEAHYAPWDGYMMFCHNLHEDDMAAFAVDYKLQNF 536

531 GYILO-EDFEDPMNPKRAVYVNRNDFHARAGNPSAESTIARVOELAEQEPYRLDELILD 589

537 GYNETTFDHPEDPRMSARPTTAGDILTARSGIFSEESIRARVNELAEQPSYSLAQVTAS 596

590 L 590

597 L 597

RESULT 8

AA018211 standard; Protein; 627 AA.

AA018211;

13-SEP-2002 (first entry)

B spicifera phenol oxidising enzyme.

Phenol oxidising enzyme; enzyme; fungus; redox reaction; detergent;

paper industry; pulp industry; textile; food industry.

Bipolaris spicifera.

US6399329-B1.

PD 04-JUN-2002.

XX 21-DEC-1999; 99US-0468578.

XX 12-DEC-1998; 98US-0220871.

XX 23-JUN-1999; 99US-0338723.

XX (GENEV) GENENCOR INT INC.

XX Wang H, Bodie EA;

XX MPI: 2002-498835/53.

XX N-PSDB; AAL47583.

XX New polynucleotides encoding phenol oxidizing enzymes, useful for
XX preventing the transfer of dyes in solution from one textile to another
XX during detergent washing -

XX Claim 1; Fig 3; 37pp; English.

XX The present invention provides the protein and coding sequences of phenol
XX oxidising enzymes from Stachybotrys chartarum, Bipolaris spicifera and
XX Curvularia pallens. These enzymes are useful in the textiles, paper,
XX pulp, detergent and food industries. In particular they are useful for
XX preventing the transfer of dyes in solution from one textile to another
XX during detergent washing (dye transfer inhibition). The present sequence
XX is the B. spicifera phenol oxidising enzyme.

XX Sequence 627 AA;

Query Match 61.3%; Score 1954.5; DB 23; Length 627;

Best Local Similarity 61.1%; Pred. No. 1e-179; Indels 21; Gaps 8;

Matches 367; Conservative 79; Mismatches 134;

2 LFKSMOLAASGLSGVLGIPMDTGSHPLEAVDPVEKTEVFADSLAAGD----- 53

6 LFSALQVLS---IAKGIYVAL--SERPAKFVDNTPDEKKA--LASTYEDDPADVNNL 58

54 -DMESPYYLLYRNALPVPKQPMIITNPYTGKDIWYEIEIKPFOORITPLRPATL 112

59 KMOSEPEYLLIRPQPLIPPAKEPNK-LTNPTYNKEIWTYELIVKFTQOVPSPSLRPAL 117

113 VGYDMSPGPTNPVPGTETVVRFTINMATVENSVLHGSPPRAPFDGMAEDVTFPGEXKD 172

118 VGYDGSIPGPTIIVPRGTAUVVRFTINMGDRRESSIHLHGSPPRAPFDGMAEDVTFPGEXKD 177

173 YTFPNYQSRLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGIPSGYGEFDIPLILT 232

178 YYYPNNAARFLMYHDHAFMYAENAYFGQAGAYLITDPAEDALGIPSGYGYDIPLVLS 237

233 AKYVADGTLRSTEGEDDLMGVDVIVNGQPMPLNVQPRKTRFRFLNAVSRAMLLYLV 292

238 SKYYNADGTLKTSVGEDKSVMGDIIVHNGQPMPLNVBERKTRFLRLNAVSRNFPALYV 297

293 RTSSPNVRIIPFOVIASDAGLLQAPVOTSNLYLAVAREYTIIDFTNFAQOTDLRNVAFET 352

298 KODNATRLRPFQVIASDAGLLTHPVOTSDMYVAAAEYRIEIVDFAPYAGOTDLRNFAPA 357

353 NVGDEDEYARTLEVMRFVYSSGTVEDNSQVSTLRDVPFRPHKEGPADKHFKERSNGH 412

358 NGIGTDDVDYANNDKVMRFVYSSQTVVDSNVPEQLSQIOFPADKT-DIDHHRFRHTNCE 416

413 YLINDGFADVNERVLAKBELGTVEVWELNSSGGSHPVHILYDFKILKRTGRCG-- 470

417 WRINGGFADVENRVLAKVPRGTVELMELENSGGSHPIVHVLVDFRVARVARGDGTG 476

471 VMPYESAGLKDVYVWVGRGFTLTTEAHQWPTGAYMMHCHNLHEDDMAVENVYAMEK 530

477 VMPYEAGAKDVYVWVGRHETVLEAHYAPWDGYMMFCHNLHEDDMAAFAVDYKLQNF 536

531 GYILO-EDFEDPMNPKRAVYVNRNDFHARAGNPSAESTIARVOELAEQEPYRLDELILD 589

537 GYNETTFDHPEDPRMSARPTTAGDILTARSGIFSEESIRARVNELAEQPSYSLAQVTAS 596

[illegible]

Db	59	KDMOSPPEPILEFREALPIPPAKKEPKK-MTNVNTKKEIYETIYVTKPPNOOYVPSLRARL	117
Qy	113	VGYDMSGGPFFFNPRGTETVRFINNATVENSVLHSGSPSRAPFDQMAEDVTFPGGYKD	172
Db	118	VGYDGISPGPFTIIVRGTEAVVRVFNQGDRESSIHLHGSPSRAPFDQMAEDLIMKGFKD	177
Qy	173	YTFPNVQASRLLLYTHDAFMKTAENATFGQAGATITNDEADALGLPSGGEFDIPLIT	232
Db	178	YTFPNVQASRLLLYTHDAFMKTAENATFGQAGATITNDEADALGLPSGGEFDIPLIT	237
Qy	223	AYYVADGTLSTEGEDDLMGDIYIHVNGQWPFLNAPRKRYRFRFLMAAVSRNMLLYLV	292
Db	238	SAFYNSDGLTQVSGEDNSLMGDYIHNVGQWPFFNVPKRYRLRFLMAAVSRNMFALYFV	297
Qy	293	RFSSPNVAIPFQVNIASDAQLOAPVQTSNLTALAVEREIIIDPTNFAGOTLDLRNVAET	352
Db	298	KQQAATATRLPFQVNIASDAQGLTTHHVQTSDIYVAAAREYEIFPDPAPYAGOTIDLRNFAK	357
Qy	353	NDVGEDEYARTLEVMARFVSSGTVEDNSQVPSFLRDVPPRPKKEGPADKHKEFERSNGH	412
Db	358	NGVYGDDEYARTMDKMRHRVSSQAVVDSSVYPALDSIQFPADTGT-IDHHRFRHRTNSE	416
Qy	413	YLINDVGFADVNERLAKRELGTVEVMELENSGSGMSPVHIIHYDKILKRTGG---RG	469
Db	417	WRINISIGPADVQNRILAAVPRGTVELMELENSGSGMSPHIVHLYDVRVAVARQDDESTRG	476
Qy	470	QVMPESASGLKDVVWLGRGETLTLEAHQPTGAYMMHCHNLIHEDNDMAVFNVTAMEE	529
Db	477	-VMPEASGLKDVVWLGRHETVLYEAHAPRPDGYVMHCHNLIHEDNDMAAADVTKLON	535
Qy	530	KGYLO-EDFEDPMNKRAVPYNNRDPHARAGNFSAESITARVOELAEQEPYKRDEILE	588
Db	536	FGYNETTFDHPDEDSRMGARPFTAADLTARSGIFSEASIRARVWELALBQYSELAQVTA	595
Qy	589	DL 590	
Db	596	SL 597	
RESULT 10			
AA96763			
ID	AA96763 standard; Protein: 627 AA.		
XX	AA96763:		
AC			
XX			
DT	09-OCT-2000 (first entry)		
XX			
DE	Curvularia pallescens phenol oxidizing enzyme.		
XX			
KM	Phenol oxidizing enzyme; colour: dye; modification; detergent; stain;		
KW	pulp; paper bleaching.		
XX			
OS	Curvularia pallescens.		
XX			
PN	MO200037654-A2.		
XX			
PD	29-JUN-2000.		
XX			
PE	20-DEC-1999; 99MO-US31009.		
XX			
PR	23-DEC-1998; 98US-0220871.		
PR	23-JUN-1999; 99US-0338723.		
XX			
PA	(GENV) GENECOR INT INC.		
XX			
PI	Wang H, Bodie EA;		
XX			
DR	WPI: 2000-452191/39.		
DR	N-PSDB; AAA51316.		
XX			
PT	New phenol oxidizing enzyme for modifying colors associated with dyes		
PT	or colored compounds, is obtained from fungus and is encoded by a		
PT	nucleic acid comprising a specific nucleotide sequence		

XX Claim 8; Fig 10; 45pp; English.
PS

This sentence is the Curvularia pallescens phenol oxidizing enzyme. Phenol oxidizing enzymes encoded by nucleic acid sequences which hybridize to the Stachybotrys chartarum DNA (AA51313) are claimed, as long as the enzyme is capable of modifying the colour associated with dyes or coloured compounds. The enzymes are useful in detergent compositions and for modifying colors associated with dyes or coloured compounds which occur in stains in a sample. The enzymes are also useful for pulp and paper bleaching, anti-dye transfer in detergent and other textile applications.

50 Sequence 627 AA;

Query Match	60.5%;	Score 1929.5;	DB 21;	Length 627;
Best Local Similarity	60.5%;	Pred. No. 2.6e-177;		
Matches 364; Conservative	81;	Mismatches 134;	Indels 23;	Gaps 9;

QY	2	LFKSNQLAAAGSLGSLGVIGIMDQSGHPIEIVDEVEYTFVFAOSLAAAGDD-----	53
Db	6	LFSLAQIAL---IAKIGTVAL--SERPAKIIDETPDEEKA--LAAIVEDPADVFRIL	58
QY	54	-DMESPYNLLRYNALPIPRPKQCKMITTNEVTKDIDWYEIEIKPPQCKIYPTLRPATL	112
Db	59	KDMQSEPRILFRELRLPIPAKKEPNK-NTNVTKKEIMWEYIYIKPNQGYLSLRARL	117
QY	113	VGIDGMSFGPFPNVRPGTETVYRFINNAIYVNSVHLHSDPSRAFDGMAEDVTPPGCYKD	172
Db	118	VGYDISISGPTIIVPRGTEAVYRFEVNGDRESSIHLHGSPSRAPFDGMAEDLIMKQFKD	177
QY	173	YVFPRVYSARLLIWHDAFMKTAENAYFGGAAVITINDEMDALGLPSGGEPIRLIT	232
Db	178	YVFPRVYQARFLMWHDAHVAHTAENAYFGGAAVLTIDPADADALGLPSGKGKDYDPLVS	237
QY	233	AKYVADGTLRSTEGEDQDLDMDGVYIHVNGQWPPLVQPRKYRFRFLNAVSRAMLLYLV	292
Db	238	SKFYNSDGTIQTSGVEDNSLMDGVYIHVNGQWPFPFNVEPRKYRLRFLMAVSRNFALFY	297
QY	293	RTSGPNVRIPPOVIASDAGLLQAPVQTSNLXLAVAERYEIIIDFTNAGOTLDIRVAET	352
Db	298	KQQAATATRLPFOVIASPDAGLLHTHPQTSIDYVAAAREYIYVDFAPYAGQTLDIRPAKA	357
QY	353	NDVGEDEDEYATLEVMKRVVSSGIYEDNSQVPTLRDVPFRPHKEGADKHFKERSNGH	412
Db	358	NGCVGIDDDYANTDKMKRHHVSSQAVVNSVYPALSOIFPADKTG-IDHHFRFHRTNSE	416
QY	413	YLINDVGFADVNERILARPELGTAEVWELENSGSGWSPHVIHLYDKRLLIKRTGG---	469
Db	417	WIKINGIGRADVONRILAVPRGTIELMELENSSGGWSPIHVLHYDFRVAARIGDESTRG	476
QY	470	QVMPEASGLKDVWMLGGETLTLEAHQOPTGAYVMHCHLLIHEDNDMDMAVFNVTAEE	529
Db	477	-VMPEASGLKDVWMLGHEHIVLEAHARPAIDGYVMFHCHLLIHEDDDMAAFVYTLQN	535
QY	530	KGYLD-EDFEDPMNKRAVDYNNRNDFHARAGNFSABSTARVOELAEQEPYNRULDIIE	588
Db	536	FGYNETTDFHDEDESRMGARPTAADLTARSGIFSEASIRARVVELAEQYSELAQVTA	595
QY	569	DL 590	
Db	596	SL 597	
RESULT 11			
AA018212			
ID AA018212 standard; Protein: 627 AA.			
XX			
AC AA018212;			
XX			
DT 13-SEP-2002 (first entry)			
1xx C pallascens phenol oxidising enzyme.			

RESULT 11

ID AA018212 standard; Protein; 627 AA.

AC AA018212;

DT 13-SEP-2002 (first entry)

C pallescens phenol oxidising enzyme.

XX Phenol oxidising enzyme; enzyme; fungus; redox reaction; detergent;
 KM paper industry; pulp industry; textile; food industry.
 XX
 OS *Curvularia pallescens*.

PN US6399329-B1.

PD 04-JUN-2002.

PF 21-DEC-1999; 99US-0468578.

PR 12-DEC-1998; 98US-0220871.

PR 23-JUN-1999; 99US-0338723.

PA (GEMV) GENENCOR INT' INC.

PI Wang H, Bodie EA;

DR WPI; 2002-498835/53

DR N-PSDB; AAL47585.

PT New polynucleotides encoding phenol oxidizing enzymes, useful for preventing the transfer of dyes in solution from one textile to another during detergent washing -

PS Example 5; Fig 10; 37pp; English.

The present invention provides the protein and coding sequences of phenol oxidising enzymes from *Stachybotrys chartarum*, *Bipolaris spizizenii* and *Curvularia pallescens*. These enzymes are useful in the textiles, paper, pulp, detergent and food industries. In particular they are useful for preventing the transfer of dyes in solution from one textile to another during detergent washing (dye transfer inhibition). The present sequence is the *C. pallescens* phenol oxidising enzyme.

Sequence 627 AA:

Query Match	60.5%;	Score 1929.5;	DB 23;	Length 627;
Best Local Similarity	60.5%;	Pred. No. 2.6e-177;		
Matches 364; Conservative	81;	Mismatches 134;	Indels 23;	Gaps 9;

[illegible]

Oy	470	QVMPRESAGLKDVMVLGRGETLTLEAHYQPWGTGAYMMHCNHLHEDNDMAVENVTAMEE	529
Dd	477	-VMPYESAGLKDVLMVLRGHETFTLVLEAHYAPMDGVYMEHCNHLHEDDDMAADVTKLON	535
Oy	530	KGYLD-EEFEDPMKPKRAVPYNNDPHARAGNSASISITARPQELAEOPYRKDEILE	588
Dd	536	FGYMETTDFHPEDSRMSAREPTAADTPRARGIFSEASIRAVNELALEOPYSELQAQVA	595
Oy	589	DL 590	
Dd	596	SL 597	
RESULT 12			
ID	AAU97312		
XX	AAU97312 standard; Protein; 583 AA.		*
AC	AAU97312;		
DX	30-JUL-2002 (first entry)		
XX	Phenol oxidising enzyme L76W/M254F mutant.		
DE			
XX			
KM	Phenol oxidising enzyme; colour modification; cleaning; textile;		
KM	dyeing treatment; decolorizing indigo waste; fabric dyeing; bleaching;		
KM	fibre modification; leather industry; paper pulp manufacture;		
KM	bluff pulp manufacture; wood processing; pump bleaching; bio-glue;		
KM	linin activation; MDF manufacturing; ink removal; paper dyeing;		
KM	adhesives; feed additive; plant material processing; oxygen scavenger;		
KM	contact lens cleaning; bread improver; food preservation; personal care;		
KM	fragrance; skin care; hair care; oral hygiene; deodorant; antiperspirant;		
KM	hair dye; skin dye; surface modification; anti-microbial agent;		
KM	odour removal; teeth whitening; cleaning; waste water treatment;		
KM	decolorification of phenolic component; bio-remediation; bio-material;		
KM	bio-catalyst; biopolymer; surface modification; biosensor;		
KM	primary alcohol production; organic syntheses; enzyme; mutant; mutain.		
OS	Stachybotrys chartarum.		
XX	Synthetic.		
XX			
FH	Key Location/Qualifiers		
FT	Misc-difference 76 /note= "Wild type Leu substituted by Trp"		
FT	Misc-difference 254 /note= "Wild type Met substituted by Phe"		
FT			
XX	MO200220755-A2.		
PX			
PD	14-MAR-2002.		
XX			
PX	30-AUG-2001; 2001WO-US27263.		
XX			
PR	07-SEP-2000; 2000US-0656640.		
XX			
PA	(GENV) GENENCOR INT INC.		
XX			
PI	Wang H, Aehle W, Rodriguez AM, Toppozada A, Van Gastel FVC;		
XX			
DR	WPI; 2002-415728/44.		
XX			
Pt	Novel enzymatically active variant of precursor phenol oxidising enzyme		
Pt	derived from Stachybotrys species to modify colour associated with		
Pt	coloured compounds such as in cleaning, e.g. for removing food stains on		
Pt	fabric -		
XX			
PS	Claim 5; Page -: 54pp; English.		
CC	The invention describes an enzymatically active variant (I) of a		
CC	precursor phenol oxidising enzyme (EI) derived from a species of		
CC	Stachybotrys. (I) is useful in: modification of colour associated with		
CC	coloured compounds; cleaning; textiles. The enzyme variants are useful		
CC	in: denim treatment; decolorizing indigo waste; fabric dyeing; textile		

Query Match	Best Local Similarity	Matches	332; Conservative	67; Mismatches	123; Indels	19; Gaps	9
57	54.4%;	Score 1735.5;	DB 23;	Length 583;			
45	61.4%;	Pred. No. 1.4e-158;					
117							
103							
175							
163							
235							
223							
295							
283							
355							
343							
405							
399							
465							
459							
525							
518							
585							
578							

XX	AA097316;
XX	
AC	
XX	30-JUL-2002 (first entry)
DT	
XX	
DE	Phenol oxidising enzyme L76W/M254F/E302V mutant.
XX	
KW	Phenol oxidising enzyme; colour modification; cleaning; textile;
KW	denim treatment; decolouring indigo waste; fabric dyeing; bleaching;
KW	fibre modification; leather industry; paper pulp manufacture;
KW	fluff pulp manufacture; wood processing; pump bleaching; bio-glu-
KW	lignin activation; MDF manufacturing; ink removal; paper dyeing;
KW	adhesives; feed additive; plant material processing; oxygen scavenger;
KW	contact lens cleaning; bread improver; food preservation; personal care;
KW	fragrance; skin care; hair care; oral hygiene; deodorant; antiperspirant;
KW	hair dye; skin dye; surface modification; anti-microbial agent;
KW	odour removal; teeth whitening; cleaning; waste water treatment;
KW	detoxification of phenolic component; bio-remediation; bio-material;
KW	bio-catalyst; biopolymer; surface modification; biosensor;
XX	primary alcohol production; organic syntheses; enzyme; mutant; mutein.
XX	
OS	Stachybotrys chartarum.
OS	Synthetic.
PH	Key Location/Qualifiers
FT	Misc-difference 76
FT	/note- "Wild type Leu substituted by Trp"
FT	Misc-difference 254
FT	/note- "Wild type Met substituted by Phe"
FT	Misc-difference 302
FT	/note- "Wild type Glu substituted by Val"
PN	WO200220755-A2.
PD	
XX	14-MAR-2002.
XX	
PF	30-AUG-2001; 2001WO-US27263.
PR	07-SEP-2000; 2000US-0656640.
XX	
PA	(GEMV) GENENCOR INT INC.
PI	
XX	Wang H, Aehle W, Rodriguez AM, Toppozada A, Van Gastel FJC;
XX	WPI: 2002-415728/44.
DR	
XX	
PT	Novel enzymatically active variant of precursor phenol oxidising enzyme
PT	derived from Stachybotrys species to modify colour associated with
PT	coloured compounds such as in cleaning, e.g. for removing food stains on
PT	fabric
XX	
PS	Claim 5; Page -; 54pp; English.
XX	
CC	The invention describes an enzymatically active variant (I) of a
CC	precursor phenol oxidising enzyme (EI) derived from a species of
CC	Stachybotrys. (I) is useful in: modification of colour associated with
CC	coloured compounds; cleaning; textiles. The enzyme variants are useful
CC	in: denim treatment; decolouring indigo waste; fabric dyeing; textile
CC	bleaching processes; fibre modification; achieving enhanced fibre or
CC	fabric properties; the leather industry; the manufacture of paper pulps
CC	and fluff pulps; wood processing; pump bleaching; wood fibre
CC	modification; bio-glu (lignin activation) for MDF manufacturing; for
CC	enhanced paper properties; ink removal; paper dyeing; adhesives; as a
CC	feed additive; processing of plant materials and food industry by
CC	products; contact lens cleaning; as a bread improver; food preservation;
CC	as an oxygen scavenger; personal care e.g in fragrances, and products of
CC	skin care, hair care, oral hygiene, personal washing and deodorant and/or
CC	antiperspirants; hair dyeing and/or bleaching; skin dyeing and/or
CC	bleaching; surface modification (e.g. as coupling reagent); as an
CC	anti-microbial agent; odour removal; teeth whitening; cleaning; waste
CC	water treatment; detoxification of phenolic components; bio-remediation;
CC	bio-materials e.g. bio-catalysts; biopolymers; surface modification;
CC	production of primary alcohols; connection with biosensors and/or organic

[illegible]

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(without alignments)
832.248 Million cell updates/sec

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3189	100.0	594	US-09-468-578-2	Sequence 2, Appl1
2	3189	100.0	594	US-09-218-702-2	Sequence 2, Appl1
3	1954.5	61.3	627	US-09-468-578-4	Sequence 4, Appl1
4	1929.5	60.5	627	US-09-468-578-7	Sequence 7, Appl1
5	1724.5	54.1	572	US-09-401-476-4	Sequence 4, Appl1
6	1716.5	53.8	583	US-09-401-476-2	Sequence 2, Appl1
7	1712.5	53.7	568	US-09-218-702-4	Sequence 4, Appl1
8	400.5	12.6	322	US-09-134-001C-2946	Sequence 2946, Ap
9	357.5	11.2	114	US-09-468-578-9	Sequence 9, Appl1
10	202	6.3	616	US-08-749-882A-2	Sequence 2, Appl1
11	202	6.3	616	US-08-539-134-2	Sequence 2, Appl1
12	202	6.3	616	US-08-991-513-2	Sequence 2, Appl1
13	202	6.3	616	US-09-032-315-9	Sequence 9, Appl1
14	202	6.3	616	US-08-993-318A-9	Sequence 9, Appl1
15	202	6.3	616	US-09-028-887-2	Sequence 2, Appl1
16	202	6.3	616	US-09-399-886-9	Sequence 9, Appl1
17	202	6.3	616	US-09-396-260-9	Sequence 9, Appl1
18	202	6.3	616	US-09-518-901-2	Sequence 2, Appl1
19	202	6.3	616	US-09-576-281-9	Sequence 9, Appl1
20	198.5	6.2	529	US-08-172-331B-14	Sequence 14, Appl1
21	198.5	6.2	529	US-08-706-037-25	Sequence 25, Appl1
22	198.5	6.2	529	US-09-005-397-25	Sequence 25, Appl1
23	198.5	6.2	529	US-09-032-315-5	Sequence 5, Appl1
24	198.5	6.2	529	US-08-993-318A-5	Sequence 5, Appl1
25	198.5	6.2	529	US-09-399-886-5	Sequence 5, Appl1
26	198.5	6.2	529	US-09-396-260-5	Sequence 5, Appl1
27	198.5	6.2	529	US-09-576-281-5	Sequence 5, Appl1

28	198	6.2	620	1	US-08-940-661A-2	Sequence 2, Appl1
29	198	6.2	620	2	US-09-083-485-2	Sequence 2, Appl1
30	198	6.2	620	2	US-08-939-218A-2	Sequence 2, Appl1
31	197	6.2	573	2	US-08-991-531-1	Sequence 1, Appl1
32	197	6.2	573	2	US-09-032-315-10	Sequence 10, Appl1
33	197	6.2	573	3	US-08-993-318A-10	Sequence 10, Appl1
34	197	6.2	573	3	US-09-028-887-1	Sequence 1, Appl1
35	197	6.2	573	4	US-09-399-886-10	Sequence 10, Appl1
36	197	6.2	573	4	US-09-396-260-10	Sequence 10, Appl1
37	197	6.2	573	4	US-09-518-901-1	Sequence 1, Appl1
38	197	6.2	573	4	US-09-576-281-10	Sequence 10, Appl1
39	197	6.2	616	5	PCT-US95-06816-2	Sequence 2, Appl1
40	197	6.2	620	1	US-08-706-037-27	Sequence 27, Appl1
41	197	6.2	620	5	US-09-005-397-27	Sequence 27, Appl1
42	197	6.2	620	5	PCT-US95-06815-2	Sequence 2, Appl1
43	194	6.1	511	1	US-08-462-484-8	Sequence 8, Appl1
44	194	6.1	511	1	US-08-441-147-8	Sequence 8, Appl1
45	194	6.1	511	5	PCT-US95-07536-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1									
US-09-468-578-2									
: Sequence 2, Application US/09468578									
: Patent No. 6399329									
: GENERAL INFORMATION:									
: APPLICANT: Wang, Huaming									
: APPLICANT: Bodie, Elizabeth A.									
: TITLE OF INVENTION: Phenol Oxidizing Enzymes									
: FILE REFERENCE: GC561-3									
: CURRENT APPLICATION NUMBER: US/09/468,578									
: CURRENT FILING DATE: 1999-12-21									
: PRIOR APPLICATION NUMBER: US 09/220,871									
: PRIOR FILING DATE: 1998-12-23									
: PRIOR APPLICATION NUMBER: US 09/338,723									
: PRIOR FILING DATE: 1999-06-23									
: NUMBER OF SEQ ID NOS: 17									
: SOFTWARE: FastSeq for Windows Version 4.0									
: SEQ ID NO 2									
: LENGTH: 594									
: TYPE: PRT									
: ORGANISM: Stachybotrys chartarum									
US-09-468-578-2									
Query Match									
Best Local Similarity 100.0%; Score 3189; DB 4; Length 594;									
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
OY	1	MLFMSQMLAAASGLSGVLGIPMDTGSHPLEAVDPVKTEVFADSLAAGDDWESPYY	60						
DB	1	MLFMSQMLAAASGLSGVLGIPMDTGSHPLEAVDPVKTEVFADSLAAGDDWESPYY	60						
OY	61	NLLRYRALPPPKOKKMITNPVTGKDIWYIEIEIKPQORITPLRATLVGYGMSPP	120						
DB	61	NLLRYRALPPPKOKKMITNPVTGKDIWYIEIEIKPQORITPLRATLVGYGMSPP	120						
OY	121	GPTFNVPRGTETVVRINNATVENSVHLGSPSRAPFDGMAEDVTPGGEYKDYFPNYS	180						
DB	121	GPTFNVPRGTETVVRINNATVENSVHLGSPSRAPFDGMAEDVTPGGEYKDYFPNYS	180						
OY	181	ARLWYHDAFMKTAENAFGQAGAYIINDEADALGSPGGEFIDPLILTRAKYYNADG	240						
DB	181	ARLWYHDAFMKTAENAFGQAGAYIINDEADALGSPGGEFIDPLILTRAKYYNADG	240						
OY	241	TLRSTGEGDODLGDVIVHNGOPWPLNVOPRKYRRRFLNAAVSRAMLTYIVRTSSPNVR	300						
DB	241	TLRSTGEGDODLGDVIVHNGOPWPLNVOPRKYRRRFLNAAVSRAMLTYIVRTSSPNVR	300						
OY	301	IPROVIASDAGLLQAPVQTSNLYLAVERYEIIIDTFNAGOTLDLRNVAETNDVDEDE	360						
DB	301	IPROVIASDAGLLQAPVQTSNLYLAVERYEIIIDTFNAGOTLDLRNVAETNDVDEDE	360						

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QY      361 YAPFLVWRVYSSGTYEDNSQVSTFLDVPFPFKESPADKHKFKFESNGHYLLINDVGF 420
      |||
      361 YAPFLVWRVYSSGTYEDNSQVSTFLDVPFPFKESPADKHKFKFESNGHYLLINDVGF 420
QY      421 ADVNERVLAKPELGVWEWLENSGGWSPVHTLIVDFKLLKPTGGGVMPYESAGLK 480
      |||
      421 ADVNERVLAKPELGVWEWLENSGGWSPVHTLIVDFKLLKPTGGGVMPYESAGLK 480
Db      421 ADVNERVLAKPELGVWEWLENSGGWSPVHTLIVDFKLLKPTGGGVMPYESAGLK 480
QY      481 DVVWLGREGTEITLIEAHYQPMTGAYWMHCNLIHEDNDMAAVNTYAMEKGYLOEDFEDP 540
      |||
      481 DVVWLGREGTEITLIEAHYQPMTGAYWMHCNLIHEDNDMAAVNTYAMEKGYLOEDFEDP 540
Db      481 DVVWLGREGTEITLIEAHYQPMTGAYWMHCNLIHEDNDMAAVNTYAMEKGYLOEDFEDP 540
QY      541 MNPKRAVPYRNNDPFHARAGNFSASTARVQOELEQEPYRNRLDEITLEDLIGEE 594
      |||
      541 MNPKRAVPYRNNDPFHARAGNFSASTARVQOELEQEPYRNRLDEITLEDLIGEE 594
Db      541 MNPKRAVPYRNNDPFHARAGNFSASTARVQOELEQEPYRNRLDEITLEDLIGEE 594

RESULT 2
US-09-218-702-2
; Sequence 2, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys sp.
US-09-218-702-2

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Query Match	Similarity	100.0%;	Score 3189;	DB 4;	Length 594;
Best Local	Similarity	100.0%;	Pred. No. 1.5e-308;		
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					Gaps
QY	1	MLFESMQLAAAGSGLISGVIGIPMDTGSHPHIEAVNDEPKTEVPADSLLAAGDDDMESPXY	60		
Db	1	MLFESMQLAAAGSGLISGVIGIPMDTGSHPHIEAVNDEPKTEVPADSLLAAGDDDMESPXY	60		
QY	61	NLLRYNAPLIPPEVKOPKMITNPVTKGDIWYIEIKPQORITPTLRPATLVGYDGMSP	120		
Db	61	NLLRYNAPLIPPEVKOPKMITNPVTKGDIWYIEIKPQORITPTLRPATLVGYDGMSP	120		
QY	121	GPTENVPRGTEEVVRFINNATVENSYHLGSSSRAPFDGMAEDYTFPGGEKQIYFPNYS	180		
Db	121	GPTENVPRGTEEVVRFINNATVENSYHLGSSSRAPFDGMAEDYTFPGGEKQIYFPNYS	180		
QY	181	ARLWVHDIAPFKTAMNAVFGQAGAVIINDEEDALGLSGGEPDIPILITAKYNNAGD	240		
Db	181	ARLWVHDIAPFKTAMNAVFGQAGAVIINDEEDALGLSGGEPDIPILITAKYNNAGD	240		
QY	241	TLRSTGEHDQIDLVGIVHNQGPMPPLNQP RKYRFRPLNAAVSRAMLLYLVRTSSPNVR	300		
Db	241	TLRSTGEHDQIDLVGIVHNQGPMPPLNQP RKYRFRPLNAAVSRAMLLYLVRTSSPNVR	300		
QY	301	IPFOVTASDAGLLQADVPQTSNLYLAAVEREYIITDFTNAGOTLDRNVAETNDVDEDE	360		
Db	301	IPFOVTASDAGLLQADVPQTSNLYLAAVEREYIITDFTNAGOTLDRNVAETNDVDEDE	360		
QY	361	YARTELVMMFVYSSGIVEDNSQVPSLRLDVPFPHPHKEGPAKDFEERSNGHLINDVGF	420		
Db	361	YARTELVMMFVYSSGIVEDNSQVPSLRLDVPFPHPHKEGPAKDFEERSNGHLINDVGF	420		
QY	421	ADVNEVRLAKPELGTVEWMELENSSGSMSPVITHLVDFTILRTGRCGVMPYESAGLK	480		
Db	421	ADVNEVRLAKPELGTVEWMELENSSGSMSPVITHLVDFTILRTGRCGVMPYESAGLK	480		
QY	481	DVAVLGRGETLITLHAYQPTGAYMMHCHLLIHEDNDMAVFNVTLAMEEGYLOQEDFEP	540		
Db	481	DVAVLGRGETLITLHAYQPTGAYMMHCHLLIHEDNDMAVFNVTLAMEEGYLOQEDFEP	540		

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Db      481    DVMVGREGLTIAHNPQPMGAWMHCHNLIHEDNDMAVFNTVADEKCYLOEDEDP
Oy      541    MNPKRAVPYRNDFPHARAGNFSASISITAROELAEOPYRLDELIEDLGIEE
                        |||
Db      541    MNPKRAVPYRNDFPHARAGNFSASISITAROELAEOPYRLDELIEDLGIEE
RESULT 3
; Sequence 4, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Bipolaris spiciifera
US-09-468-578-4

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[illegible]

Db 537 GYNETTDFHDPEDPRKMSARPTAGDULANSGIFSEESIRARVNEALAEOPYSELAQVITAS 596
QY 590 L 590
Db 597 L 597

RESULT 4
US-09-468-578-7
; Sequence 7, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodle, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Curvularia pallescens
US-09-468-578-7

Query Match 60.5%; Score 1929.5; DB 4; Length 627;
Best Local Similarity 60.5%; Pred. No. 3,9e-183;
Matches 364; Conservative 81; Mismatches 134; Indels 23; Gaps 9;

QY 2 LFSKQOLAASGLISGVIGIPMDTSGHPLEAVDPREKTVFPAQSLAAGD----- 53
Db 6 LFSALQAS--IAKIGYVAL--SERPAKYIDETPDEKAA--LAAIEDDPADVFRIL 58
QY 54 -DMESPVYLRLNALPPIPVKOPKMIINPVTKGDIWYEIEIKFPQORIPYTLRPAUL 112
Db 59 KMOSPEYIILREALPIPAKAPNK-KTNPVTNKEIWIYEIYIKFNOQVPSLPAPL 117
QY 113 VGYDMSGPPTENPRGTETVVRFINNATVENSVLHSGSPRAPEDGMAEDVTFPEGYD 172
Db 118 VGYDGISPCPTIIVRGFAVVRVFNQGDRESSIHLHSGSPRAPFGWAMEDLIMKQFMD 177
QY 173 YFEPYQSRLLYTHDAFMKTAENAYFGQAGAYIINDAEDALGLPSYGERDIPLLIT 232
Db 178 YYPNNQAAARFLMYHDHMHVTAENAYFGQAGAYLITDPAEDALGLPSYGRGKIDIPVL 237
QY 223 AKYUADGTLSTEGEDDOLMGDVIHNGQPMPLNVORPKYRFRFLNAVSRAMLLYLV 292
Db 228 SKFYNSDGLTQTSVGEDNSLMGQDVHNGQPMPEFVNERPKYRFRFLNAVSRAMLLYLV 297
QY 293 RTSSPNVRIPEOVIVASDAGLQAPVQTSNLYLAVEREYIIDFTFAGQOTDLRLVAET 352
Db 298 KQQAATATRLPEQVIVASDAGLLTHPQTSIYVAAERVETIVDEFAPYQOTIDLRFAKA 357
QY 333 NDVGDEDEYARFLLEVYMRVYSSGTVEDNSQVSTLRDVPFPHKESGRADKHFEERSNGH 412
Db 338 NGVGTDDDAANDKVMRFVSSQAAVVDNSVPAQLSQIOFPADKTG-IDHHRFRHHTNSE 416
QY 413 YLINVGFAVNERVLAKPELGTVEVWELSSGGSHVHILHVDKFLIKTRTG---SG 469
Db 417 WHINIGFAVDVNRILAKPRGTVELWELSSGGSHPIHVLDFRVARGDDESTRG 476
QY 470 QVMPYESAGLKDVNLGRGETLITIAHQPTGAYVMCHNLIHEDNDMAVFNVTAMEE 529
Db 477 -VMPYESAGLKDVNLGRGETLITIAHQPTGAYVMCHNLIHEDNDMAVFNVTAMEE 535
QY 530 KGYLO-EDFEDPMRKRVAAPYRNDFHARAGNFSAESITARVOELAEOPYRNRLDEILE 588
Db 536 FGYNETTFHDPEDSRMSARPTADLTARSGIFSEASIRARVNEALAEOPYSELAQVITA 595

QY 589 DL 590
Db 596 SL 597

RESULT 5
US-09-401-476-4
; Sequence 4, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: No. 6168936el Phenol Oxidizing Enzymes
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Stachybotrys charatum
US-09-401-476-4

Query Match 54.1%; Score 1724.5; DB 4; Length 572;
Best Local Similarity 60.3%; Pred. No. 8,6e-163;
Matches 322; Conservative 75; Mismatches 126; Indels 9; Gaps 7;

QY 57 SPBYNLLYNALPPIPVKOPKMIINPVTKGDIWYEIEIKFPQORIPYTLRPAULVGD 116
Db 43 SPQYP-MFTVPLPIPVKOPRLVTNPVNGQEIWYEIEIKFTHQVYDGLGADLVGD 101
QY 117 GMSPGPTENPRGTETVVRFINNATVENSVLHSGSPRAPFGWAMEDVTFPEGYKDYTP 176
Db 102 GMSPGPTENPRGTETVVRFINNATVENSVLHSGSPRAPFGWAMEDVTFPEGYKDYTP 161
QY 177 NYOSARLLYHDAFMKTAENAYFGQAGAYIINDAEDALGLPSYGERDIPLLITAKY 236
Db 162 NQASATLWYHDAFMKTAENAYFGQAGAYIINDAEDALGLPSYGERDIPLLITAKY 221
QY 237 NADGTRSTEGEDDOLMGDVIHNGQPMPLNVORPKYRFRFLNAVSRAMLLYLVTS 296
Db 222 TANGNLVTNGELNSFWGQVHNGQPMPEKKNVPRKRYRFRFLDAVSRSGFLYFADTDA 281
QY 297 PNVRIPFOYIVASDAGLQAPVQTSNLYLAVEREYIIDFTFAGQOTDLRLVAET 355
Db 282 IDRLPEFYVIVASDAGLQAPVQTSNLYLAVEREYIIDFTFAGQOTDLRLVAET 341
QY 356 GDEDEYARFLLEVYMRVYSSGTVEDNSQVSTLRDVPF-PHKEGRADKHFEERSNGH 413
Db 342 GDTDTVDNTDKVMRFVYVADDTQPTDSVYVPAKLRDVPFSPITNTP--RQFRGRGTPTW 399
QY 414 LINDVGFAVNERVLAKPELGTVEVWELSSGGSHVHILHVDKFLIKTRTG--- 471
Db 400 TINGVAFADVQNLALANVPGTVERWELINAGNGWTHPIHILHVDKFLIKTRTG--- 459
QY 472 MPYESAGLKDVNLGRGETLITIAHQPTGAYVMCHNLIHEDNDMAVFNVTAMEE 531
Db 460 MPYES-GLKDVNLGRGETLITIAHQPTGAYVMCHNLIHEDNDMAVFNVTAMEE 518
QY 532 YLOEDEDPMRKRVAAPYRNDFHARAGNFSAESITARVOELAEOPYRNRLDEILE 585
Db 519 YNATVVDMEELMKARPELGEFGQAGAYIINDAEDALGLPSYGERDIPLLITAKY 572

RESULT 6
US-09-401-476-2
; Sequence 2, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584

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; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-401-476-2
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Query Match          53.8%; Score 1716.5; DB 4; Length 583;
Best Local Similarity 61.0%; Pred. No. 5,5e-162;
Matches 330; Conservative 67; Mismatches 125; Indels 19; Gaps 9;
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QY 57 SPPYLLRNALPIPPVOKPMIITNPVTGKDIWYEIEIKFPQORIYPTLRPATLVGYD 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 45 SPLL-ALVEPLPIPLPKPN--TVNPNTGEDILYEMERIRFSSHQIYDLEPANWGYD 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 117 GMSRPTFVPRGTETVYAFINNA--TVENSYHLGSPSRAPFDGMAEDVTTPGEYKDY 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 103 GMSRPTTIIVPRGTESVYAFVNSGENTSPNSVHLGFSRPAFDGMAEDTTPGGEYKDY 162
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 175 FPNYSARLLWYHDHAFMKTAENAYFGQAGAYIINDEADALGPSYGEFDIPLITFAK 234
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 163 YPNRQAAKMLWYHDHAFMKTAENAYFGQAGAYIINDEADALGPSYGEFDIPLITFAK 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 235 YYNADGTLRSTEGEDODLMDGVIVHNGQPMFPLVOPRRKYRFRFLNAAVSRAMLVYRT 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 223 RYNAGDTLESTNGEVSSEFPGDIVIQVNGQPMPLVNOPRRKYRFRFLNAAVSRFALYATS 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 295 SSPNRIPIPOVIASDAGLLQAPVQTSNLYLAVEREIIIDTFNFAQOTLDLRNVAETND 354
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 EDSETRLPQVIADAGLLEGVDTDTLYISMAERREVVIDSTPAQOSIDIRNLPGAOG 342
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 355 VQDEDEYARTLEVMRFVYSSGTYE--DNSQVPTLRDVPFPKHKEG---PA----DKHF 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 343 LGEVEPFDITDKVMRFVDE-VLESPTSEVPANLRDVEFP---EGGNMPPANPTDDETF 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 405 KEERSNGHYLINDVGFADYNERVLAKPELGTVEVWELENSSGGWSHPVHILVDKILKR 464
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 399 TFGRRAGQWITNGVTFSDVENRLLRVPRDTVEIMLENNNSMGWTHPVHILHVDKFLSR 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 465 TGGRGQVMEYASGLKDYVWLGRGETLTIEAHYQPTGAYMWHCHNLHEDNDMAVENV 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 459 STARG-VEPYEAGLKDVMYLARREVYVEAHYAPPGVYMLCHNLHEDNDMAAFNV 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 525 TAMEEKYLOEDFEDPMNPKRAVPYNRNDFHARAGNFAESITARQELAEQEPYRNL 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 518 TVLGDGVYTFEIDPMERLMPRPFLGLGFENGSGDFSELATIDRIQDMASFNRYAQAD 577
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QY 585 E 585
DB 578 D 578
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RESULT 7
US-09-218-702-4
; Sequence 4, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Bilirubin oxidase
US-09-218-702-4
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Query Match          53.7%; Score 1712.5; DB 4; Length 568;
Best Local Similarity 59.7%; Pred. No. 1.3e-161;
Matches 318; Conservative 76; Mismatches 128; Indels 11; Gaps 6;
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QY 57 SPPYLLRNALPIPPVOKPMIITNPVTGKDIWYEIEIKFPQORIYPTLRPATLVGYD 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 43 SPQYP-MFTVPLPIPPVOKPLTVTNPNVNGQETIWEYIEIKFTQYVYDLSADLVGYD 101
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 117 GMSRPTFVPRGTETVYAFINNAATVENSVHLGSPSRAPFDGMAEDVTTPGEYKDYFP 176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 102 GMSRPTFQVPRGTETVYAFINNAEAPNSVHLGFSRPAFDGMAEDITEPSPFDYYP 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 NQOSARLLWYHDHAFMKTAENAYFGQAGAYIINDEADALGPSYGEFDIPLITATKY 236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 162 NQOSARLLWYHDHAFMKTAENAYFGQAGAYIINDEADALGPSYGEFDIPLITATKY 221
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 NADGTLRSTEGEDODLMDGVIVHNGQPMFPLVOPRRKYRFRFLNAAVSRAMLVYRTSS 296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 222 TANGNLVTTNGELNSFWGDVIVHNGQPMFPRKRYRFRFLDAVSRFGLYADTDA 281
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 297 PVRIPIFOVIASDAGLLQAPVQTSNLYLAVEREIIIDTFNFAQOTLDLRNVAETNDV 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 282 IDTRLPIFKVIASDGLLEHPADTSLIYISMAERYEVFEDSDYAGKTIELRLNGSIGI 341
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 356 GDEDEYARTLEVMRFVYSSGTYE--DNSQVPTLRDVPFPKHKEGADKHFKERSNGHYL 414
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 342 GDTDTYDNTDKVMRFVADDTTPPTSVVPAHLRDVFP--SPTNRQFRGRGPTWT 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 415 INDVGFADYNERVLAKPELGTVEVWELENSSGGWSHPVHILVDKILKRTGGRG--QVM 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 399 INGVAFADYQNLNLANVPRGTYERHMLINAGGWTHPHIHLVDKVISRTSGNARRYM 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 473 PYESAGLKDVMYLGRGETLTIEAHYQPTGAYMWHCHNLHEDNDMAVENVYAMEEKY 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 459 PYES--KDVYMLGRETVVEAHYAPPGVYMFCHNLHEDNDMAAFNATVLPDYGY 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 533 LOEDEDEPMNPKRAVPYNRNDFHARAGNFAESITARQELAEQEPYRNLDE 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 516 NATVEVDPMEELMQARPELGEFOASQGSVQAVANGERTIQTMAERYRPAADE 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 8
US-09-134-001C-2946
; Sequence 2946, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2946
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2946
```

```
Query Match          12.6%; Score 400.5; DB 4; Length 322;
Best Local Similarity 32.9%; Pred. No. 2e-31;
Matches 118; Conservative 43; Mismatches 151; Indels 47; Gaps 12;
```

```
QY 171 KDYEPNYSARLLWYHDHAFMKTAENAYFGQAGAYIINDEADALGPSYGEFDIPLI 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6 KTIKFEVNDASATLWYHNPSPNTAQQVYNGLSGLIYIDSKN--NPSNNGKNDLPII 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 231 LTAKYINADGTLRSTEGEOD--LMDGVIVHNGQPMFPLVOPRRKYRFRFLNAAVSRAML 289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 64 IODKTF-VSKKLNYSKTEDEDTQGDJVLVNCIVNPKLTAKKEKIRLLRLNGSNARDNL 122
QY 290 YLVRTSSPNVRIRPFOVIASDAGLLQAPVOTSNLYLAVEREYIIIDFTFAQOTDLRNV 349
Db 123 KLSNNOS-----FEYIASDGGOLNNAKLKEINLAPSERKEIVIDLKMKKEKISL--- 173
QY 350 AETNDVGEDEDEARLEWMEFVSSGTVEDNSQVSTLADVPFPFKKEGPARKHFEERS 409
Db 174 -----VONDK-----TYLPISSNKEKSSNKGNTPK-----VSKTKILEGM 208
QY 410 NGHYLINDVGADVNERVLAKPELCTVEWELEN---SSGWSHPVHILVDPEKILKRTG 466
Db 209 NDHYTINGNKF-DPN-RIDFTQKLNQKEWMEIENVKDKMGKHPFHIGTQFVLSVD- 265
QY 467 GRGQVMPRESAGLKVWNLGRGETLTLEAHYQPMTGAYMCHNLHEDNDMAAFNVNT 525
Db 266 -GEKPPKDMRGKDVISLEPGOKAKIEVFERN-TGYTFHCHLLEHEDNGMKGOIKYVT 321

RESULT 9

US-09-468-578-9
: Sequence 9, Application US/09468578
: Patent No. 6393329
: GENERAL INFORMATION:
: APPLICANT: Wang, Huming
: APPLICANT: Bodle, Elizabeth A.
: TITLE OF INVENTION: Phenol Oxidizing Enzymes
: FILE REFERENCE: GC561-3
: CURRENT APPLICATION NUMBER: US/09/468, 578
: PRIORITY FILING DATE: 1999-12-21
: PRIOR APPLICATION NUMBER: US 09/220, 871
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: US 09/338, 723
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 114
: TYPE: PRT
: ORGANISM: Amersporium atrum
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (1)...(114)
: OTHER INFORMATION: Xaa - space of unknown number of aa
US-09-468-578-9

Query Match 11.2%; Score 357.5; DB 4; Length 114;
Best Local Similarity 32.2%; Pred. No. 6.8e-28;
Matches 85; Conservative 13; Mismatches 15; Indels 151; Gaps 4;

QY 194 TAENNYFQOAGAYIINDAEADALGIPSGYGERDIPILITAKYNNADGTLRSTEGEDDILW 253
Db 1 TAENNYFQOAGFYIILHDAEDALGLPS--GKYDPLALSLKAYNSDGLTFDEKDETSIF 58
QY 254 GDVIVNGCPMPELVNORPKYRFRFLNAVASRAWLLVLRSSPNVRIRPFOVIADAGLL 313
Db 59 GDVIVNGCPMPELVNORPKYRFRFLNAVASRAWLLVLRSSPNVRIRPFOVIADAGLL 313
QY 314 QAPVOTSNLYLAVEREYIIIDFTFAQOTDLRNVAVETNDVGEDEDEARLEWMEFVSS 373
Db 92 ----- 91
QY 374 SGTVEDNSQVSTLADVPFPFKKEGPARKHFEERSNGHYLINDVGADVNERVLAKPEL 433
Db 92 -----FK----- 93
QY 434 GTVEWELEN-SSGWSHPVHIL 456
Db 94 ---XWMELENTSSGWSHPVHIL 114

RESULT 10
US-08-749-882A-2

: Sequence 2, Application US/08749882A
: Patent No. 5750388
: GENERAL INFORMATION:
: APPLICANT: Berka, Randy
: APPLICANT: Thompson, Sheryl
: APPLICANT: Xu, Feng
: TITLE OF INVENTION: Purified Scytalidium laccases
: TITLE OF INVENTION: And Nucleic Acids Encoding Same
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 57503880 No. 5750388disk Of No. 5750388th America, Inc.
: STREET: 405 Lexington Avenue - 64th Fl.
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10174
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/749, 882A
: FILING DATE: 15-NOV-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias J
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4186, 020-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-878-9652
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 616 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Scytalidium thermophilum
US-08-749-882A-2

Query Match 6.3%; Score 202; DB 1; Length 616;
Best Local Similarity 23.1%; Pred. No. 3.4e-11;
Matches 147; Conservative 77; Mismatches 237; Indels 174; Gaps 35;

QY 8 LAAASGLL-SGYLGIIPMDGSHPIEAVDPEVKEVFADSLAAAGDDMESPPYLLLRN 66
Db 9 LLLAGLNSGLAAP---STHP--RSNPDIILERDDHSLTSRQG--SCHSPSNRACWS 61
QY 67 ALRPPVQPKMIITNPVYTKDWMYEIEIKFOQRIYP--TLRPATLVGYDMSGPGTF 124
Db 62 GFDINTVDETK---TPNPGV--VRRYTFDITVDNRPPGDPYIKRKMMLINDKLL-GFTV 115
QY 125 NVPRGTEIVVRINN--ATVENSVLHSGSPSRAP--FDGMAEDVTF----DEKYDYVFP 176
Db 116 FANWG-DTIEVTVNNHRLRTNGTSIMHGHQKGTNYHNG-ANGVTECPPIPGGSRYVSFR 173
QY 177 NYQASRLMYHDHAFMAKNAENYFQOAGAYIINDAEADALGIPSGYGERDIPIL-ILTKAK- 234
Db 174 ARQYG-TSNYHSH-FSAQYGN---GVSQAIQINGPA---SLP-----YDIDLGLVPLD 219
QY 235 --YVNADGTLRSTEGEDDILMGDVIVNGO-----PMPFLNVOP-RKYRFRFLNAA 282
Db 220 WYKASADOLVETTLAKGNAPFSDNVLINGTAKHPTTGGGEVAIVLTPDKRRLRLIMMS 279
QY 283 VSRALLVLRSSPNVRIRPFOVIASDAGLLQAPVOTSNLYLAVEREYIIIDFT----- 337
Db 280 VENNFOVSLAKHT-----MTVIAADWVPVNA-MTVISLFWAVGQRYDVIDASQAVGN 331
QY 338 -----NFAGO-----TIDLNRVAVETN 353

Db 332 YWFNITFGQOKCGFSHPAPALIFRYEGAPDALPTDGAAPKDHQCLDTLIDLSPVYOKN 391
Qy 354 DVGDEDEYARTLEWRFVYSSGTVEDNSQVSTLRDVPFPPHKEGPAKHFKERSNG-- 411
Db 392 -----VPVDFGVKEPG-----NTLPVTL-----HVQAAAPHVFTWKINGSA 428
Qy 412 -----HYLINDYGFADVNERVYLAKPELGTVEWELENSSG--MSHPVHILV 457
Db 429 ADVMDRPLEYVNMNDLSIPVKNNIVYVDGVNEMTYWLVENDEGRSLSPHMHLSGH 488
Qy 458 DFKILRTGGRGOVVPYESAGL-----KDVVWL-GRGETLTTEAHYQ 498
Db 489 DFEVLGRS---PDVSPDSETRFVFPDAVDLPRLRGHNFRRDVTMLPARGWLLAFRTDN 545
Qy 499 PWTGAYMWHCHNLHEDNDMAVFNVTAMEEKGYL 533
Db 546 P-GAMLFHCHIAHWVSGLSVDFLERPDELRGQL 578

RESULT 11
US-08-539-134-2
Sequence 2, Application US/08539134
Patent No. 5843745
GENERAL INFORMATION:
APPLICANT: Berka, Randy
APPLICANT: Thompson, Sheryl
APPLICANT: Xu, Feng
TITLE OF INVENTION: Purified Scytalidium Laccases
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: No. 58437450 No. 5843745disk Of No. 5843745th America, Inc.
STREET: 405 Lexington Avenue - 64th Fl.
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,134
FILING DATE: 04-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4186,010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9652
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 616 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Scytalidium thermophilum
US-08-539-134-2

Query March 6,34; Score 202; DB 2; Length 616;
Best Local Similarity 23.18; Pred. No.3.4e-11;
Matches 147; Conservative 77; Mismatches 237; Indels 174; Gaps 35;

Qy 8 LAASGGLTSGVILPMDTGSHPTEAVPEVTEFVADSLAAAGDDDWESPYYMLLYRN 66
Db 9 LLLAGLINSGLAP---STHP--RSNPDLILERDHSLSRGS--SCHSSNACMS 61
Qy 67 ALPIPVKOPKMITNPVTGKDIWYEIEIKPQRIY--TLRPATLVGIDGMSPGPTF 124

Db 62 GEDINFDYETK---TPMTGV-VRRYTFDITEVDNRPGPDGVIEKMLINDKLL-GETV 115
Qy 125 NVPRCTETVREFINN--ATVENSVLHGSPSRAP--FDGMAEDVTF---DGEKDYVFP 176
Db 116 FANNG-DTIEYTVNNHLRTNGTSHMHGLHOKGTIVHDG-ANGVTECIIPPGGSNYSFR 173
Qy 177 NYQARLLMYHDHAEFMKTAENAYFGQAGAYITIDEADALGPSYGEFDIPL-ILTK- 234
Db 174 AROYG-TSMYHSH-FSAQYGN--GVSQAIOINGPA---SLP-----YDIDLGLVPLQD 219
Qy 235 --YINADGTLASTEGEDDDINGDVIHVNGQ-----PPFPLNVOP-RKYRREFLNAA 282
Db 220 WYKSAQDLVIETLAKGNAPPSDNVLLNGTAKHPTTGEGEYAIKLPDKRRLRLNMS 279
Qy 283 VSRAMLTVLRTSSPNVRIPECVIASDAGLLQAPVQTSNLVLAVEREITIDFT----- 337
Db 280 VENHFOVSLAKHT-----MTVIAADNVPYNA-MTVSLMAVQQRVDYITIDASQAVGN 331
Qy 338 ----NFAQG-----TDLRNVAETN 353
Db 332 YWFNITFGQOKCGFSHPAPALIFRYEGAPDALPTDGAAPKDHQCLDTLIDLSPVYOKN 391
Qy 354 DVGDEDEYARTLEWRFVYSSGTVEDNSQVSTLRDVPFPPHKEGPAKHFKERSNG-- 411
Db 392 -----VPVDFGVKEPG-----NTLPVTL-----HVQAAAPHVFTWKINGSA 428
Qy 412 -----HYLINDYGFADVNERVYLAKPELGTVEWELENSSG--MSHPVHILV 457
Db 429 ADVMDRPLEYVNMNDLSIPVKNNIVYVDGVNEMTYWLVENDEGRSLSPHMHLSGH 488
Qy 458 DFKILRTGGRGOVVPYESAGL-----KDVVWL-GRGETLTTEAHYQ 498
Db 489 DFEVLGRS---PDVSPDSETRFVFPDAVDLPRLRGHNFRRDVTMLPARGWLLAFRTDN 545
Qy 499 PWTGAYMWHCHNLHEDNDMAVFNVTAMEEKGYL 533
Db 546 P-GAMLFHCHIAHWVSGLSVDFLERPDELRGQL 578

RESULT 12
US-08-991-531-2
Sequence 2, Application US/08991531
Patent No. 5925554
GENERAL INFORMATION:
APPLICANT: Pedersen, Anders Hjelholt
APPLICANT: Svendsen, Allan
APPLICANT: Schneider, Palle
APPLICANT: Rasmussen, Grethe
TITLE OF INVENTION: Myceliophthora And Scytalidium Laccase
TITLE OF INVENTION: Variants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: No. 59255540 No. 5925554disk Of No. 5925554th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,531
FILING DATE: 16-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5125,200-US


```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 616 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-531-2

Query Match      6.3%; Score 202; DB 2; Length 616;
Best Local Similarity 23.0%; Pred. No. 3.4e-11;
Matches 146; Conservative 76; Mismatches 239; Indels 174; Gaps 34;

QY 8 LAAASGLL-SGVLGIPMDTGSHPTEAVDEVKTEVFADSLAAAGDDMESPPYLLRYN 66
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9 LLLAAGLLNSGALAAP---STHP--RSNPDLIERDHSITLSRQG--SCHSPSNRACWCS 61

QY 67 ALPIPVKQPKMITNPVTKGDIWYEIEIKRQORLYP--TLRPATLVGYDMSGPTFF 124
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 62 GEDINTDYETK---TPNTGV-VRRYTFDTEVDNRPGRGVYKELMLINDKLL-GPTV 115

QY 125 NVPRGTEFVRFIN--ATVENSVLHSGSPSRAP--FDGMAEDVTF---PGEYKDYFP 176
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 116 FANWG-DTIEVYNNHLNRLNGTSHHGHLOKNTYHDG-ANGVTCSPIRPGSGRYYSFR 173

QY 177 NQASARLLYHDAEMFKTLEMAVFGQAGAYIINDEAEDALGSPSGYGERDIPL---ILT 232
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 174 ARQYG-TSWYHSH-FSAQYGN--GVSGAIQINGPA---SLP---YDIDGLVPLXD 219

QY 233 AKYUNADGTLRSTEGEDQDLKMGDVHIVNGO-----PWFLNVPQ-RKYRFRFLNA 282
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 220 WYKKSADQVLETLLKGNAPFSDNVLINGTAKHPPTGEGEYAIKLTTPKRRRLRLNMS 279

QY 283 VSRAMLVLVTRTSSPNVRIIPQVIASDAGLLQAPVQTSNLYLAVERYEIITDFT----- 337
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 280 VENHFGVSLAKHT-----MTVIADMYPVNA-MTVDSLPAVQGRYDVTIDASQAVGN 331

QY 338 -----NFAQO-----TLDIRNVAETN 353
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 332 YWFNITFFGQOKCGFSHNPAPAIFRYEGAPDALPTDGAAPKDHQCLDTLDSLVYQKN 391

QY 354 DVGDEDEYARTLEVMEFVYSSGTVEDNSQVPTSLRDVPRPPKREGADNHFERSNG--- 411
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 392 -----VPVDEYFAEPG-----NTLPVTL-----HYDDAADAAPHVFTWKINGSA 428

QY 412 -----HYLINDVGFADYNERVLAKPELGTVEVMELENSSG---WSHPVHIHLV 457
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 429 ADVDMDRPYLEVVMNNDLSSIPVKNIVAVDGVNEMTYLVLENDEBGRSLSLRPHMLHGH 488

QY 458 DKILKRTGRCQVMPYESAGL-----KDYVWL-GRGETLTTEAHYQ 498
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 489 DEFVLGRS---PDVSPDSETRFVFPADVLDLRLRGHNPRVRDVTMLPARGMILLAFRTDN 545

QY 499 PWTGAYVMHCHNLIEHDNDMAVFNVTAMEEKGYL 533
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 546 P--GAWLFHCHIAHXVSGLSYDFLERPEDELRGOL 578

RESULT 13
US-09-032-315-9
Sequence 9, Application US/09032315
Patent No. 5985818
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59858180 No. 5985818disk of No. 5985818th America, Inc.
STREET: 405 Lexington Avenue
```

```
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,315
FILING DATE: 27-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 616 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-032-315-9

Query Match      6.3%; Score 202; DB 2; Length 616;
Best Local Similarity 23.0%; Pred. No. 3.4e-11;
Matches 146; Conservative 76; Mismatches 239; Indels 174; Gaps 34;
```

```
QY 8 LAAASGLL-SGVLGIPMDTGSHPTEAVDEVKTEVFADSLAAAGDDMESPPYLLRYN 66
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9 LLLAAGLLNSGALAAP---STHP--RSNPDLIERDHSITLSRQG--SCHSPSNRACWCS 61

QY 67 ALPIPVKQPKMITNPVTKGDIWYEIEIKRQORLYP--TLRPATLVGYDMSGPTFF 124
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 62 GEDINTDYETK---TPNTGV-VRRYTFDTEVDNRPGRGVYKELMLINDKLL-GPTV 115

QY 125 NVPRGTEFVRFIN--ATVENSVLHSGSPSRAP--FDGMAEDVTF---PGEYKDYFP 176
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 116 FANWG-DTIEVYNNHLNRLNGTSHHGHLOKNTYHDG-ANGVTCSPIRPGSGRYYSFR 173

QY 177 NQASARLLYHDAEMFKTLEMAVFGQAGAYIINDEAEDALGSPSGYGERDIPL---ILT 232
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 174 ARQYG-TSWYHSH-FSAQYGN--GVSGAIQINGPA---SLP---YDIDGLVPLXD 219

QY 233 AKYUNADGTLRSTEGEDQDLKMGDVHIVNGO-----PWFLNVPQ-RKYRFRFLNA 282
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 220 WYKKSADQVLETLLKGNAPFSDNVLINGTAKHPPTGEGEYAIKLTTPKRRRLRLNMS 279

QY 283 VSRAMLVLVTRTSSPNVRIIPQVIASDAGLLQAPVQTSNLYLAVERYEIITDFT----- 337
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 280 VENHFGVSLAKHT-----MTVIADMYPVNA-MTVDSLPAVQGRYDVTIDASQAVGN 331

QY 338 -----NFAQO-----TLDIRNVAETN 353
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DB 332 YWFNITFFGQOKCGFSHNPAPAIFRYEGAPDALPTDGAAPKDHQCLDTLDSLVYQKN 391

QY 354 DVGDEDEYARTLEVMEFVYSSGTVEDNSQVPTSLRDVPRPPKREGADNHFERSNG--- 411
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 392 -----VPVDEYFAEPG-----NTLPVTL-----HYDDAADAAPHVFTWKINGSA 428

QY 412 -----HYLINDVGFADYNERVLAKPELGTVEVMELENSSG---WSHPVHIHLV 457
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DB 429 ADVDMDRPYLEVVMNNDLSSIPVKNIVAVDGVNEMTYLVLENDEBGRSLSLRPHMLHGH 488

QY 458 DKILKRTGRCQVMPYESAGL-----KDYVWL-GRGETLTTEAHYQ 498
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DB 489 DEFVLGRS---PDVSPDSETRFVFPADVLDLRLRGHNPRVRDVTMLPARGMILLAFRTDN 545
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Oy      499  PWTGAYMWHCHNLIHEDNDMAVENVTAMEEKGYL 533
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Db      546  P--GAWLFCHIAHXVSGSLVDFLERPDRLRQL 578

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RESULT 14
US-08-993

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1      : Sequence 9 Application US/08993318A
2      : Patent No. 5998353
3      :
4      : GENERAL INFORMATION:
5      : APPLICANT: Pedersen, Anders
6      : APPLICANT: Svendsen, Allan
7      : APPLICANT: Schneider, Palle
8      : APPLICANT: Rasmussen, Grethe
9      : APPLICANT: Cherry, Joel
10     :
11     : TITLE OF INVENTION: LACCASE MUTANTS
12     :
13     : NUMBER OF SEQUENCES: 10
14     :
15     : CORRESPONDENCE ADDRESSES:
16     : ADDRESSSEE: No. 5998353o No. 5998353disk of No. 5998353lth Americaa
17     : STREET: 405 Lexington Avenue
18     : CITY: New York
19     :
20     : COUNTRY: USA
21     :
22     : ZIP: 10174
23     :
24     : COMPUTER READABLE FORM:
25     : MEDIUM TYPE: Floppy disk
26     : COMPUTER: IBM PC compatible
27     : OPERATING SYSTEM: PC-DOS/MS-DOS
28     : SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
29     :
30     : CURRENT APPLICATION DATA:
31     : APPLICATION NUMBER: US/08/993,318A
32     : FILING DATE: December 18, 1997
33     : CLASSIFICATION: 435
34     : ATTORNEY/AGENT INFORMATION:
35     : NAME: Gregg, Valeta A.
36     : REGISTRATION NUMBER: 33,728
37     : REFERENCE/DOCKET NUMBER: 5032.200-US
38     : TELECOMMUNICATION INFORMATION:
39     : TELEPHONE: 212-867-0123
40     : TELEFAX: 212-878-9655
41     :
42     : TELEX:
43     :
44     : INFORMATION FOR SEQ ID NO: 9:
45     : SEQUENCE CHARACTERISTICS:
46     : LENGTH: 616 amino acids
47     : TYPE: amino acid
48     : STRANDEDNESS: single
49     : TOPOLOGY: linear
50     :
51     : MOLECULE TYPE: protein
52     :
53     : US-08-993-318A-9

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Query Match	6.3%	Score 202;	DB 2;	Length 616;
Best Local Similarity	23.0%;	Pred. No. 3.4e-11;		
Matches 146;	Conservative 76;	Mismatches 239;	Indels 174;	Gaps 34

[illegible]

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QY 283 VSNAMLLYLVARTSSPNRNIIPROYIASAGLLQAPVQSNLYIAVEEYELIIDFT----- 337
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Db 280 VENNHOVSALACT-----MTVIAADKVPVNA-MTVDSLFMAVGORTDVTIDASOAVCN 331
      | : : : : : | : : : : : | : : : : : | : : : : : |
QY 338 -----NFGQ-----TLDLRNVAETN 353
      | | | | | | | | | | | | | | | |
Db 332 YWENTTFEGGQOKCFESHNPAPALFREGAGDALPTDGPAAKDHOCLOTLDLSPVQKN 351
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Db 392 -----VPDQGFYKEPG-----NTLPVTL-----HYDQAAAPHVFTWKINGS 428
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QY 412 -----HYLINDYGFADNERYVLAKELCTGEVWELENSSG-----WSRPVNHILV 457
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QY 456 DKIKLKRTGGROQVWPYESAGL-----KDYVWL-GRGETTLTEAHYQ 498
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Db 489 DEEVLGRS---PDVSPDSETRFVEDPAVDLRLKQHNRPVRDRVTMLPARGMLLLAERTDN 545
      | : : : : : | : : : : : | : : : : : | : : : : : |
QY 499 PWTGAYMMHCHNLHEDNDMMAVFENVTAMEEGYL 533
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RESULT 15
US-09-028

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1Sequence 2, Application US/09028887
2Patent No. 6060442
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4GENERAL INFORMATION:
5APPLICANT: Svendsen, Allan
6TITLE OF INVENTION: LACCASE MUTANTS
7NUMBER OF SEQUENCES: 2
8CORRESPONDENCE ADDRESS:
9ADDRESSSEE: No. 60604420 No. 6060442disk of No. 6060442th America
10STREET: 405 Lexington Avenue
11CITY: New York
12STATE: NY
13COUNTRY: USA
14ZIP: 10174
15
16COMPUTER READABLE FORM:
17MEDIUM TYPE: Floppy disk
18COMPUTER: IBM PC compatible
19OPERATING SYSTEM: PC-DOS/MS-DOS
20SOFTWARE: PatentIn Release #1.0, Version #1.30 (Epo)
21CURRENT APPLICATION DATA:
22APPLICATION NUMBER: US/09/028,887
23FILING DATE: 24-February-1998
24
25CLASSIFICATION:
26ATTORNEY/AGENT INFORMATION:
27NAME: Gregg, Valeta A.
28REGISTRATION NUMBER: 35,127
29REFERENCE/DOCKET NUMBER: 5201.200-US
30INFORMATION FOR SEQ ID NO: 2:
31SEQUENCE CHARACTERISTICS:
32LENGTH: 616 amino acids
33TYPE: amino acid
34STRANDEDNESS:
35TOPOLOGY: linear
36
37MOLECULE TYPE: protein
38
39US-09-028-887-2

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Query Match	6.38;	Score 202;	DB 3;	Length 616;
Best Local Similarity	23.08;	Pred. No. 3.4e-11;		
Matches 146;	Conservative 76;	Mismatches 239;	Indels 174;	Gaps 34;

[illegible]

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 05:15:58 ; Search time 46 Seconds
(without alignments)
329.914 Million cell updates/sec

Title: US-09-218-702-2

Perfect score: 3189
Sequence: 1 MLFSWQLAAAGSLSGVIG.....AEQEPYNRLEDELDGIEE 594

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 2554876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCOT_NEW_PUB.pep:*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3189	100.0	594	10 US-09-338-723A-2	Sequence 2, Appli
2	3189	100.0	594	12 US-10-080-210-2	Sequence 2, Appli
3	3189	100.0	594	12 US-10-080-233-2	Sequence 2, Appli
4	1954.5	61.3	627	10 US-09-338-723A-4	Sequence 4, Appli
5	1954.5	61.3	627	12 US-10-080-210-4	Sequence 4, Appli
6	1929.5	60.5	627	12 US-10-080-210-7	Sequence 4, Appli
7	1724.5	54.1	572	9 US-09-942-185-4	Sequence 7, Appli
8	1716.5	53.8	583	9 US-09-942-185-2	Sequence 4, Appli
9	1712.5	53.7	568	12 US-10-080-233-4	Sequence 2, Appli
10	500	15.7	511	9 US-09-738-626-4553	Sequence 4, Appli
11	357.5	11.2	114	12 US-10-080-210-9	Sequence 4, Appli
12	202	6.3	616	9 US-09-869-877-9	Sequence 9, Appli
13	202	6.3	616	10 US-09-732-350-9	Sequence 9, Appli
14	198.5	6.2	529	9 US-09-869-877-5	Sequence 5, Appli
15	198.5	6.2	529	10 US-09-732-350-5	Sequence 5, Appli
16	197	6.2	573	9 US-09-869-877-10	Sequence 10, Appli
17	197	6.2	573	10 US-09-732-350-10	Sequence 10, Appli
18	192.5	6.0	499	9 US-09-869-877-2	Sequence 2, Appli
19	192.5	6.0	499	10 US-09-732-350-2	Sequence 2, Appli

20	187.5	5.9	539	9 US-09-869-877-1	Sequence 1, Appli
21	187.5	5.9	539	10 US-09-732-350-1	Sequence 1, Appli
22	179	5.6	548	9 US-09-869-877-4	Sequence 4, Appli
23	179	5.6	548	10 US-09-732-350-4	Sequence 4, Appli
24	174.5	5.5	499	9 US-09-869-877-3	Sequence 3, Appli
25	174.5	5.5	499	10 US-09-732-350-3	Sequence 3, Appli
26	162	5.1	564	9 US-09-944-160-12	Sequence 12, Appli
27	147	4.6	493	9 US-09-738-626-6780	Sequence 6780, Ap
28	126.5	4.0	572	9 US-09-869-877-7	Sequence 7, Appli
29	126.5	4.0	572	10 US-09-732-350-7	Sequence 7, Appli
30	121.5	3.8	886	9 US-10-002-3098-2	Sequence 2, Appli
31	119.5	3.7	575	9 US-09-869-877-8	Sequence 8, Appli
32	119.5	3.7	575	10 US-09-732-350-8	Sequence 8, Appli
33	111	3.5	599	9 US-09-869-877-6	Sequence 6, Appli
34	111	3.5	599	10 US-09-732-350-6	Sequence 6, Appli
35	105	3.3	2764	9 US-09-808-602-80	Sequence 80, Appli
36	104.5	3.3	1938	9 US-10-014-436-2	Sequence 2, Appli
37	103	3.2	19	10 US-09-338-723A-6	Sequence 2, Appli
38	103	3.2	19	12 US-10-080-210-10	Sequence 6, Appli
39	100.5	3.2	1600	9 US-09-738-626-4310	Sequence 4310, Ap
40	100.5	3.2	1653	10 US-09-741-669-402	Sequence 402, Ap
41	100	3.1	2765	9 US-09-808-602-84	Sequence 84, Appli
42	99	3.1	1092	9 US-09-423-126-5	Sequence 5, Appli
43	98	3.1	1198	9 US-09-975-719-405	Sequence 405, App
44	97.5	3.1	2724	9 US-09-808-602-13	Sequence 13, Appli
45	97.5	3.1	2733	9 US-09-808-602-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1				
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; Sequence 2, Application US/09338723A				
; Patent No. US20020019038A1				
; GENERAL INFORMATION:				
; APPLICANT: Huaming, Wang				
; TITLE OF INVENTION: Phenol Oxidizing Enzymes				
; FILE REFERENCE: GC561-2				
; CURRENT APPLICATION NUMBER: US/09/338,723A				
; CURRENT FILING DATE: 1999-06-23				
; PRIOR APPLICATION NUMBER: 09/220,871				
; PRIOR FILING DATE: 1998-12-23				
; NUMBER OF SEQ ID NOS: 11				
; SOFTWARE: FastSeq for Windows Version 3.0				
; SEQ ID NO 2				
; LENGTH: 594				
; TYPE: PRT				
; ORGANISM: Stachybotrys chartarum				
US-09-338-723A-2				
Query Match 100.0%; Score 3189; DB 10; Length 594;				
Best Local Similarity 100.0%; Pred. No. 2.2e-256;				
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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QY	61	NLLRYRALPIPPKQPKMITNPVTGKDIWYIEIEKPPQOARIYPTLRPATLVGDGMSF	120	
DB	61	NLLRYRALPIPPKQPKMITNPVTGKDIWYIEIEKPPQOARIYPTLRPATLVGDGMSF	120	
QY	121	GPTFNPVPGTETVVRFINNATVENSYHLGSPSRAPDFGMAEDVTFPGCYKDYFPNVS	180	
DB	121	GPTFNPVPGTETVVRFINNATVENSYHLGSPSRAPDFGMAEDVTFPGCYKDYFPNVS	180	
QY	181	ARLWHDHAFKKTANNAFEGGAGATIIINDEADALGSPGGEPIPLITAKKYNADG	240	
DB	181	ARLWHDHAFKKTANNAFEGGAGATIIINDEADALGSPGGEPIPLITAKKYNADG	240	
QY	241	TLRSTGEODLMDGVIIHNGOPWPLNQPCKRYRFLNAVSRAMLTYLVRTSSPNVR	300	
DB	241	TLRSTGEODLMDGVIIHNGOPWPLNQPCKRYRFLNAVSRAMLTYLVRTSSPNVR	300	

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Dh 301 IFFOVIASDAGLLQAPVQTSNLYLAAVEREYELIIDFTNAGOTLDRNVAETNDVDEDE 360
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Dh 361 YARTLEVMRFVYVSSGTVEDNSQVPTLRDVPPEPPHKEGPADKHFFERSNGHYLLINDVGF 420
Oy 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
Dh 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
Oy 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAAVENVTAMEKGYLQEDFEDP 540
Dh 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAAVENVTAMEKGYLQEDFEDP 540
Oy 541 MNPKNRAVPYNNRNDPHARAGNFSAESITARVOELAEQEPYNNRLDEILDGIEE 594
Dh 541 MNPKNRAVPYNNRNDPHARAGNFSAESITARVOELAEQEPYNNRLDEILDGIEE 594
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RESULT 2
US-10-080-210-2
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; Sequence 2, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-10-080-210-2
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Query Match 100.0%; Score 3189; DB 12; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.2e-256;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dh 61 NLLYRNALPIPPYKOPKMITNPNVTGKDIWYIEIKPQORLYPTLRPATLVGYDGMS 120
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Dh 121 GPTFNVPRTGETVVRFINNATVENSYHLHGSRAFDGMAEDVTFPGEEKDYFEPNYS 180
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Dh 181 ARLLWYHDAEFKTKTANAFGQAGATYINDEADALGSPGGEFDIPILITRAKYNNAG 240
Oy 241 TLRSTEGEDQDLMDGVYIHVNGQPWPFLLNVQPRKRYFRFLNAAVSRAMLLYLVRTSSPNVR 300
Dh 241 TLRSTEGEDQDLMDGVYIHVNGQPWPFLLNVQPRKRYFRFLNAAVSRAMLLYLVRTSSPNVR 300
Oy 301 IFFOVIASDAGLLQAPVQTSNLYLAAVEREYELIIDFTNAGOTLDRNVAETNDVDEDE 360
Dh 301 IFFOVIASDAGLLQAPVQTSNLYLAAVEREYELIIDFTNAGOTLDRNVAETNDVDEDE 360
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Dh 361 YARTLEVMRFVYVSSGTVEDNSQVPTLRDVPPEPPHKEGPADKHFFERSNGHYLLINDVGF 420
Oy 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
Dh 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
Oy 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAAVENVTAMEKGYLQEDFEDP 540
Dh 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAAVENVTAMEKGYLQEDFEDP 540
Oy 541 MNPKNRAVPYNNRNDPHARAGNFSAESITARVOELAEQEPYNNRLDEILDGIEE 594
Dh 541 MNPKNRAVPYNNRNDPHARAGNFSAESITARVOELAEQEPYNNRLDEILDGIEE 594
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RESULT 3
US-10-080-233-2
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; Sequence 2, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1 Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys sp.
US-10-080-233-2
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Query Match 100.0%; Score 3189; DB 12; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.2e-256;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dh 361 YARTLEVMRFVYVSSGTVEDNSQVPTLRDVPPEPPHKEGPADKHFFERSNGHYLLINDVGF 420
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Dh 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
Oy 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAAVENVTAMEKGYLQEDFEDP 540
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Db 541 MNPKNRAVYNNRNDPHARAGNFSAESITARVOELAEQEPYNRLEDELDIGIE 594

RESULT 4
US-09-338-723A-4
; Sequence 4, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huangming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRF
; ORGANISM: Bipolaris spicifera
US-09-338-723A-4

Query Match 61.3%; Score 1954.5; DB 10; Length 627;
Best Local Similarity 61.1%; Pred. No. 4.7e-154;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

Qy 2 LFKSQOLAASGLSGVLGIPMDTGSPIEAVDPEVKTEVPFDSLLAAGDD----- 53
Db 6 LFSALQLV-----IAKGIYVAL--SERPAKEVDNTPDEKAA--LASTIVEDDPADVVMNL 58
Qy 54 -DMESPYYNLKLYRNALPIPPVKQPKMIITNPYTKDIIWYEIEIKPFOQRIYPTLRATL 112
Db 59 KMWQSEYELIRQPLPIPAKEPNK-LTNPYTNKEIWIYELIKFTQOYVPSLRAPL 117
Qy 113 VGIDGMSPEPTNPVPGTIVVRFINNAIVENSVLHSGSPRAPFDGMAEDVTFGEYKD 172
Db 118 VGIDGISPPTIIVPGTAVVRFINQGDRESSIHLSGSPRAPFDGMDMIMKEYKD 177
Qy 173 YFEPNQSARLMLYHDHAAFKTAENAYFGQAGAYIINDAEALGLPSGYGEFDPIILIT 232
Db 178 YFYPNQAARFLMYHDHAAHVTAEENAYFGQAGAYLITDPAEDALGLPSGYGKTDIPLVLS 237
Qy 233 AKYNNADGTLRSTEGEDDGLMGDVIHVGQPPFLNVQPRKXRFRLNAVASRAMLLYLV 292
Db 238 SKYNNADGTLKTSVGEDKSVMGDIIHVGQPPFLNVBERKXRLRLNAVASRNFALYFV 297
Qy 293 RTSSPNVRIPEFOVIASDAGLLQAPVOTSNLYLAVEREYIIIDFTNFACQTLDRNVAET 352
Db 298 KQDNATRIPEFOVIASDAGLLTHPVQTSMDYVAAERYEIVDFAPYAGQTLDRNFAPA 357
Qy 353 NDVGDEDEARLLEVMRFVSSGTVEDNSQVSTLRDVFPPPHKESPRADKHKFEKSNCH 412
Db 358 NGIGTDDDTAANDKVMRFVSSQTVVANSVPEQLSQIQFPAKDT-DIDHNRFRHRTNCE 416
Qy 413 YLINDVGFADVNERVLAKBELGTVEVMELENSSGMSHNVHILVDFKILKRTGGRGQ-- 470
Db 417 WRINGGFAVDENRVLAKPRGTVELMELENSSGMSHNIHVILVDFRVAVARYGDEGTG 476
Qy 471 VMPYESAGLKDVVWLGSGTLLTEAHYQPTGATYMWCHNLHEDNDMAVFNVTAMERK 530
Db 477 VMPYEAAGLKDVVWLGSRHETVLEAHYAPWDGVYMFHCHNLHEDODMMAAFDVTKLQNF 536
Qy 531 GYLQ--EDFEDPMNPKRAVRYNNRNDPHARAGNFSAESITARVOELAEQEPYNRLEDELD 589
Db 537 GYNETTTDFHDPEDPKMSARPTAGDLTARSGLFSEESIRARVNEALALQOPYSELAQVYAS 596
Qy 590 L 590
```

```
Db 597 L 597

RESULT 5
US-10-080-210-4
; Sequence 4, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huangming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRF
; ORGANISM: Bipolaris spicifera
US-10-080-210-4

Query Match 61.3%; Score 1954.5; DB 12; Length 627;
Best Local Similarity 61.1%; Pred. No. 4.7e-154;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

Qy 2 LFKSQOLAASGLSGVLGIPMDTGSPIEAVDPEVKTEVPFDSLLAAGDD----- 53
Db 6 LFSALQLV-----IAKGIYVAL--SERPAKEVDNTPDEKAA--LASTIVEDDPADVVMNL 58
Qy 54 -DMESPYYNLKLYRNALPIPPVKQPKMIITNPYTKDIIWYEIEIKPFOQRIYPTLRATL 112
Db 59 KMWQSEYELIRQPLPIPAKEPNK-LTNPYTNKEIWIYELIKFTQOYVPSLRAPL 117
Qy 113 VGIDGMSPEPTNPVPGTIVVRFINNAIVENSVLHSGSPRAPFDGMAEDVTFGEYKD 172
Db 118 VGIDGISPPTIIVPGTAVVRFINQGDRESSIHLSGSPRAPFDGMDMIMKEYKD 177
Qy 173 YFEPNQSARLMLYHDHAAFKTAENAYFGQAGAYIINDAEALGLPSGYGEFDPIILIT 232
Db 178 YFYPNQAARFLMYHDHAAHVTAEENAYFGQAGAYLITDPAEDALGLPSGYGKTDIPLVLS 237
Qy 233 AKYNNADGTLRSTEGEDDGLMGDVIHVGQPPFLNVQPRKXRFRLNAVASRAMLLYLV 292
Db 238 SKYNNADGTLKTSVGEDKSVMGDIIHVGQPPFLNVBERKXRLRLNAVASRNFALYFV 297
Qy 293 RTSSPNVRIPEFOVIASDAGLLQAPVOTSNLYLAVEREYIIIDFTNFACQTLDRNVAET 352
Db 298 KQDNATRIPEFOVIASDAGLLTHPVQTSMDYVAAERYEIVDFAPYAGQTLDRNFAPA 357
Qy 353 NDVGDEDEARLLEVMRFVSSGTVEDNSQVSTLRDVFPPPHKESPRADKHKFEKSNCH 412
Db 358 NGIGTDDDTAANDKVMRFVSSQTVVANSVPEQLSQIQFPAKDT-DIDHNRFRHRTNCE 416
Qy 413 YLINDVGFADVNERVLAKBELGTVEVMELENSSGMSHNVHILVDFKILKRTGGRGQ-- 470
Db 417 WRINGGFAVDENRVLAKPRGTVELMELENSSGMSHNIHVILVDFRVAVARYGDEGTG 476
Qy 471 VMPYESAGLKDVVWLGSGTLLTEAHYQPTGATYMWCHNLHEDNDMAVFNVTAMERK 530
Db 477 VMPYEAAGLKDVVWLGSRHETVLEAHYAPWDGVYMFHCHNLHEDODMMAAFDVTKLQNF 536
Qy 531 GYLQ--EDFEDPMNPKRAVRYNNRNDPHARAGNFSAESITARVOELAEQEPYNRLEDELD 589
Db 537 GYNETTTDFHDPEDPKMSARPTAGDLTARSGLFSEESIRARVNEALALQOPYSELAQVYAS 596
Qy 590 L 590
```

Db 597 L 597

RESULT 6

US-10-080-210-7

; Sequence 7, Application US/10080210
; Patent No. US2002014243A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Huaming

; APPLICANT: Bodie, Elizabeth A.

; TITLE OF INVENTION: Phenol Oxidizing Enzymes

; FILE REFERENCE: GC561-3

; CURRENT APPLICATION NUMBER: US/10/080, 210

; CURRENT FILING DATE: 2002-02-19

; PRIOR APPLICATION NUMBER: US 09/220,871

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: US 09/338,723

; PRIOR FILING DATE: 1999-06-23

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 627

; TYPE: PRT

; ORGANISM: Curvularia pallescens

US-10-080-210-7

Query Match 60.5%; Score 1929.5; DB 12; Length 627;

Best Local Similarity 60.5%; Pred. No. 5.5e-152;

Matches 364; Conservative 81; Mismatches 134; Indels 23; Gaps 9;

QY 2 LKSNQLAASGLSGVLGIPMDTGSHPLEAVDPEVTEVFADSLAAGD----- 53

Db 6 LPSALQLAS---LAKGIYVAL--SERPAKYIDETPDEEKA--LAAIVEDDPADVFRLL 58

QY 54 -TWESPPVLLLRNMLPRTPVYKQPKMITNVTGKDIWYELIKRFOQRITPTLRPATL 112

Db 59 KMWQSEPPILREAPLPPAKPEPK-MTNPTNKEIWEYELVKEFNQVPSPLPATL 117

QY 113 VGYDGSPPPTFNVRPGTEVVRFINNATVENSVLHGSRAPEFGMAEDVTFPEGEYKD 172

Db 118 VGYDGSPPPTITVIRGTFVAVVRFNQGDRESSIHLHGSRAPEFGMAEDLIMNGOFKD 177

QY 173 YFPVYQASRLMYHDHAFMKTAENNAFSGOAGAYIINDEADALGPSYGEEDIPLIIT 232

Db 178 YFPVYQASRLMYHDHAFMKTAENNAFSGOAGAYIITDPAEDALGPSYGEEDIPLIIT 237

QY 233 AKYYNADGTLRSTEGEDDOLMGDVHVNQOPWPEFLNVQPRKTRFRRLNAVSRAMELYLV 292

Db 238 SKFYNSDGTLLQTSVGEDNSLWGDVHVNQOPWPEFVNEPRKTRFRRLNAVSRAMELYLV 297

QY 293 RTSSPVRIRIPFOVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNAVET 352

Db 298 KQQAATRIPLPFOVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNAVET 357

QY 353 NDVGEDEYARLLEVYRFRVYSSGTVEDNSQVPTLRDVPFPPHKEGPADKHKFEERSNGH 412

Db 358 NGVGTDDVYANTDKVMRFVYSSQAAVYDVPASQIQPADKGT-IDHHRFRHRTNSE 416

QY 413 YLINDVGFADYNERVLAKELGVEYWELENSGSGSHVHILHVDKILKRTGSG---RG 469

Db 417 WRINGIGFADYNERVLAKELGVEYWELENSGSGSHVHILHVDKILKRTGSG---RG 476

QY 470 QWVPYSAGIKDVVWLGREFTLIEAHYQPTGAYVMHCHNLHEDNDMAAVENVTAMEEK 529

Db 477 -WVPYSAGIKDVVWLGREFTLIEAHYQPTGAYVMHCHNLHEDNDMAAVENVTAMEEK 535

QY 530 KGYLQ-EDFEDPMKRAVPYRNDFHARAGNFSASITARVQELAEQEPYNRIDELLE 588

Db 536 FGYNETTDHDPDSRMSARPFADULTARSGIFSEASTIRARVNELALQPYSELAQVTA 595

QY 589 DL 590

Db 596 SL 597

RESULT 7

US-09-942-185-4

; Sequence 4, Application US/09942185
; Patent No. US20020165113A1

; GENERAL INFORMATION:

; APPLICANT: Aehle, Wolfgang

; APPLICANT: Convents, Daniel

; APPLICANT: Doornink, Monique

; APPLICANT: van Gastel, Frans

; APPLICANT: Rodrigues, Ana

; APPLICANT: Topozada, Amr

; APPLICANT: De Vries, Cornelis Hendrikus

; FILE REFERENCE: C7567

; CURRENT APPLICATION NUMBER: US/09/942,185

; CURRENT FILING DATE: 2001-08-29

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 572

; TYPE: PRT

; ORGANISM: Myrothecium verucaria

US-09-942-185-4

Query Match 54.1%; Score 1724.5; DB 9; Length 572;

Best Local Similarity 60.3%; Pred. No. 4.7e-135;

Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;

QY 57 SPPVYLLRNALPDPVVKQPKMITNVTGKDIWYELIKRFOQRITPTLRPATLVGYD 116

Db 43 SPQY-MFTVPLPDPVVKQPKMITNVTGKDIWYELIKRFOQRITPTLRPATLVGYD 101

QY 117 GMSPPPTFNVRPGTEVVRFINNATVENSVLHGSRAPEFGMAEDVTFPEGEYKD 176

Db 102 GMSPPPTFNVRPGTEVVRFINNATVENSVLHGSRAPEFGMAEDVTFPEGEYKD 161

QY 177 NQASRLMYHDHAFMKTAENNAFSGOAGAYIINDEADALGPSYGEEDIPLIITANY 236

Db 162 NQASRLMYHDHAFMKTAENNAFSGOAGAYIINDEADALGPSYGEEDIPMIITSQY 221

QY 237 NADGTLRSTEGEDDOLMGDVHVNQOPWPEFLNVQPRKTRFRRLNAVSRAMELYLV 296

Db 222 TANGNLVTTNGELNSGWDVHVNQOPWPEFVNEPRKTRFRRLNAVSRAMELYLV 281

QY 297 PVRIRIPFOVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNAV- 355

Db 282 IDTRLPFKVIASDGLLEHPRADTSLIYISMAERYEVFPDSYAGKTILRLNLGSGIGI 341

QY 356 GDEDEYARLLEVYRFRVYSSGTVEDNSQVPTLRDVPFPPHKEGPADKHKFEERSNGH 413

Db 342 GDTDTYNDTKVMRFVYSSQAAVYDVPASQIQPADKGT-IDHHRFRHRTNSE 399

QY 414 LINDVGFADYNERVLAKELGVEYWELENSGSGSHVHILHVDKILKRTGSG--QY 471

Db 400 TINGVAFADYNERVLAKELGVEYWELENSGSGSHVHILHVDKILKRTGSG--QY 459

QY 472 MPYESAGIKDVVWLGREFTLIEAHYQPTGAYVMHCHNLHEDNDMAAVENVTAMEEK 531

Db 460 MPYES-GLKDVVWLGREFTLIEAHYQPTGAYVMHCHNLHEDNDMAAVENVTAMEEK 518

QY 532 YLQEDFEDPMKRAVPYRNDFHARAGNFSASITARVQELAEQEPYNRIDELLE 585

Db 519 YNATYVDPMEELMQARPELGEPQASQSFQVQATERTIQTMAERYRYLAAD 572

QY 589 DL 590

Db 596 SL 597

QY 596 SL 597

Db 596 SL 597

QY 596 SL 597

Db 596 SL 597

QY 596 SL 597

Db 596 SL 597

QY 596 SL 597

Db 596 SL 597

QY 596 SL 597

Db 596 SL 597

QY 596 SL 597

Db 596 SL 597

;; TYPE: PRF
;; ORGANISM: Rhizoctonia solani
US-09-869-877-5

Query Match 6.2%; Score 198.5; DB 9; Length 529;
Best Local Similarity 21.4%; Pred. No. 1.2e-08;
Matches 116; Conservative 78; Mismatches 222; Indels 127; Gaps 25;

```
QY 92 YEIEIKPFOQRIYPTLRPATLVGYDGMSPGFENVPKGTETVVRFINNAVTEN-----SV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 25 YKFDIK--NVNAPDGFQFSIVSNGLVPGTLITANKGDTLRINVTNOLDPSMRRAFTI 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 HLHG--SPSRAPFDG-----WAEVTFPEGEYKDYFPNQSARLLMYHDHAFMKTAE 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 83 HHMGLEQATTAEDEGPAFVTCQPIAQNLSY-----TYEIPRLGQGTGMVYH--LAS 133
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 197 NAFYQAGAYIIND-----EAEDALGRLSGYGEFDIPL-ILTAKYNNADGTLRSTF 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 134 QYVDGIRGLVLYDPNDPKHSRYDDVDASTVVMLEDWYHTPAVLEKQMFSTNNATALLSP 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 247 GEDODLMGDIYHNGQ-----PMPLNY-QPRKYRFRFLNAASRAMLLYLVRTSS 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 194 VPDSSL-----INGKRYVGGPAVRSYINVKRGRYRLRVINMSAIGSFIFSIEGHS- 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 297 PNVRIPEOVIASDAGLLQAPVQTSNLYLAVEREYELIDFTNFAQTDLRLNV----- 349
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 247 -----LVYIAD-GILHQLAVDSFOIYAGORYSYIVE-----ANQTANYIIRAPMTVA 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 350 -AETNDVGDEDEYARTLEVMRFVSSGTVEDNSQVPSLTDV-----PFPHKREGPAD 401
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 296 GAGTANALDPTNVFAVLHVEGAPNAEPTTEGSAIGTALVEENLHALINPGAPGSGAPAD 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 402 -----KHKFERSGHYLI-----NDYGFADYNERVLAKPEL 433
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 356 VSLNLAIGRSTVDGILRTFENNIKYEAPSLPTLLKILANNASNDADFTF-NEHTIVLPIN 414
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 434 GYVEVWELENSSGGMSHPVHILVDFKILKRTGGQVMPYESAGLKDYVWL-GRGETLT 492
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 415 KYIEL-----NITGGADHP:HLHGHEVDIVKSLGGTPN--YVNPRRDVRVGGTGVLR 467
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 493 IEAHYQPTGAYMMHCNHLIHEDNDMAAVFNVTAMEKGYLOEDFEDPNV-----PKWR 546
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 468 FKTDN---PGPMFVHCHIDMHLHLEAGLALVFAEAPSQIRGVQS--VQPNNANNQLCPKTA 522
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 547 AVP 549
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 523 ALP 525
```

RESULT 15
US-09-732-350-5
; Sequence 5, Application US/09732350
; Patent No. US20010031490A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490A1tr
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,350
; FILING DATE:

;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/032,315
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rozek, Carol
;; REGISTRATION NUMBER: 36,993
;; REFERENCE/DOCKET NUMBER: 5200,200-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-9655
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 529 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-732-350-5

Query Match 6.2%; Score 198.5; DB 10; Length 529;
Best Local Similarity 21.4%; Pred. No. 1.2e-08;
Matches 116; Conservative 78; Mismatches 222; Indels 127; Gaps 25;

```
QY 92 YEIEIKPFOQRIYPTLRPATLVGYDGMSPGFENVPKGTETVVRFINNAVTEN-----SV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 25 YKFDIK--NVNAPDGFQFSIVSNGLVPGTLITANKGDTLRINVTNOLDPSMRRAFTI 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 HLHG--SPSRAPFDG-----WAEVTFPEGEYKDYFPNQSARLLMYHDHAFMKTAE 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 83 HHMGLEQATTAEDEGPAFVTCQPIAQNLSY-----TYEIPRLGQGTGMVYH--LAS 133
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 197 NAFYQAGAYIIND-----EAEDALGRLSGYGEFDIPL-ILTAKYNNADGTLRSTF 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 134 QYVDGIRGLVLYDPNDPKHSRYDDVDASTVVMLEDWYHTPAVLEKQMFSTNNATALLSP 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 247 GEDODLMGDIYHNGQ-----PMPLNY-QPRKYRFRFLNAASRAMLLYLVRTSS 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 194 VPDSSL-----INGKRYVGGPAVRSYINVKRGRYRLRVINMSAIGSFIFSIEGHS- 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 297 PNVRIPEOVIASDAGLLQAPVQTSNLYLAVEREYELIDFTNFAQTDLRLNV----- 349
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 247 -----LVYIAD-GILHQLAVDSFOIYAGORYSYIVE-----ANQTANYIIRAPMTVA 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 350 -AETNDVGDEDEYARTLEVMRFVSSGTVEDNSQVPSLTDV-----PFPHKREGPAD 401
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 296 GAGTANALDPTNVFAVLHVEGAPNAEPTTEGSAIGTALVEENLHALINPGAPGSGAPAD 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 402 -----KHKFERSGHYLI-----NDYGFADYNERVLAKPEL 433
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 356 VSLNLAIGRSTVDGILRTFENNIKYEAPSLPTLLKILANNASNDADFTF-NEHTIVLPIN 414
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 434 GYVEVWELENSSGGMSHPVHILVDFKILKRTGGQVMPYESAGLKDYVWL-GRGETLT 492
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 415 KYIEL-----NITGGADHP:HLHGHEVDIVKSLGGTPN--YVNPRRDVRVGGTGVLR 467
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 493 IEAHYQPTGAYMMHCNHLIHEDNDMAAVFNVTAMEKGYLOEDFEDPNV-----PKWR 546
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 468 FKTDN---PGPMFVHCHIDMHLHLEAGLALVFAEAPSQIRGVQS--VQPNNANNQLCPKTA 522
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 547 AVP 549
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 523 ALP 525
```

Search completed: February 13, 2003, 06:35:08
Job time : 47 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 03:10:27 : Search time 38 Seconds
(without alignments)
1502.733 Million cell updates/sec

Title: US-09-218-702-2

Perfect score: 3189

Sequence: 1 MLFQWQVLAASGLSLGVG.....AEQEPYNRLELDLIGIEE 594

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1724.5	54.1	572	2	B48521 bilirubin oxidase
2	713	22.4	513	2	F69604 spore coat protein
3	480	15.1	568	2	B86364 hypothetical prote
4	450	14.1	591	2	G96734 spore coat protein
5	439.5	13.8	527	2	C70397 periplasmic cell d
6	405.5	12.7	533	2	AC0414 probable exported
7	402	12.6	494	2	AC3582 probable blue-copp
8	391	12.3	536	2	AF0523 probable multicop
9	388.5	12.2	516	2	C64735 probable copper-bi
10	385.5	12.1	516	2	G90644 hypothetical prote
11	385.5	12.1	516	2	G85495 hypothetical prote
12	340.5	10.7	470	2	G65088 sufl protein precu
13	335.5	10.5	470	2	B81116 suppressor of ftsi
14	335.5	10.5	470	2	E85961 suppressor of ftsi
15	323.5	10.1	470	2	AD0888 sufl protein limpo
16	315.5	9.9	513	2	G81298 probable periplasm
17	303	9.5	474	2	AD0083 probable cell divi
18	284	8.9	1662	2	T18540 moA protein precu
19	241	7.6	311	2	H64157 sufl protein homol
20	231.5	7.3	370	2	H87368 copper-binding pro
21	223	7.0	460	2	B83910 hypothetical prote
22	216.5	6.8	503	2	G83175 probable metallo-o
23	215.5	6.8	611	2	C82845 copper resistance
24	214	6.7	721	2	H82528 L-ascorbate oxidas
25	195.5	6.1	632	2	F83387 copper resistance
26	192	6.0	609	1	KSPSCR copper resistance
27	190.5	6.0	529	2	S68120 laccase (EC 1.10.3
28	189.5	5.9	635	2	A36868 copA homolog - Xan
29	188.5	5.9	520	2	S59533 laccase (EC 1.10.3

30	188.5	5.9	520	2	JC5356 laccase (EC 1.10.3
31	187.5	5.9	504	2	F70813 hypothetical prote
32	185	5.8	527	2	JC5357 laccase (EC 1.10.3
33	184.5	5.8	573	2	T02743 laccase (EC 1.10.3
34	183	5.7	619	1	KSNCTO laccase (EC 1.10.3
35	180	5.6	533	2	S62371 laccase (EC 1.10.3
36	180	5.6	621	2	S72493 laccase (EC 1.10.3
37	179.5	5.6	605	2	S52253 copper resistance
38	179	5.6	548	2	S18746 laccase (EC 1.10.3
39	176	5.5	551	2	T02752 probable laccase (
40	176	5.5	619	1	KSNCLT laccase (EC 1.10.3
41	172.5	5.4	520	2	A35883 laccase (EC 1.10.3
42	172.5	5.4	520	2	B35883 ligninolytic pheno
43	171.5	5.4	552	2	A51027 L-ascorbate oxidas
44	169.5	5.3	579	2	S11027 L-ascorbate oxidas
45	167	5.2	512	2	JC5355 laccase (EC 1.10.3

ALIGNMENTS

RESULT 1

B48521
bilirubin oxidase (EC 1.3.3.5) - fungus (Myrothecium verrucaria)
C:Species: Myrothecium verrucaria
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B48521; A48521
R:Koike, S.; Ando, K.; Kajii, H.; Inoue, T.; Murao, S.; Takeuchi, K.; Samejima, T.
J. Biol. Chem. 268, 18801-18809, 1993
A:Title: Molecular cloning of the gene for bilirubin oxidase from Myrothecium verruca
A:Reference number: A48521; MUID:93366794; PMID:8360171
A:Accession: B48521
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-572 <KO11>
A:Cross-references: GB:D14081; NID:G436236; PIDN:BAA03166.1; PID:G456710
A>Note: sequence extracted from NCBI backbone (NCBIN:136730, NCBIPI:136732)
A:Accession: A48521
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-572 <KO12>
A:Cross-references: GB:D14081; NID:G436236; PIDN:BAA03166.1; PID:G456710
A>Note: sequence extracted from NCBI backbone (NCBIN:136728, NCBIPI:136729)
C:Keywords: oxidoreductase

Query Match	54.1%	Score 1724.5:	DB 2:	Length 572:
Best Local Similarity	60.3%	Pred. No. 1.4e-123:		
Matches 322:	Conservative 75:	Mismatches 128:	Indels 9:	Gaps 7:
OY	57	SPPYNLVYRNALPIPPVAKPKMTITNPVYTKGDIWYEIFEIKFPQORITPTLRPAFLVGD	116	
DB	43	SPQYR-MFTVPLPIPPVAKPKMTITNPVYTKGDIWYEIFEIKFPQORITPTLRPAFLVGD	101	
OY	117	GSPGPTFNVPVPGTEVFVFFINNATVENSVHLGSPSRAPFGMAEDYTFPEYDYDYP	176	
DB	102	GASPGPTFVPPGVETVYVAFINNAEAPNSVHLGSPSRAPFGMAEDYTFPEYDYDYP	161	
OY	177	NYQASARLLVYHDAFMKTAENAYFGQAGAYIINDEADALGPSYGEEDIPLITLANY	236	
DB	162	NMQSARTLWYHDHAMHTAENAYRGQAGLYMLTDPADALNLPSTYGEEDIPMLITSQY	221	
OY	237	NADGTLRSTREGEDQDLKGDVHVNGCPMPFLVNOVRKTRFRFLNAVAASRAVLLVTRSS	296	
DB	222	TANGMLVYTTNGELNSFVGQVHVNGQPMPEFKVYRFRFLDAVAASRSFCLYFADDA	281	
OY	297	PVVRIPFOVIASDAGLQAPVOTSMLYLAVEREITIDFTFAGOTLDLRNV-AETNDV	355	
DB	282	IDTRLPPKVIYASDGLHPADTSLITYISMAERYEVDYFSYAKTITELRNLSGISTGI	341	
OY	356	GDEDFYARTLEVAFVSSGIVE-DNSQVPTLRDVPFP-PKKEGPAADKHFKEFSNGHY	413	
DB	342	GNDTVDNMDKVMRRVVDVDDTTPQDTSVVPANLROVPPSPPTTNP--RQFFRGRTGPTW	399	

QY 414 LINDGEPADYNERVLAKEPLGTEVMELENSGGSHPHYHLVDPKILKTGGG--QV 471

Db 400 TINGAFAADVONRLRLANPVGTEVERMELIAGNGCTHPHILHLDPEKVISRTSGNNARTV 459

QY 472 MEYSAGAKDVAWGLRGELFTTEAHYOPMTGAYMMHCHNLHEDNDMAVFNVTAMEKG 531

Db 460 MPYES-GLKDVAVMLRRETIVVEAHYAPPGVYMHCHNLHEDNDMAAFNATVLPDYG 518

QY 532 YLQEDFEDPMNPKRAVPYNRNDFHARAGNFSAESITRANVCELAQEPNRLDE 585

Db 519 YNATVFDPMEMELMQARPELGEFQAQSGQSFVQAATERIDGMALRYPAADE 572

RESULT 2

F69604

spore coat protein (outer) cotA - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999

C:Accession: F69604; A27393; S02538

R:Kunst, F.; Ogatawara, N.; Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertele, C.; Bron, S.; Brulliet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chai, E.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallenbach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Laubert, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee, S.; Mawar, K.; Ogatawara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon, A.; Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Serron, A.; Serron, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Yoshikawa, H.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: F69604

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-513 <KUN>

A:Cross-references: GB:299107; GB:AL009126; MID:g2632866; PIDN:CAB12449.1; PID:el182609.

A:Experimental source: strain 168

R:Donovan, W.; Zheng, L.; Sandman, K.; Losick, R.

J: Mol. Biol. 196, 1-10, 1987

A:Title: Genes encoding spore coat polypeptides from Bacillus subtilis.

A:Reference number: A27393; MUID:88011308; PMID:2821284

A:Accession: A27393

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-37 <DON>

R:Sandman, K.; Kroos, L.; Cutting, S.; Youngman, P.; Losick, R.

J: Mol. Biol. 200, 461-473, 1988

A:Title: Identification of the promoter for a spore coat protein gene in Bacillus subtilis

A:Reference number: S02538; MUID:88286730; PMID:3135411

A:Accession: S02538

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-32 <SAN>

C:Comment: this spore coat protein is responsible for the characteristic brown pigment C:Genetics:

C:Keywords: sporulation

Query Match 22.4%; Score 713; DB 2; Length 513; Best Local Similarity 34.6%; Pred. No. 2e-46; Mismatches 175; Indels 96; Gaps 18; Matches 183; Conservative 75;

QY 66 NALPPIP---PYKQPKMITNPVTGKDIWYIEIKPFOQRIYPLRATLVGYDGMSPG 121

Db 8 DALPPIPIKPYQO-----SKEKTYEVMEECTHQLNRPRLPTRLMGVNGLPFG 57

QY 122 PTFNVPRTGETVYVRINNA-----TYVNS-----VHLGSPSRAPPDG 159

Db 58 PTIEVKRNNENVYKKMMNLLPSTHELPIDHDTIHNSQSHDEPEVKTVYLLHGSGVPDDSDG 117

OY 160 WAE-----DYPERGGY----KOYFPNYSARLLWHDHIAFKKTAENAFGAGAYIINDE 211
:
:
Dd 118 YPEAFMSKDFEQTGYEFKREYVHYHPNOQGAALILWWHDHAMALLTRLNVAGLVGAYIIHDR 177
:
:
OY 212 ABDALGLRSGCYGEPIPLITLAKYYNAOGTL---RSTEGEDODL-----MGDVINH 259
:
:
Dd 178 KEKRKLKLS--DEVIVPRLIIDRTINEDGS.LFYSPAPNPSPSLPNPSIVAFPGETILLV 235
:
:
OY 260 NGQPMPFLINVOPRKRYFRFFLAAYSRAWLLYLVTSSPNVRIPFOVIASDAGLLDAQYT 319
:
:
Dd 236 NCKVMPLYEVFERKKRYFRRVINASNTRYNLSDNGCD-----FIQGSDGGLLPISRVKL 289
:
:
OY 320 SNLYLAVERVEYLIIDFNFAQOTLDLRNVAET-NDVDDEDERATLEVMRFVVSSGIVE 378
:
:
Dd 290 NSFSLAPEREDVIIIDTFAVEGESIILIANSAGCGGDVPEND---ANIMOFRTVKPLAQ 345
:
:
OY 379 -DNSGVPTLRDPVPPPKHEGPADKHFFKEESNGHY-----LINDVGADVENEVLAKPE 432
:
:
Dd 346 KDESRRKYTIASSYPVQHNERIONITLTLAGTDODEYGRPVLLLNNKKRHND---PYTEPRK 402
:
:
OY 433 LGTFWEWELENSSGWSHPVHIHLVDFKI LR-----TGGRGOVMPEYES 476
:
:
Dd 403 VGTFTWIHSIIINPTRS-TPHIHLLTVSFVRLDRRPEDIARYOEGSEL.SYTCGPAVPPSEK 461
:
:
OY 477 AGLKVWMLGREGELTIEAHYOPTGMAMMCHNI.IHDDNMMAVFNT 525
:
:
Dd 462 -GWKDITIQAHHAGEVLRIRATFGPSRYVMWHCHILEHEDYMNRPMIDT 509
:
:

RESULT 3

B86364

hypothetical protein F19G10_5 - Arabidopsis thaliana

C:Species: Arabidopsi s thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

R:Ccessionion: B86364

R:Theologias: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dekar,ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Matil, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B86364

A>Status: preliminary

A:Molecule type: DNA

A:Cross-references: GB:AE005172; NID:g2462832; PID:NAB72167.1; GSPDB:GN00141 C:Genetics:

A:Map position: 1

Query Match 15.1%; Score 480; DB 2; Length 568;
Best Local Similarity 28.0%; Pred.No.1,4e-28;
Matches 146; Conservative 76; Mismatches 167; Indels 130; Gaps 20;

OY 109 PATLVGYDGMS-----GGPTFNVRGTYEVVRFINN-----AT-----V 142
||| ||| | : | : | : | : | : | : | :
Dd 71 PATPFYAAGTSRSKATVPGPIETIYGVDTYVTRRNHLPKSHILPMDPTISPAPIRKHGCI 130
||||| : | : | : | : | : | : | :
OY 143 ENSVHLGSPSRAPPDGAEDVTTPGEYKD-----YFPNYQSARLLMYHDHAFMK 193
||| | : | : | : | : | : | : | :
Dd 131 PTVALHIGIGEPTS DGNA-DAMFTAGREFRGPKWTKTTLHEYENKQOPGMWYKDHDMGL 189
||| | : | : | : | : | : | : | :
OY 194 TAENAVFPOGACAYIINDA-EDALGLRSGCYGEPIPLITLAKYYNAOGTL-RSTEGEDOD 251
||| | : | : | : | : | : | : | :
Dd 190 TRVNLLACLVAAYIIRHNHAVESPQLPTG-DEFBRPLLIFDSRSRKGGSIYMNATGNPNS 248
||| | : | : | : | : | : | : | :
OY 252 L-----WDVIVNQCPMLINVOPRKRYFRFFLAAYSAEWRAVLLVLTSTSPNVRIPIF 303
:||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

Db 249 IHQWQPEYFGDVIIVNGKAMPRLNVRRRKRYRRIINASNAPEKFEF-----SNGLD 302
Qy 304 QVIASDAGLLQAPVOTSNLYLAVEREIIIDFTNAGOTLDIRNVA-----ETNDVGDE 358
Db 303 IYVGSASLRSKRVMTKSIILSPSELVDVVDYKSPSKRTVLANAPRYPSGDVNEE 362
Qy 359 DEYARTLEVMRFVSSGTVEDNSQVSTLRDVPFPKREGRADKHFEER--SNG-----H 412
Db 363 NG-----KVMKFIINNESEDCTIPKRLINYNADSVNVLRYISMVYVNSDEPT 417
Qy 413 YLINDVGF-ADVNERVLAKPELCTVEWELENSGSGSHPHVHLVDKILKRTGGQV 471
Db 418 LVLNGSLPYEARPYTE---IPKSGTVEWEVINTLED-NHPLHILGLGFKVEQTA----- 467
Qy 472 MPYESAGLKD-----VVMIGRGFTLITEAHYQPMTG----- 502
Db 468 --LLAAGLEEFKECMTKQNDVAKCQISKYARGKTATATAEHRGKMKVFKMPCGHVTRILV 525
Qy 503 -----AYMHCNHLIHEDNDMAVFN 524
Db 526 RFSYHTNMSYRPDPQOEPRGVYVHCHILHEDMMMRPLKV 566

RESULT 4

G96734
Species: Arabidopsis thaliana (mouse-ear cross)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: G96734
R.Theologidis, A.; Ecker, J.R.; Palm, C.D.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Hulzer, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L., Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kraykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A66141; MUID:21016719; PMID:11130712
A.Accession: G96734
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-591 <STOS>
A.Cross-references: GB:AE005173; NID:g6714313; PIDN:AAF26006.1; GSPDB:GN00141
C.Genetics:
A.Gene: F23N20.3
A.Map position: 1

Query Match 14.1%; Score 450; DB 2; Length 591;

Best Local Similarity 27.4%; Pred. No. 2,9e-26;
Matches 142; Conservative 74; Mismatches 182; Indels 120; Gaps 18;

Qy 109 PATLVGYDMS-----PGTFNVPRGTETVVRFIN-----NATV 142
Db 86 PATPVAYGTSGTSATVPRPTIEAYGVDPITYWRNHLRLPHLTPMDPTSPALPKHGI 145
Qy 143 ENSVHLHGSPSRAPFGMAEDYTFPEKYD-----YFPNYSARLLMTHDAFMK 193
Db 146 PTVVHLHGSIHEFTSDGN--DSWETAGFKETGSKMTKTHYVKNKOOPGMWVHDAAGL 204
Qy 194 TAENAFGQAGAYII-NDAAEDALGPGSGEFDIPLILAKYVNDGTL-RSTEGD-- 249
Db 205 TRNNLLAGLLGSIILHSSVESPLRLPTG-RETPRDLVITDRSFRKDGSIYMATGNPT 263
Qy 250 -----ODLMGDVIVHNGOPWPELVQPRKRYRRLNAAVSRAMLLYLVTTSSPNRIP 303
Db 264 IHQWQPEYFGDVIIVNGKAMPRLNVRRRKRYRRIINASNAPEKFEF-----SNGLD 317
Qy 304 QVIASDAGLLQAPVOTSNLYLAVEREIIIDFTNAGOTLDIRNVAETNDVDEDEYAR 363
Db 318 IYVGSASLRSKRVMTKSIILSPSELVDVVDYKSPSKRTVLANAPRYPSGDVNEE 377

Qy 364 TLEVMRFVSSGTVEDNSQVSTLRDVPFPKREGRADKHFEER--KFSRNG-----HYLIN 416
Db 378 NSKVMKRIIVKSEVDISIIIPKKLIEPR-PAHVSTRTRTYIMAFVESSIDEPHTLYIN 436
Qy 417 DVGADVNERVLAKPELCTVE-----VWELENSGSGSHPHVHLVDKILKRTG 466
Db 437 GLPY---NAVETEPKIGTSEFSKSLMTIKWVEVINTLED-NHPLHILGLGFKVEQTA 492
Qy 467 -----GRQVMPYESAGLKDV-----W 484
Db 493 LVKSEEFECMTKQNDVAKCEISKYARGKTATATAEHRGKMKVFKMPCGHVTRILV 552
Qy 485 IGRGETLIEAHYQPMTGAYMHCNHLIHEDNDMAVFN 522
Db 553 IHSNESISPDATQEP---GYVHCHILHEDNDMMMRPF 587

RESULT 5

C70397
Species: Aquifex aeolicus
C.Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C.Accession: C70397
R.Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.

Nature 392, 353-358, 1998
A.Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A.Reference number: A70300; MUID:98196666; PMID:9537320
A.Accession: C70397
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-527 <NOF>

A.Cross-references: GB:AE000724; NID:g2983585; PIDN:AAC07157.1; PID:g2983586; GB:AE00
A.Experimental source: strain VFS
C.Genetics:
A.Gene: sufi

Query Match 13.8%; Score 439.5; DB 2; Length 527;

Best Local Similarity 30.1%; Pred. No. 1.6e-25;
Matches 147; Conservative 72; Mismatches 191; Indels 79; Gaps 21;

Qy 98 PFOQRIYPTLRPATLVGYDMSF-----GPTFNVPRGTETVVRFINNATVENS 146
Db 58 PDQGRVSIKAKWTLEIIPKSTDMLYELDNEYNPIFLRKQGTSSADPVNNSGDSII 117
Qy 147 HLHGSPSRAPF--DGAEDYTFPEKYDVFVNV---QSARLLMTHDAFMKTAENAF 201
Db 118 HWHG--FRAPWKSQGHRYVAVKDG--TYSYRPTIIRSGTYFVHNRPHGRGQVYVG 173
Qy 202 QACAYIINDAEDAL--GLPSGGEFDIPLILAKYVNDGTLRSTEGEDQIDMGVINY 259
Db 174 LAMIIIEDEDENLQALDLEGVIDIPILIDKPFSSGQLVNPMGIMGFGOTILV 233
Qy 260 NGOPWPELVQPRKRYRRLNAAVSRAMLLYLVRTSSPNRIPFOYIASDAGLLQAPVOT 319
Db 234 NLPRNMYMDERKIYFRILNCSNAPRYRALLR---GNRMRFVYIVGVDGLDTPRKEV 290
Qy 320 SNLYLAVEREIIIDFT-----NEAGOTLIDL-----RNAETN--- 353
Db 291 NEILVAPGERIDILVDFRDASVNDVIKLVFNPLILGIMGIMGRMGIMGRMGIMGIM 350
Qy 354 -DVG--DEDEYATFLVMRFVSSGTVEDNSQVSTLRDVPFPKREGRADKHFEERSV 410
Db 351 MDGMADNSEF---EVMERVTAKSAVDS-IPORLSEVT-PIINDGAVOQVITLGMRR 404
Qy 411 GHYLIN---DVGFA--DYNE-RVLAKPELCTVEWELENSGSGSHPHVHLVDKIL 462
Db 405 MVTITGETMEDGYANDQDINPKVLVEQNGSGDVYIIEYVNNIGM-HPNHNIGRFOYL 463
Qy 463 KRTGGRQVMPYESA--GLKDVWLGRGETLITE---AHQPMTGAYMHCNHLIHEDND 517
Db 464 ERSIIG-----PLRATDLGWKQDVIVAPMETVRIAVDMSHPYNEHQIYLLCHILEHND 518


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OY 137 INNAIVENSV-----HLHGSPSR--APPDGCAEDVTPGGEYKDYIFPNYOSARLLW 185
Db 92 SNRLLENKSNMVAQLOVBGPMLGGEPARMSPADAP-----VLPIROMAARLL 140
OY 186 YHDAHFMTAENAVEGCGAGAYIINDEAEDALGPRSGCEPDIPLITAKYNAOGLTST 245
Db 141 YHANTPNTAOQVYINGLAGMWLDEDEVSKSLPIPHNYGVDDPVTYIQDRIDNFTPREYN 200
OY 246 EGEDDOLMGDVIHVNGCPMPFLNVQPRKYRFRFLNAAASRAMLYLVTRSSPNVRIPFOV 305
Db 201 EPGSGGFVGDTLVNGVQSPYEVYSGRWRLRLNLANSRRQQLQM-----NDRPLHY 254
OY 306 IASDAGLLQAPVQTSNLYLVAERETIITFTNFRAGOTLDIRNAETNDVGD-----DE 360
Db 235 ISGDGFPLPAPYSVQQLSLAPGERREILVDMSN-----GDEVSIITGE 297
OY 361 YARTEVVRPFVYSSGTVSDNSOVSTL-----RDVPRPHKEGPAD 401
Db 298 AASIVDRIR-----GFEPPSSILVSTLVTLRPRGCLPLVYDLSLPRMLLPYEMAGSPF- 351
OY 402 KHFKEERSNGHYLLINDVFA-----DVNERVLAKPELGTVIEWEELNESSGGSHPHYHLL 457
Db 352 -----RSRDISLGDGDPINGQIMQVNV-RIDVTAQOGTWEKMTVANADE---PQAFHIEGV 401
OY 458 DFKILKRTGSGRQVWPY-ESAGLKDVMVL-GRGEFL 491
Db 402 MFOIRNVNG---AMPFEPEDRGMKDTVMVVDGOVELL 433

```

```

RESULT 13
E91116
suppressor of ftsi [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
R:Accession: E91116
R:Author: T. Makino, K. Ohnishi, M. Kurokawa, K., Ishii, K., Yokoyama, K., Han, C.G.
gasaikari, N., Yasunaga, T., Kunihara, S., Shiba, T., Hattori, M., Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genoc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E91116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1,470 <NAV>
A:Cross-references: GB:BA000007; PIDN:BA837324.1; PID:913363373; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS3901

Query Match 10.5% Score 335.5; DB 2; Length 470;
Best Local Similarity 26.7% Pred. No. 1,1e-17;
Matches 138; Conservative 63; Mismatches 176; Indels 139; Gaps 20;

QY 20 GIPMDTGSHPLEADVDEPKTEVFADSLAAGDDDMESPNNLYLRNALPIRPVKOPKMI 79
||: | :||:
D 13 GIALCAGAVPLKA-----SAAGQ-----QQPLRPPLLESR-- 43

QY 80 ITNPVTKDITVYELEIKRFOQRITPTLR--ATLVGDDGMSGPFFNVBREGTEVVR 136
||: | :||:
D 44 -----RCQPLFM-----TVORAHMSEFTPCTRASVWGINRGLYPTTRVYKGDVRLIY 91

QY 137 INNAITVENS-----HLHGSPSR--APFDGAEDVTPFGEKKOYVFNYSARLLW 185
||: | :||:
D 92 SNRLTENSMKVYAGLQVPGPLMGGRAMSPNADWP-----VLPIDONATLW 140

QY 186 YHDAFMKTAENAYFGQAGAYIINDEADALGSPSGGEFDIPLITAKYYNADGTLRST 245
||: | :||:
D 141 YHANTPNRTAQOAVYNGLGMVLVEDEVSKSLPIPNHYGVDDPFVLIODKRLDNGFTPEYN 200

QY 246 EGEODDLMDGVITVHNGCPWPLNQQPKYRFRPLNAVSRMMLLYLVTSPPNKRIPQV 305
||: | :||:
D 201 EPGSGGVEGVDITLVNGVQSPVVEYSRGWVRLRLNLANSRKYQLOM-----SGQRLPHV 254

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QY 306 IASDAGLLQAPVQYSNLYLAVAERYEIIIDTFNAGOTLDRNVAETNDVGD-----DE 360
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 255 ISGDGFLPAPSVYKQLSLAGEERREILLMSN-----GDEVSINCGE 297
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 361 YARLEWVRFWSSQSTVDNSQVYSTL-----RDVPFPFKBEPAD 401
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 298 AASIVDRIR-----GFEFSSILVSTLVTLRPMGLLPLVTDLSLPMRLPTEIMAGSP- 351
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 402 KHFEKERENGHLLINDVEFA-----DVNERVLAKPELGTVEWMELENSGGMSHPVHIHLV 457
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 352 -----RSRDISLGDDEPINGQLMDVNRIDVTANQOGTMEWRTYRADE---PQAFHIEGV 401
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 458 DFKILKRTGGRQVMPY-ESAGLKDVYL-GRGETL 491
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 402 MFOIRNVNG-----AMPFEDGMDKDTVAWQVQVILL 433
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

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RESULT 14
E85961
suppressor of ftsI [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85961
R:Perla, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamotis, K.; Apodaca
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85961
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-470 <STO>
A:Cross-references: GB:A8005174; NID:q12517596; PIDN:AAG58153.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: sufl

Query Match 10.5%; Score 335.5; DB 2; Length 470;
Best Local Similarity 26.7%; Pred. No. 1,1e-17;
Matches 138; Conservative 63; Mismatches 176; Indels 139; Gaps 20;

OY 20 GTPMDTGHPIEAVDPEKVEFADSLAAGDDDESPPNLLRYNALPIPPVKQPMI 79
DB 13 GIALCGAVPLKA-----SAAGQ-----QQPLPVPPLLESr- 43
OY 80 ITNPVTGDIWYEIEIKPFOORITPLRP--ATLVGYDDKMSGPFNVPRTETVVRf 136
DB 44 -----RCQPLEM-----TVORAHWSTPGTRASVWGINGRIYGLPTIRVKGGDDVKILY 91
OY 137 INNAIVENSr-----HLGSPSR--APFDGAEDVTPEGEKDYVFPFYOSARLLM 185
DB 92 SRRLEENYSMTVAGLQVGPCLMGCPARMMSPNADAP-----VLPTRQNAATLM 140
OY 166 YHDHAFMKTAEAAVYGCAGAYIINDEADALCPGSGCEPDIPLITAKYYNAGOTLRST 245
DB 141 YHAMPNRTAQGVYVINGLGMWLEDEVSKSLPIPHYGVDDPVALYIDKRLDNGETPEYN 200
OY 246 EGEDDLMDGVYHVNGQMPPLNVQPRKYRFRFLAAASRAMLLYLVYNTSSPNVRIPOV 305
DB 201 EPGSGGFVGDITLVNGVQSPYEVESRGWVRLLRLNANSRSRYQLQM-----SDGRPLHV 254
OY 306 IASDGLLQAPYQTSNLYLAVEREIIIDPTNFAGOTLDLRNVAETNDVDE-----DE 360
DB 255 ISGDGGLPAPYVKQLSLAPGERREILVDSN-----GDEVSYTCGE 297
OY 361 YARTLEVVRFFVSSGTVEDNSOVSTL-----RDVPPPHKEGPA 401
DB 298 AASIVDRIR-----GFPEPSLIVSTLVLTLPRTGLPLVYVDSLPKRLLPFEIMAGSI- 351
OY 402 KHEKERSNGHYLVNDGFA----DVNERVLAKPELGTVEVWELSENSGSGMSPHVHLV 457
DB 352 -----RRDLSISLGGDPPINGQLMDVNV--RIVVTAQOGTWERMWTARDE---PQAFHIEGV 401

```


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OM protein - protein search, using sw model

Run on: February 13, 2003, 01:08:17 ; Search time 20 seconds

(without alignments)
1231.847 Million cell updates/sec

Title: US-09-218-702-2

Perfect score: 3189

Sequence: 1 MLFRSMQLAASGLSLGVG.....AEQEPYNRDLIEDLGIEE 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1724.5	54.1	572	1	BLRO_MYRVE
2	713	22.4	513	1	COTL_BACSU
3	519	16.3	642	1	PHSA_STRAT
4	405.5	12.7	533	1	CUEO_YERPE
5	391	12.3	536	1	CUEO_SALRT
6	390	12.2	536	1	CUEO_SALRT
7	388.5	12.2	516	1	CUEO_SALRT
8	385.5	12.1	516	1	CUEO_SALRT
9	340.5	10.7	470	1	SUFI_ECOS7
10	323.5	10.1	470	1	SUFI_ECOS7
11	241	7.6	311	1	SUFI_HAETN
12	192.5	6.0	520	1	LAC1_TRAVI
13	192	6.0	609	1	LAC1_TRAVI
14	190	6.0	527	1	COPA_PSEBM
15	188.5	5.9	520	1	LAC4_TRAVI
16	188.5	5.9	520	1	LAC4_TRAVI
17	185	5.8	527	1	LAC5_TRAVI
18	180	5.6	533	1	LAC2_PLEOS
19	180	5.6	621	1	LAC2_PLEOS
20	179.5	5.6	605	1	LAC2_PLEOS
21	179	5.6	648	1	PCOA_ECOS7
22	177.5	5.6	520	1	LAC1_PHLRA
23	177	5.6	619	1	LAC2_AGABI
24	176.5	5.5	519	1	LAC2_AGABI
25	176.5	5.5	520	1	LAC2_AGABI
26	176	5.5	619	1	LAC2_AGABI
27	174	5.5	591	1	LAC1_CRYPA
28	172.5	5.4	520	1	LAC1_CRYPA
29	171.5	5.4	552	1	ASO_GUCPM
30	169.5	5.3	519	1	LAC2_TRAVE
31	169.5	5.3	579	1	ASO_GUCPM
32	166.5	5.2	622	1	FET3_YEAST
33	163.5	5.1	624	1	FET3_CANAL

RESULT 1	ID	BLRO_MYRVE	STANDARD:	PRT:	572 AA.
AC	012737:				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	Bilirubin oxidase precursor (EC 1.3.3.5).				
OS	Myrothecium verrucaria.				
OC	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.				
OX	NCBI_TaxID=5532;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=MT-1;				
RX	MEDLINE=9336794; PubMed=8360171;				
RA	Koike S., Ando K., Kaji H., Inoue T., Murao S., Takeuchi K., Samejima T.;				
RT	"Molecular cloning of the gene for bilirubin oxidase from Myrothecium verrucaria and its expression in yeast."				
RL	J. Biol. Chem. 268:18801-18809(1993).				
CC	- FUNCTION: OXIDATION OF BILIRUBIN AND OTHER TETRAPYRROLES.				
CC	- CATALYTIC ACTIVITY: Bilirubin + O(2) -> biliverdin + H(2)O.				
CC	- CORFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR. CONTAINS 2 BLUE COPPER ATOMS PER MOLECULE.				
CC	- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.				
CC	- SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).				
CC	EMBL: D14081; BAA03166.1; -				
DR	EMBL: D12579; BAA02123.1; -				
DR	HSP: P36649; 1kv7				
DR	InterPro: IPR001117; Cu-oxidase.				
DR	Pfam: PF00394; Cu-oxidase; 1.				
KW	SIGNAL; Copper; Metal-binding; Oxidoreductase; Glycoprotein; Repeat.				
FT	SIGNAL	1	19		
FT	PROPEP	20	38		
FT	CHAIN	39	572		
FT	DOMAIN	39	194		
FT	DOMAIN	98	526		
FT	DOMAIN	404	572		
FT	DOMAIN	132	132		
FT	METAL	132	134		
FT	METAL	172	172		
FT	METAL	174	174		
FT	METAL	174	174		
FT	METAL	436	436		
FT	METAL	439	439		
FT	METAL	441	441		
FT	METAL	494	494		
FT	METAL	494	494		

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FT METAL 495 495 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 496 496 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 500 500 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 503 503 COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 510 510 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 572 AA; 63947 MW; 5842b6413035EEFF CRC64;

Query Match 54.1%; Score 1724.5; DB 1; Length 572;
Best Local Similarity 60.3%; Pred. No. 8.6e-119;
Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;

OY 57 SPFYMLLRNALPPIPVKOPKMTITNPYTKDKITWYEIFRPFQORITPTLRPALVCGD 116
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 43 SPQYV-MFVVPRLPIPVKOPKMTITNPYTKDKITWYEIFRPFQORITPTLRPALVCGD 101
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 117 GMSPGPTFVNPRTGTEVYVAFINNAVENSVHLHGSPRPFQMAEDVFPPEYKDYRPP 176
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 102 GMSPGPTFVNPRTGTEVYVAFINNAVENSVHLHGSPRPFQMAEDVFPPEYKDYRPP 161
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 177 NYQSARLLMYHDHAFMKTAENAFYFGAGAYIINDEADALGSPGGERDIPILITAKYY 236
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 162 NYQSARLLMYHDHAFMKTAENAFYFGAGAYIINDEADALGSPGGERDIPILITAKYY 221
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 237 NADGTLRSTEGEDQDKGDVHVNCGPMPFLVNPQPKYFRFLNAAVSAFLLIYVRS 296
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 222 TANGNLYVTNGCLNSFWGVIVHNGCPMPFKVNEPRKYFRFLDAVSRFGLYFADTDA 281
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 297 PAVRIPEVYIASDAGLAPVOTSNLYLAVARVEYIIFTFNACOTLRLRV-LETNV 355
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 282 ITRLPFKYIASDAGLAPVOTSNLYLAVARVEYIIFTFNACOTLRLRV-LETNV 341
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 356 GDEDEYARTLEVYRVESSGYE-DNSQVPSLRLDVPF-PKREGPADKHFEERSNGHY 413
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 342 GDTDYDNDTKVMRFVYADDTQPTSVYVPAFLRDVPFSPPTTNPF-RQFRGRTGPTW 399
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 414 LINDGFAYVNRVLAKEPLGTEVWELENSGSGMHPHILYDPKILKRTGGRG-QY 471
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 400 TINGFAFADVQNRLLANVGVTEVERELINAGNGWHPHILYDPKILKRTGGRG-QY 459
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 472 MYEASGLKDVYMLRGFTLTTEAHQWPTGAYMMHCHLIEDNDMMAFVNTAAEKG 531
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 460 MYEASGLKDVYMLRGFTLTTEAHQWPTGAYMMHCHLIEDNDMMAFVNTAAEKG 518
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 532 YLQEDFEDPMNRKRAVPYRNRFHARAGNFSAESITTAQVQELAEQEPYNRIDE 585
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 519 YNATVVDMEELMQARPYELGEGFQASQGSQVQAVTERIQFWAEYRPAADE 572
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

RESULT 2
COTA_BACSU STANDARD: PRT; 513 AA.
AC P07788; 024818;
DT 01-AUG-1988 (Rel. 08. Created)
DT 30-MAY-2000 (Rel. 39. Last sequence update)
DT 16-OCT-2001 (Rel. 40. Last annotation update)
DE Spore coat protein A.
GN COTA OR PIG.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97124186; PubMed=8969499;
RA Borris R., Portmollik S., Schroeter R.;
RT "The 52 degrees-55 degrees segment of the Bacillus subtilis
   chromosome: a region devoted to purine uptake and metabolism, and
   containing the genes cota, gabp and guaA and the pur gene cluster
   within a 34960 bp nucleotide sequence.";
RL Microbiology 142:3027-3031(1996).
RP SEQUENCE FROM N.A.

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RC STRAIN=168 / Marburg;
RX MEDLINE=98116660; PubMed=9455482;
RA Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadaie Y.;
RT "Sequence analysis of the groESL-cota region of the Bacillus subtilis
   genome, containing the restriction/modification system genes.";
RL DNA Res. 4:335-339(1997).
RN [3]
RP SEQUENCE OF 1-37 FROM N.A.
RX MEDLINE=88011308; PubMed=2821284;
RA Donovan W., Zheng L., Sandman K., Losick R.;
RT "Genes encoding spore coat polypeptides from Bacillus subtilis.";
RL J. Mol. Biol. 196:1-10(1987).
RN [4]
RP SEQUENCE OF 1-34 FROM N.A.
RX MEDLINE=88286730; PubMed=3135411;
RA Sandman K., Kroos L., Cutting S.M., Youngman P., Losick R.;
RT "Identification of the promoter for a spore coat protein gene in
   Bacillus subtilis and studies on the regulation of its induction at a
   late stage of sporulation.";
RL J. Mol. Biol. 200:461-473(1988).
RN [5]
RP SEQUENCE OF 1-10 FROM N.A.
RX STRAIN=168;
RA Wray L.V., Ferson A.E., Fisher S.H.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBD databases.
CC -I- FUNCTION: INVOLVED IN BROWN PIGMENTATION DURING SPOROGENESIS.
CC -I- SIMILARITY: TO S.ANTIBIOTICUS PHENOXAZINONE SYNTHASE (PHSA).
CC -----
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CC -----
DR EMBL: U51115; AAA62305.1; -.
DR EMBL: AB007638; BAA22774.1; ALT_INIT.
DR EMBL: Z99107; CAB12449.1; -.
DR EMBL: X05678; CAA29165.1; ALT_INIT.
DR EMBL: X07512; CAA30392.1; -.
DR EMBL: U31756; AAC44642.1; -.
DR PIR: A27393; A27393.
DR HSP: P36649; 1KV7.
DR Subtilist; BG10490; cota.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 1.
KW Sporulation; Complete proteome.
FT CONFLICT 347 367 DESRRKYLASPSVQHERIQ -> TKAESRSTSPHLRYS
FT FT MKDT (IN REF. 1).
FT CONFLICT 414 420 PIRGTHP -> RHAHIL (IN REF. 1).
FT FT GFAVPPPP -> VRCPAA (IN REF. 1).
SQ SEQUENCE 513 AA; 58499 MW; 836B83B458D75F87 CRC64;

Query Match 22.4%; Score 713; DB 1; Length 513;
Best Local Similarity 34.6%; Pred. No. 9e-45;
Matches 183; Conservative 75; Mismatches 175; Indels 96; Gaps 18;

OY 66 NALPIP-----PYKOPMITNPYTKDKITWYEIFRPFQORITPTLRPALVCGDMSG 121
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 8 DALPIPDILKIPYQ-----SKEKTYEVTMECHQHLDRLPRLRWGYNCLFPG 57
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 122 PTFNVPRTGTEVYVAFINNA-----TVENS-----VHLGSPSRAPFPG 159
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 58 PTFNVPRTGTEVYVAFINNA-----TVENS-----VHLGSPSRAPFPG 117
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 160 MAF-----DVTPGGEY-----KDYFFPYQASARLLMYHDHAFMKTAENAFYFGAGAYITNDE 211
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 118 YPAWFSKQFEGTGPYFKREVYHYFPQOQCALIWTYHDHAFMKTAENAFYFGAGAYITNDE 177
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

OY 212 AEDALGPSYGEFDIPLITAKYVNAAGTL--RSTEGEDDL-----WGCVIHY 259
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 178 KEKRLKLPF--DEYDVPDLITDRTINEDSLFYPSPAPENPSPSLPSPSLVPAFCGFTILV 235
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

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CUEO_ID	YERPE	STANDARD:	PRT:	533 AA.
AC	CUEO_YERPE_082BK0:			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Blue copper oxidase cued precursor (Copper efflux oxidase).			
GN	CUED OR YPO3409.			
OS	Yersinia pests.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Yersinia.			
OX	NCBI_TaxID=632;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CO-92 / Biovar Orientalis;			
RX	MEDLINE-21470413: PubMed-11585360.			
RA	Pathell J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,			
RA	Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,			
RA	Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,			
RA	Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,			
RA	Felwell T., Hamlin N., Holtroyd S., Jagels K., Katlyshev A.V.,			
RA	Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,			
RA	Simmons M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;			
RL	"Genome sequence of Yersinia pests, the causative agent of plague.";			
RL	Nature 413:523-527(2001).			
CC	-I- FUNCTION: Probably involved in periplasmic detoxification of			
CC	copper by oxidizing Cu(I) to Cu(II), and thus preventing its uptake			
CC	into the cytoplasm. Possesses phenoloxidase and ferroxidase			
CC	activities and might be involved in the production of polyphenolic			
CC	compounds and the prevention of oxidative damage in the periplasm			
CC	(By similarity).			
CC	-I- COFACTOR: This protein belongs to the multicopper oxidases which			
CC	contain three distinct Cu centers known as type 1 or blue, type 2			
CC	or normal, and type 3 or coupled binuclear (by similarity).			
CC	-I- SUBUNIT: Monomer (Probable).			
CC	-I- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat			
CC	pathway (By similarity).			
CC	-I- INDUCTION: By cuer, at increased levels of cytoplasmic cuprous			
CC	ions (Probable).			
CC	-I- DOMAIN: The methionine-rich domain could provide binding sites for			
CC	exogenous copper ions. This methionine-rich region is probably			
CC	important for copper tolerance in bacteria.			
CC	-I- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.			
CC	-I- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.			
CC	-I- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/sib-stb.ch).			
CC	or send an email to license@sib-stb.ch).			
DR	EMBL: AJ414157; CAC92639.1: -			
DR	InterPro: IPR001117; Cu-oxidase.			
DR	InterPro: IPR002355; Multicu-oxidse2.			
DR	Pfam: PF00394; Cu-oxidase; 1.			
DR	PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.			
KW	Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;			
KW	Complete proteome.			
FT	SIGNAL	1..28	BY SIMILARITY.	
FT	CHAIN	29..533	BLUE COPPER OXIDASE CUED.	
FT	DOMAIN	68..164	PLASTOCYANIN-LIKE 1.	
FT	DOMAIN	165..425	PLASTOCYANIN-LIKE 2.	
FT	DOMAIN	426..533	PLASTOCYANIN-LIKE 3.	
FT	DOMAIN	356..415	MET-RICH	
FT	METAL	102..102	COPPER (TYPE 2) (BY SIMILARITY).	
FT	METAL	104..104	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	142..142	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	144..144	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	458..458	COPPER (TYPE 1) (BY SIMILARITY).	
FT	METAL	461..461	COPPER (TYPE 2) (BY SIMILARITY).	
FT	METAL	463..463	COPPER (TYPE 3) (BY SIMILARITY).	

Query Match	12.7%	Score 405.5	DB 1	Length 533
Best Local Similarity	27.1%	Pred. No. 3.2e-22		
Matches 146	Conservative 57	Mismatches 217	Indels 119	Gaps
QY	68	LPBPVQOPK---MITNPVTGKDIWYEEIEIKFPQORITPILRPATLV---GYDMSFG	121	
DB	34	LPBPVQOPK---MITNPVTGKDIWYEEIEIKFPQORITPILRPATLV---GYDMSFG	121	
QY	122	PTFVNPQCTETVVFPIINNAIVENSYHLHGSPSAPRFDGNAEDVTPFGEKQDVYFFRYQSA	181	
DB	77	PAIRLQKRAVTTIDITNALPBPATVHHNGLEIPGEVDGQALIQGAKROYTFEAVEQPA	136	
QY	182	RLWVHDAEKKTAENAVFQAGAYIITNDEAEALGPGSGEFDPLITLTKAYVADGT	241	
DB	137	ATCWHPHTHSHKTHQYAVMGLGGLVLTDDSDSETLPLPKOMGVDDLPVLLQDKLIDKHGO	196	
QY	242	LRTSEGEDODL-----WGDVYHNGQWPFLVQNPCKY-RREFNLAAVSRWLVLY	291	
DB	197	V-----DYQDVTMTAAVNGMGDBMLNGVPRP-QQITPRGWRLRLNGCNARSNLAL	249	
QY	292	VRTSSPNVRIPFOVIASDAGLCAVPQTSNLYLAVEREITIIDFNPAQOTLIDLRNVAE	351	
DB	250	-----SDGRPMYVIASDGLLAPVYVRLPILMGREFVAVLDTRD--GQSLDVLTPV	301	
QY	352	TNDVDEDEVARTLEVMRFVSVSTVEDNSQV--PSTLRDVPFRPKRGADKHF-----	404	
DB	302	TQMGHTLAPBPQPLPVLKIQPS---LAIGSVLPDESILVPIELADVTGQVERMFOQLMDP	358	
QY	405	KFERNSGHYLI-----NDVGFAD-----	422	
DB	359	KLDMLGMALVAVARGKRMKAMNMNNHNDMGMDGNRPDMQSGKMKMGNDGTWNGAPAFN	418	
QY	423	-----VNERVLAKPE-----LQTVEMLELSSGGMSHPVHILHYDKILKRTGGRCQ	470	
DB	419	FSHANRINGKAFKSMTEPAFDKQCKYEKWTISGEGDMILHPFHVHGQFRIILENG----	474	
QY	471	VMPYE-SAGLADYVWL--GREFTLIEAHQVPTGCAVMMCHNLIHEDNDMAVFNVTA	526	
DB	475	KPPAHRGKMDIVAVEGARSEILVRENYLAPASTPYMAACHLLEHEDTGMILGFTVSA	533	
RESULT 5				
ID	CUEO_SALTI	STANDARD	PRT	536 AA.
AC	Q829E1			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Blue copper oxidase cueo precursor (Copper efflux oxidase).			
GN	CUEO OR SFY0190.			
OS	Salmonella typhi.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Salmonella.			
OX	NCBI_TaxID=601;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CT18;			
RX	MEDLINE=21534947; PubMed=11677608;			
RA	Parthill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.			
RA	Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,			
RA	Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,			
RA	Crofton A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,			
RA	Feltwell T., Hamlin N., Hogue A., Hoen T.T., Holroyd S., Jagels K.,			
RA	Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,			
RA	Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,			
RA	Whitehead S., Barrett B.G.;			

RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhimurium CT18.";
RL Nature 413:848-852(2001).
CC -1- FUNCTION: Probably involved in periplasmic detoxification of
CC copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake
CC into the cytoplasm. Possesses phenoloxidase and ferroxidase
CC activities and might be involved in the production of polyphenolic
CC compounds and the prevention of oxidative damage in the periplasm
CC (By similarity).
CC -1- COFACTOR: This protein belongs to the multicopper oxidases which
CC contain three distinct Cu centers known as type 1 or blue, type 2
CC or normal, and type 3 or coupled binuclear (By similarity).
CC -1- SUBUNIT: Monomer (Probable).
CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat
CC pathway (By similarity).
CC -1- INDUCTION: By copper, at increased levels of cytoplasmic cuprous
CC ions (Probable).
CC -1- DOMAIN: The methionine-rich domain could provide binding sites for
CC exogenous copper ions. This methionine-rich region is probably
CC important for copper tolerance in bacteria.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL627265; CAD01326.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; MultiCu_Oxidase2.
DR Pfam: PF00394; Cu-oxidase; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;
KW Complete proteome.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 536 BLUE COPPER OXIDASE CUEO.
FT DOMAIN 67 163 PLASTOCYANIN-LIKE 1.
FT DOMAIN 164 430 PLASTOCYANIN-LIKE 2.
FT DOMAIN 431 536 PLASTOCYANIN-LIKE 3.
FT METAL 355 420 MET-RICH.
FT METAL 101 101 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 103 103 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 141 141 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 143 143 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 463 463 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 466 466 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 468 468 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 519 519 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 520 520 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 521 521 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 525 525 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 530 530 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 530 530 COPPER (TYPE 1) (BY SIMILARITY).
SQ SEQUENCE 536 AA; 58624 MW; 2410581D287C3E80 CRC64;
Query Match 12.3%; Score 391; DB 1; Length 536;
Best Local Similarity 25.8%; Pred. No. 3.7e-21;
Matches 140; Conservative 68; Mismatches 215; Indels 120; Gaps 18;

QY 245 TSEEDQD-----WGDVIVHNGQPPPLNVQPRKRYRFRPLNAVASRAWLLYVRS 295
DB 197 ----DQDLMITPAVNGFEDTLTNGAITPOHSAPKGMRLRLRLNCNARS-----LNIA 248
QY 296 SPNVRIPEVIVASDGLDAPVQTSNMLYLAVEREIIIDTFNAGQOTDLRNVAFETNDV 355
DB 249 SDN -RLVIVASDGLLAPVKVTEPLPLMGREFVLVDID--GKADLVTL-PSVGM 303
QY 356 G-----DEDEVARTLEVMRFVVSSTVEDNSOVPTLRDVPVPPRKESGRADKHFE--- 406
DB 304 GMAIAFDPKRPVHMRIQPLR-ITASQT-----LPDTLTMPALPSLEGLTVRNLIKLSMD 356
QY 407 -----ERSNGHYLINDVGRAD----- 422
DB 357 PRLDMGMOMLKKKGGAQMSGMDHDSMAHHOGGMNGHGDHGMDSHNGMAGMGM 416
QY 423 -----VNERV--LAKP-----ELGTVEVWELNSSGSMSPVHILVDFKILK 463
DB 417 NNGKRFDPNANFINQVQEDMKPMFAQGRHRENVISGVDDMLHPRHINGTORILS 476
QY 464 RTGGRGQVMPYESAGLKDYYWL--GGETLTLEAHYQPTGAVMMHCHNLIEDNDMAV 521
DB 477 E--NKGAPAAHRTGKDVVEGEGISEVLVXFHDPAKREHAYMAHCHLLEHEDGMIMG 533
QY 522 FNV 524
DB 534 FTV 536
RESULT 6
CUEO_SALTY
ID CUEO_SALTY STANDARD; PRT; 536 AA.
AC Q8ZRS2; Q938E6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Blue copper oxidase cueo precursor (copper efflux oxidase).
GN CUEO OR CU1D OR STM0168.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxId=602;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee I.S., Lim S.Y., Choi S.-Y.;
RT "cu1d, a gene encoding a multicopper oxidase from S. typhimurium:
RT cloning and characterization.";
RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
CC -1- FUNCTION: Probably involved in periplasmic detoxification of
CC copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake
CC into the cytoplasm. Possesses phenoloxidase and ferroxidase
CC activities and might be involved in the production of polyphenolic
CC compounds and the prevention of oxidative damage in the periplasm
CC (By similarity).
CC -1- COFACTOR: This protein belongs to the multicopper oxidases which
CC contain three distinct Cu centers known as type 1 or blue, type 2
CC or normal, and type 3 or coupled binuclear (By similarity).
CC -1- SUBUNIT: Monomer (Probable).
CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat
CC pathway (By similarity).

Query Match	Best Local Similarity	Score	DB 1:	Length	536:
Matches 140: Conservative	68:	Mismatches 215:	Indels 120:	Gaps 18:	
65 RNALPPIPKOPKMITNTNVGKDIWYIEIKFQORIRYPLTRPATLVGDMGSPGPF	124	12.2%:	Score 390:	DB 1:	Length 536:
31 RPALPIPD-----LITAAASNR-----MGLIYKAGSGTF--AGKNAITTMGYNGLGPAV	78	25.8%:	Pred. No. 4,4e-21:		
125 NVPRGTEVYRFINNAATVENSVAHLGSPSRADPDGAEDVTPPEGEKYDFPNYGSARLL	184				
79 QLHKGSYVVDIHNOIAEDTTLHMHGLEIPGIYDGGPQGLIPAGGTRVTFPEQRAATC	138				
185 WYDHDAFMKTAENAYGCGAGATIIINDEADALCLPBGSGEFDPIPLTLAKYINADSTELS	244				
139 WHPHNGHGTGROVANGLAGLVLEDEDEIRKLRLPQWQIDIVPVLIIQKRSADGQI--	196				
245 TEGEDDDL-----MGSDVITHVNGQMPPLFVNGRKKYRFRFLNAAVSRAWLLYVPTS	295				
197 ----DYQDILMTAAVNGFEDTLITNKCAIRPOHSAPRGWRLRLKLNCCNARS-----LNTAA	248				
296 SPNVRIPIFOVIASDAGLLQAPVQTSMLYLAVEREYIIIDFTNFAQOTLDLRNVAETNDV	355				
249 SDN--RPLVVIASDGLLAEPVKVTLEPLIMGRERFEVLVDSI--GKARDIVTL--PVSGM	303				
356 G-----DEDEVARTILEWRFVYSSGTEVDNSOVPTSLDVPPEPPHKEGPRADKHKEF---	406				

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Db 304 GMAIHPEDKPRHPVMIQPLR-ITASGT-----LPDLITTPALPSLEGLVVRNLKLSMD 350
Oy 407 -----ERSNGHYLINDVGFAD----- 422
Db 357 PRLDMGQMLMKKYGQAOMSGMDHSDMNAHMOGNGMGHGDHGMNDHSGMNHGAMGMM 410
Oy 423 -----VNERV--LAKP-----ELGTVEVWELENSGSGSHPVHILHVDKFLK 460
Db 417 NHGKFEFHMANFINGOVEDMKKPFPAQKGKHEHWIVISGVDMILHPEFHILHGTQFRILS 470
Oy 464 RTGSGQGVMPYESALAKJVWVL--GRGFTLTITEAYPQWTAAYMHMCHNLIHEDNDIMAV 520
Db 477 E---NGKAPAAHRTQKQTVRREGGISSEVLVKFDPDAKKEHAHYAHACHLLHEHDGMILG 530
Oy 522 FNV 524
Db 534 FTV 536

RESULT 7
CUEO_ECOLI STANDARD: PRT: 516 AA.
AC P36649: P75655;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Blue copper oxidase cueo precursor (Copper efflux oxidase).
GN CUEO OR B0123.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=94261430; PubMed=8202364;
RA Fujita N., Mori H., Yura T., Ishihama A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
RL the 2.4-4.1 mln (110,917-193,643 bp) region.";
RN Nucleic Acids Res. 22:1637-1639(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[3]
RP SEQUENCE OF 29-40.
RC STRAIN=K12 / EMG2;
RX MEDLINE=974433975; PubMed=9298646;
RA Link A.J., Robinson K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RL in the genome of Escherichia coli K-12.";
RN Electrophoresis 18:1259-1313(1997).
[4]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10493123;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RL hydroxapatite chromatography.";
RN Electrophoresis 20:2181-2195(1999).
[5]
RP POSSIBLE FUNCTION IN COPPER HOMEOSTASIS.
RX MEDLINE=21125583; PubMed=11222619;
RA Grass G., Rensing C.;
RT "Genes involved in copper homeostasis in Escherichia coli.";
RL J. Bacteriol. 183:2145-2147(2001).
[6]
RP POSSIBLE FUNCTION IN COPPER HOMEOSTASIS.

```

CC STRAIN-K12;
 RX MEDLINE=21391920; PubMed=11399769;
 RA Outten F.W., Huffman D.L., Hale J.A., O'Halloran T.V.;
 RT "The independent cue and cus systems confer copper tolerance during
 RT aerobic and anaerobic growth in *Escherichia coli*.";
 RL J. Biol. Chem. 276:30670-30677(2001).
 RN [7]
 RP CHARACTERIZATION.
 RC STRAIN-K12 / DH5-alpha;
 RX MEDLINE=20469457; PubMed=10915804;
 RA Outten F.W., Outten C.E., Hale J.A., O'Halloran T.V.;
 RT "Transcriptional activation of an *Escherichia coli* copper efflux
 RT regulon by the chromosomal *mer* homologue, *cueR*.";
 RL J. Biol. Chem. 275:31024-31029(2000).
 RN [8]
 RP CHARACTERIZATION.
 RC STRAIN-K12 / C600;
 RX MEDLINE=21359329; PubMed=11466290;
 RA Kim C., Lorenz W.W., Hoopes J.T., Dean J.F.D.;
 RT "Oxidation of phenolate siderophores by the multicopper oxidase
 RT encoded by the *Escherichia coli* *yacK* gene.";
 RL J. Bacteriol. 183:4866-4875(2001).
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-500 AND HIS-501.
 RC STRAIN-K12 / W3110;
 RX MEDLINE=21418784; PubMed=11527384;
 RA Grass G., Rensing C.;
 RT "CueO is a multicopper oxidase that confers copper tolerance in
 RT *Escherichia coli*.";
 RL Biochem. Biophys. Res. Commun. 286:902-908(2001).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
 RC STRAIN-K12 / W3110;
 RX MEDLINE=21874132; PubMed=11867755;
 RA Roberts S.A., Weichsel A., Grass G., Thakali K., Hazzard J.T.,
 RA Tolin G., Rensing C., Montfort W.R.;
 RT "Crystal structure and electron transfer kinetics of CueO, a
 RT multicopper oxidase required for copper homeostasis in *Escherichia*
 RT *coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:2766-2771(2002).
 CC -1- FUNCTION: Probably involved in periplasmic detoxification of
 CC copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake
 CC into the cytoplasm. Possesses phenoloxidase and ferrioxalase
 CC activities and might be involved in the production of polypheolic
 CC compounds and the prevention of oxidative damage in the periplasm.
 CC -1- COFACTOR: This protein belongs to the multicopper oxidases which
 CC contain three distinct Cu centers known as type 1 or blue, type 2
 CC or normal, and type 3 or coupled binuclear.
 CC -1- SUBUNIT: Monomer (Probable).
 CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat
 CC pathway.
 CC -1- INDUCTION: By *cueR*, at increased levels of cytoplasmic cuprous
 CC ions.
 CC -1- DOMAIN: The methionine-rich domain could provide binding sites for
 CC exogenous copper ions. This methionine-rich region is probably
 CC important for copper tolerance in bacteria.
 CC -1- MISCELLANEOUS: This protein is sensitive to oxygen deprivation. It
 CC probably plays a significant role in copper efflux under aerobic
 CC conditions.
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
 CC FRAMESHIFT IN POSITION 464.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; D26562; BAA05579.1; ALT_FRAME.

DR EMBL: AE000121: AAC73234.1; -
 DR PIR: S45200; S45200.
 DR PDB: 1KV7: 06-FEB-02.
 DR Ecogene; E612318; *cueO*.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR002355; MultiCu-oxidase2.
 DR Pfam; PF00394; Cu-oxidase; 1.
 DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
 KW Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;
 KW 3D-structure; Complete proteome.
 FT SIGNAL 1
 FT CHAIN 28
 FT DOMAIN 67 163 BLUE COPPER OXIDASE CUEO.
 FT DOMAIN 164 410 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 411 516 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 355 400 MET-RICH.
 FT METAL 101 103 COPPER (TYPE 2).
 FT METAL 103 103 COPPER (TYPE 3).
 FT METAL 141 141 COPPER (TYPE 3).
 FT METAL 143 143 COPPER (TYPE 3).
 FT METAL 443 443 COPPER (TYPE 1).
 FT METAL 446 446 COPPER (TYPE 2).
 FT METAL 448 448 COPPER (TYPE 2).
 FT METAL 499 499 COPPER (TYPE 3).
 FT METAL 500 500 COPPER (TYPE 1).
 FT METAL 501 501 COPPER (TYPE 3).
 FT METAL 505 505 COPPER (TYPE 1).
 FT METAL 510 510 COPPER (TYPE 1).
 FT METAL 501 501 CH-SR: RESIDUAL ACTIVITY AND LOSS OF
 FT MUTAGEN 500 RESISTANCE TO COPPER.
 SQ SEQUENCE 516 AA; 56556 MW; 37D96B1C331CF30B CnC64;

Query Match 12.2%; Score 368.5; DB 1; Length 516;
 Best Local Similarity 26.1%; Pred. No. 5.3e-21;
 Matches 142; Conservative 65; Mismatches 208; Indels 129; Gaps 19;
 66 NALPI-----PPYOPKMITNPVTGKDIWYEIEIKPFOORTYPTL----- 107
 17 SALPLMSRAVFAERPTLPIDLLTTDA-----RNRIOLITGAGQSTFG 60
 108 -RPATLVGYDGMSPPTENVPRGTETVAFINNAIVENSVLHGSPRAPFDGMAEDVTF 166
 61 GKTATWVGNGMLRPAYVLQGRKAVTVQIVQLEETLTHMHGLEGVEVDGPGQGIIP 120
 167 PEETDYFRPNQASRLMYHDAFMKTRANAYFQOAGAVIINDAEDALGIPSTGEPD 226
 121 PGKRSVTLNVQDPATCFHFPHQHGKGRQVAMGLVIEDEILKMLPKOMGIDD 180
 227 IPLILTAKYNADGTLRSTEGEDDL-----WGDIYHNGQWPPLVNPQPKY-RF 276
 181 VPIYVQDKKFSADGQI-----DYQLDVTAAVGFQDILLTNGAIVP-QHAPRGMLRL 233
 277 RFLNAVSRAMLVLTVRTSSPNVRIIPFOVIASDAGILQAPVQTSMLYLAVEREYIIDF 336
 234 RLNCGNMR-----LNFAITSDN--RPLVYIASDGLPEPVVSELPLVMGRFEVLEEV 287
 337 TN---FAGQTLDRVNAETENDVGEDEYARTLETWRFPVYVSSGTVEDNSQVSTLDRVPP 393
 288 DNKRFEDLVTLFVSOMGMA--IAPEDKRPVRIQPIAISA-----SGALPDTLSSLPAL 340
 394 PKKEPRA-----DKH----- 403
 341 PSLEGITVARKQLQSLMDPMLDMGMQMLEKYGDDQAMAGDSOMMGHMGCMNMHNGG 400
 404 -FKPERSNGHYLDINDGVADVNERVLAKPELTGVEVWELENSGGSHPRHILVDVFKIL 462
 401 KDFPHNAN---KINGQAF-DNKKRPFYAAK-GQYERWVISGDMILRPNHIGQFPIIL 455
 463 KKTGGCGVMPEPSAGLDVYWL--GRGETLTIEHYQPTWGAIVYAGCHNLIHEDNDMA 520
 456 SE--NGKRPAAHRAGMWDYKVEGVNSEVILVKFNHDAPEKRAVYAHACHLLEHEDTGML 512
 521 VENV 524

Db 513 GFTV 516

RESULT 8
CUBO_ECO57 STANDARD: PRT: 516 AA.
AC 08X947;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Blue copper oxidase cuco precursor (Copper efflux oxidase).
GN CUBO OR Z0133 OR ECS0127.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Pena N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Grobbeck E.J., Davis N.W., Lim A., Dimalanca E.T., Potamoustis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RT Nature 409:529-533(2001).
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsuto E., Nakayama K., Murata T., Tanaka M., Tohe T., Iida T., Takami H., Honda T., Sasaki G., Ogasawara N., Yasunaga T., Kihara S., Shiba T., Hattori M., Shinagawa H.;
RA "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
RT DNA Res. 8:11-22(2001).
RL [1]
CC -I- FUNCTION: Probably involved in periplasmic detoxification of copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake into the cytoplasm. Possesses phenoloxidase and ferroxidase activities and might be involved in the production of polyphenolic compounds and the prevention of oxidative damage in the periplasm (By similarity).
CC -I- COFACTOR: This protein belongs to the multicopper oxidases which contain three distinct Cu centers known as type 1 or blue, type 2 or normal, and type 3 or coupled binuclear (By similarity).
CC -I- SUBUNIT: Monomer (Probable).
CC -I- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat pathway (By similarity).
CC -I- INDUCTION: By copper, at increased levels of cytoplasmic cuprous ions (Probable).
CC -I- DOMAIN: The methionine-rich domain could provide binding sites for exogenous copper ions. This methionine-rich region is probably important for copper tolerance in bacteria.
CC -I- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -I- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; AE005188; BAB54427.1; -
CC EMBL; AP002550; BAB33550.1; -
CC InterPro: IPR001117; Cu-oxidase.
CC InterPro: IPR002355; Multicou_oxidse2.
CC Pfam; PF00394; Cu-oxidase; 1.
CC -----

DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;
KW Complete proteome.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 516 BLUE COPPER OXIDASE CUBO.
FT DOMAIN 67 163 PLASTOCYANIN-LIKE 1.
FT DOMAIN 164 410 PLASTOCYANIN-LIKE 2.
FT DOMAIN 411 516 PLASTOCYANIN-LIKE 3.
FT DOMAIN 355 400 MET-RICH.
FT METAL 101 101 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 103 103 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 141 141 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 143 143 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 443 443 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 446 446 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 448 448 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 499 499 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 500 500 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 501 501 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 505 505 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 510 510 COPPER (TYPE 1) (BY SIMILARITY).
SQ SEQUENCE 516 AA; 56702 MW; 7AD387C799780386 CRC64;
Query Match 12.1%; Score 385.5; DB 1; Length 516;
Best Local Similarity 25.9%; Pred. No. 6.8e-21;
Matches 141; Conservative 66; Mismatches 208; Indels 129; Gaps 19;
Oy 66 NALPI-----PPKOPKMITNPVTKGDIWYEIEIKPFQORLYPTL----- 107
Db 17 SALPLMSRAVFAAERKPTLPIDLLTTDA-----RNKQLTLTGACQSTFC 60
Oy 108 -RPATLVGYDMSPGPTFNVPRGTETVVRFINNATVENSVHLHGSPRAPDGAEDVTF 166
Db 61 EKTATWGWYNGNLGPAVKLQKRAVTVDIYNQLEETTLHHHGLEVGEVGPQGIIP 120
Oy 167 PGKYDYTFPNTQSRRLMYHDHAFMKTAEENAYFEQAAAYIINDEADALGPSYGEFD 226
Db 121 PGKRSVTLNVDQPAATCWPFPHQHGKGRVAMGLAVLVEDELLKMLPKQWGIDD 180
Oy 227 IPLILTAKYUNADGTLRSTEGEDDL-----WGDVHNGQMPFLNVPKRY-RF 276
Db 181 VPVIVQDKKFSADQI-----DYGLDVMTAAVGFQGTLLTNGAIYV-QHAAPRGWRL 233
Oy 277 RFLNAASRAMLLVLTSTSPNVRIRPFQVIASDAGLLAPVQTSNULYLAVEREIIIDF 336
Db 234 RLNGCNARS-----INFATSDN--RPLVVIASDGLLPEPVKVNELPVLMEERFEVLEV 287
Oy 337 TN---FACQITDLRVAVETNDVGDEDEYARLVEVRFVSSGTVEDNSQVSTLADVPFP 393
Db 288 NDNKPFDLVTLPLVSQWMA--TAPDKRHPVVRIOPIAISA-----SGALPDTLSSLPAL 340
Oy 394 PHEKGRP-----DKH----- 403
Db 341 PSLEGLTVRKILQDSMDPLMDMNGMQMLMEKYGDDQAMVGMDSQMMHGCHGMMNMHNGG 400
Oy 404 -KFKERSGHVLLINDVGFADVNERVLAKRELGTVEFWELNENSGGWSHPVHILVDKIL 462
Db 401 KEDFHNAN---KINGQAF--DNMKRPFYAAK--GQYERAVISGVDGMLRPHFNGTFRIL 455
Oy 463 KRTGGQVMPEESAGLDVYWL--GRGETLTLEAHYQPMWGAAYWGHNLHENDDMA 520
Db 456 SE---NGKRPRAAHRAGMKRDTYKVEGNSVSEVLAKFNHNDAPKERAYMAHCHLLEDGTGML 512
Oy 521 VFNV 524
Db 513 GFTV 516
RESULT 9
SUFI_ECOLI STANDARD: PRT: 470 AA.
AC P26648; 01-AUG-1992 (Rel. 23, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein sufi precursor.
CN SUFI OR B3017.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE OF 1-89 FROM N.A.
RX MEDLINE=92212294; PubMed=1557036;
RA Coleman J.;
RT "Characterization of the Escherichia coli gene for
RT 1-acyl-sn-glycerol-3-phosphate acyltransferase (pisc).";
RL Mol. Genet. 237:295-303(1992).
RN [3]
RP SEQUENCE OF 28-39.
RC STRAIN-K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
CC -1- FUNCTION: INVOLVED IN CELL DIVISION. SUPPRESSES A FIRST MUTATION.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: U28377; AAA69185.1;
DR EMBL: AE000384; AAC76053.1;
DR EMBL: M63491; AAA24398.1;
DR PIR: S20461; S20461.
DR HSSP: P36649; IKV7.
DR Ecogen; EG11376; SUFI.
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 1.
KW Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 470 PROTEIN SUFI.
FT DOMAIN 68 164 PLASTOCYANIN-LIKE.
SQ SEQUENCE 470 AA; 51858 MW; C643A54CBI46688 CRC64;

Query Match 10.7%; Score 340.5; DB 1; Length 470;
Best Local Similarity 26.9%; Pred. No. 1.5e-17;
Matches 139; Conservative 62; Mismatches 176; Indels 139; Gaps 20;

QY 20 GIPMDTGHPLFVAVDEPKTEVFADSLAAGDDDESPYNLLYRNALPTIPVKQPKMI 79
DB 13 GIALCAGVPLKA-----SAAGQ-----QQLPVPPLLESR-- 43
QY 80 ITNPVTGMDIVYEIEIKPFOQRIYPLR--ATLVGYDGSPPGFTNVGRGTFVYRF 136
DB 44 -----RGQPLM-----TYORAHWSFTPTGRASVWINGYLGPTLVWVGDDVKLIY 91
QY 137 INNAIVENS-----HLHGSFSR--APFDGAEDVTFEGEYKDYFFNYQSARLLW 185

DB 92 SNRLTENVSMTFVAGLQVPGPLMGSPARMSPNADWAP-----VLPIRMQAATLM 140
QY 186 YHDAHFMAKTAENAFYGOAGATIIINDEADALGPGCYGEFDIPLLTAKYINADOTLAST 245
DB 141 YHAMPNRTAQQVYNGVGLGMVLVEDEVSKSLIPNHGVDPFVITIOKRLDNFGTPEYN 200
QY 246 ECEDDDLMDGVYHNVGQWMPFLNVQPRKRYRPFRLAAVSRAMLVLTVTSPPNVAIPQV 305
DB 201 EPGSGGFVGDITLVNGVOSPIYEVSRGWVRLRLNANSRRKQLOM-----NDGRPLHV 254
QY 306 IASDAGLLQAPVQTSNLYLAVEREIIIDFTNAGQTLDRNNAETNDVGE-----DE 360
DB 225 ISDGGFLPAPVSVQSLAPGERREILVDSN-----GDEVSTGCE 297
QY 361 YARTLEWAFVWSSGVTEDNSOVFTL-----RQVPPPKEGPAD 401
DB 298 AASIVDRIR-----GFPESSITVSTLVLTLPKPTGLPLVYDLSLPMRLPTEIMAGSP- 351
QY 402 KHFFERSNGHYLINDVGA-----DVNERVLAKPELGTVEVWELENSSGMSHPVHILV 457
DB 352 -----RSRDISLGDDPGINGQLMDVN-RIDVTAQCGTWERWTYRADE---PQAFHICV 401
QY 458 DEKILKRTGGRGQVMPY-ESAGLKDVMWL-GRGETL 491
DB 402 MGIIRNVG-----AMPPEDRGMKDTVMVQGVVELL 433

RESULT 10
SUF1_SALTY STANDARD: PRT: 470 AA.
AC P40799;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein sufi precursor.
GN SUFI OR SPM3172 OR STY3349.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
NCBI_Taxid=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=L72;
RA Cong J., Schmidt M.B.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=L72 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Aili J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT L72.";
RL Nature 413:852-856(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jorgels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).

CC -1- FUNCTION: INVOLVED IN CELL DIVISION, SUPPRESSES A FTSI MUTATION
(BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in position 413.
CC -----
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CC -----
DR EMBL: U09309; AAA56679.1; ALT_FRAME.
DR EMBL: AE008845; AAL22046.1; -
DR EMBL: AL672777; CAD03004.1; -
DR HSSP: P36649; 1K7.
DR StyGene: SG10522; sufl.
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 1.
KW Periplasmic; signal; Complete proteome.
FT SIGNAL 1 27 BY SIMILARITY.
FT CHAIN 28 470 PROTEIN SUFI.
FT DOMAIN 68 164 PLASTOCYANIN-LIKE.
SQ SEQUENCE 470 AA; 51858 MW; 61E84D4D2B025FB CRC64;

Query Match 10.1%; Score 323.5; DB 1; Length 470;
Best Local Similarity 25.8%; Pred. No. 2.7e-16;
Matches 142; Conservative 58; Mismatches 190; Indels 161; Gaps 21;

QY 1 MLFQSMQAAASGLSGVLPMDTGSHPTEAVDPEKTEVFADSLAAGDDWESPYPY 60
DB 1 MSFSRQFLQAS-----GIALCAGALPLRA-----NAAG----- 30
QY 61 NLLYNNAIPPIPVKPKMTITNPYTKDIIWYEIEIKPQQRITFTLR-----PA 110
DB 31 ----OQPLVPPLELSRR-----GQPLEMTLDPAHWSFTQGTTRA 65
QY 111 TLVGYDGSPPGTFFNVPGETETVRFINNATVENS-----HLHGSPSR--APFDG 159
DB 66 PVMGVNGRYLGTITVWKGDDVKLLYSNRRLAENVSMYTAGLLPGLMGPARMMSPNAD 125
QY 160 WAEDVTPGEYKDYFPVYQASRLWYHDHAFMKTAEANAYFGQAGAYIINDEAEDALGP 219
DB 126 WAP-----VLPIROSATLWYHANTPNRTAQOYVNGIAGMWLVEDDISKTLPIP 174
QY 220 SGYGFEDIPILITAKYVYAADGFLRSTEGEDQDLMGDVIHVNGQPPFLNVQPKRRFRFL 279
DB 175 NHYGVDDPEVITIQDKRLNFGTPEXSEPGSGEVDTLVNGAQSPPYEVSRGWVRLRL 234
QY 280 NAAVSRAWLLVLRTPSSPNVRIPFOVIASDAGLLQAPVQTSMLYLAVEREYIIIDFTNF 339
DB 235 NASNSRRRQLOQMSDRA-----LHVISGDSGFLLPAPYSVYKSLAPGERRIILVDMTN- 287
QY 340 AGQTLDLRNVAETNDVGE-----DEVARTLEVMRFVYVSSGTEVENSQVPTL----- 387
DB 288 -----GDEVSTTCGEAASIYDRIR-----GFEBSISLIVSTLVLTLRPT 326
QY 388 -----RDVPFPKHKEGPADKHFPERKNGHYLLINDVGA-----DYNENYLAKP 431
DB 327 GLPLVLTNPLRRLPLTEIMSGAPV-----RSRDISLGDDPGINGOLMDVN-HIDITTA 378
QY 432 ELGTVEVELEMSGGSMHPVHILVDFKILKRTGCGRGQVMPY-RSAGLKDVVMIGRGRT 490
DB 379 QOGTEKRTIVR---ADMQPSFHIEGVSFLIRNVNG-----AMPFEDRGKKDITVWD-GQV 430
QY 491 LITEAHYOP-W 500
DB 431 ELVYVYQGPWSM 441

RESULT 11
SUFI_HAEIN
ID SUFI_HAEIN STANDARD: PRT: 311 AA.
AC P44847;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein sufi homolog precursor.
GN SUFI OR H10733.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC Haemophilus
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC -1- SIMILARITY: STRONG, TO E.COLI AND S.TYHIMORIUM SUFI.
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: U32756; AAC22390.1; -
DR HSSP: P36649; 1K7.
DR TIGR: H10733;
KW Periplasmic; signal; Complete proteome.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 311 PROTEIN SUFI HOMOLOG.
FT DOMAIN 68 164 PLASTOCYANIN-LIKE.
SQ SEQUENCE 311 AA; 34496 MW; 436173F59F1E1772 CRC64;

Query Match 7.6%; Score 241; DB 1; Length 311;
Best Local Similarity 28.6%; Pred. No. 1.6e-10;
Matches 78; Conservative 39; Mismatches 134; Indels 22; Gaps 5;

QY 65 RNALPIPVKOPKMTITNPYTKDIIWYEIEIKPQQRITFTLR-----LRPATVGYDGMSPG 122
DB 31 REKLIVVPPLEIVR-----RGRPI-----VLTMOENYPLDGSNHWTFGFGNENYLCP 77
QY 123 TFNVNPGTETVRFINNATVENSIVHLHGSPSRAPDGAEDVTPGEYKDYFPVYQASR 182
DB 78 TIKISGSAFKANTYNNLNPQSAVLSIOGLQASGEFLGCAARLKKKGESMAPVPIEQPAA 137
QY 183 LLMYHDHAFMKTAEANAYFGQAGAYIINDEAEDALGPSYGEFDPILITLAKYVYAADGTL 242
DB 138 SCWYSASATLANSAYOTYRGLAGMWLIEDQSLKANLPMKYGVDDIPILIDMEFNNDC-L 196
QY 243 RSTEGEDDLMGDVIHVNGQPPFLNVQPKRRFPFLNAAVSRAWLLVLRTPSSPNVRIP 302
DB 197 QLFKONQPHFVGNRLVNGIEAPYLDVARGWIRLRLNLAASLARAYDRLDNDQ----- 250
QY 303 FOVIASDAGLLQAPVQTSMLYLAVEREYIIID 335
DB 251 MLTIADUGLGLPKAKSVKSLVSPGERAEIILVN 283

FT	CARBOHYD	75	75	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	229	229	N-LINKED (GLCNAC. . .) <td>(POTENTIAL)</td>	(POTENTIAL)
FT	CARBOHYD	238	238	N-LINKED (GLCNAC. . .) <td>(POTENTIAL)</td>	(POTENTIAL)
FT	CARBOHYD	354	354	N-LINKED (GLCNAC. . .) <td>(POTENTIAL)</td>	(POTENTIAL)
FT	CARBOHYD	361	361	N-LINKED (GLCNAC. . .) <td>(POTENTIAL)</td>	(POTENTIAL)
FT	CARBOHYD	457	457	N-LINKED (GLCNAC. . .) <td>(POTENTIAL)</td>	(POTENTIAL)
SO	SEQUENCE	520 AA;	55545 MM;	046AB6D/4737C60E	CRC64;
Query Match					
Best Local Similarity		21.5%	Pred. No. 1,2e-06;	DB 1;	Length 520;
Matches 111;		Conservative 65;	Mismatches 209;	Indels 131;	Gaps
QY	108	RPAITGVGDGMSPCPTFVNPVPGCTETVVRFINNAT-----VENSYHILGSSSRAPFQDMAE	162	162	162
DB	43	KQAVVY--NGSTPGLTGKNGDRFLQVLVDINLNIHTWVKSTSHMGFPQKG--TNWAD	98	98	98
QY	163	DVTF-----PGEKDDYFPFNYSOSARLLWHDHAFKTAEMAFYGOAGAYII--NDEA	212	212	212
DB	99	GRAFINCPRISSGSHFLDQVPPQAGFVHSHLSIQYCD-----GLRGFFVYDPRDPA	154	154	154
QY	213	EDALGPSGYGEFDIPLILTAKYVNADGTLKSTEGEDODLMGVYIHVGO-----P	263	263	263
DB	155	ADLYVDVN-----DDVTIVLDVYHVAKL-----GPAFLGADATLILNGKRSPTTTAD	205	205	205
QY	264	WPLNVQP-RKRRRFLNLAANSRAMLLXYRTSSPNVRIRPQ-----VIASDAGLQAPV	317	317	317
DB	206	LSVVISYVPGKRYRRLVSL-----SCDPNTFFSIDGNMNTIETDS--INVAFL	252	252	252
QY	318	QTSNLYAVARREIILIDFTNFAQOTLD-----LRVAEHNVDGDE-----DEYART	364	364	364
DB	253	VVDSIQTFMAORTSFVLE---AAQAVDNTWIRANPNFGNNGFTGGINSAILRYDGAAY	308	308	308
QY	365	LEVAREVSSQTVEDNSQVSTLRLDVFPPPKES---PADKHEKFEKSNHYLINDGFA	421	421	421
DB	309	EPTTQTQTSTAPLMEVNLNHLPLVTTAVFGSPYAGVDLAINMAFNENQTN--FPINGSTFT	366	366	366
QY	422	DYNERVL-----AKPELGTVEWLELSSSG-----GMSPHVHILVDFK	460	460	460
DB	367	PPTVAVLLQIISGQNMODLLPSSGSVYSLPSMDIEISFPATAAPAPHPFHLGHAF	426	426	426
QY	461	ILKRTGKGQVWPESAGIKQVYVLG---GGETLTIEAHQ---PWTGAAIMMHCHNIHE	514	514	514
DB	427	VVRSAG--STYYNTDNPFRFVYSTGTPAAGDNTITFRPDNGPW---FLCHIDIFHL	480	480	480
QY	515	DNDMAVFENYATMEKGYLODFED-----PMNPKW	545	545	545
DB	481	EAGFAVVF-----ADDIPDVASANDVPQAW	505	505	505
RESULT 13					
COPA_PSESM		STANDARD; PRT; 609 AA.			
ID	COPA_PSESM	STANDARD;	PRT;	609	AA.
AC	P12374;				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-OCT-1989 (Rel. 12, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Copper resistance protein A precursor.				
GN	COPA.				
OS	Pseudomonas syringae (pv. tomato).				
OC	Plasmid PPT23D.				
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;				
OC	Pseudomonas.				
OX	NCBI_TaxID=323;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88227880; PubMed=3372485;				
RA	Mellano M.A., Cooksey D.A.;				
RT	"Nucleotide sequence and organization of copper resistance genes from				
RT	Pseudomonas syringae pv. tomato."				
RL	J. Bacteriol. 170:2879-2883(1988).				
RN	[2]				
RP	CHARACTERIZATION, AND SEQUENCE OF 33-37.				
RC	STRAIN=PT23.2;				

```

RX MEDLINE-92020961; PubMed-1924351;
RA Cha J.-S., Cooksey D.A.;
RT "Copper resistance in Pseudomonas syringae mediated by periplasmic and
RT outer membrane proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8915-8919(1991).
CC -1- FUNCTION: MEDIATES COPPER RESISTANCE BY SEQUESTRATION OF COPPER IN
CC THE PERIPLASM ALONG WITH THE COPPER-BINDING PROTEIN COPC. MAY HAVE
CC OXIDASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- INDUCTION: BY COPPER.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES. COPA
CC SUPERFAMILY.
-----
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-----
CC EMBL, M19930; AAA25806.1; -.
CC PIR, A32018; KSPSCY.
CC HSSP: P36649; 1KV7.
CC InterPro: IPR001117; Cu-oxidase.
CC InterPro: IPR002355; Multicopper oxidase2.
CC Pfam: PF00394; Cu-oxidase; 2.
CC PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
CC PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
CC Oxidoreductase: Copper; Repeat; Signal; Plasmid; Metal-binding;
CC Periplasmic.
CC SIGNAL 1 32
CC CHAIN 33 609 COPPER RESISTANCE PROTEIN A.
CC DOMAIN 367 434 5 X 8 AA TANDEM REPEATS OF D-H-X-X-M-X-
CC G-M.
CC REPEAT 367 374 1.
CC REPEAT 375 382 2.
CC REPEAT 408 415 3.
CC REPEAT 419 426 4.
CC REPEAT 427 434 5.
CC METAL 100 100 COPPER (TYPE 2) (BY SIMILARITY).
CC METAL 102 102 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 142 142 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 144 144 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 542 542 COPPER (TYPE 1) (POTENTIAL).
CC METAL 545 545 COPPER (TYPE 2) (POTENTIAL).
CC METAL 547 547 COPPER (TYPE 3) (POTENTIAL).
CC METAL 590 590 COPPER (TYPE 3) (POTENTIAL).
CC METAL 591 591 COPPER (TYPE 1) (POTENTIAL).
CC METAL 592 592 COPPER (TYPE 3) (POTENTIAL).
CC METAL 596 596 COPPER (TYPE 1) (POTENTIAL).
CC METAL 601 601 COPPER (TYPE 1) (POTENTIAL).
CC SEQUENCE 609 AA; 67354 MW; 9C086528E8135252 CRC64;

```

Query Match 6.0%; Score 192; DB 1; Length 609;
 Best Local Similarity 20.5%; Pred. No. 1.7e-06;
 Matches 138; Conservative 80; Mismatches 214; Indels 242; Gaps 35;

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QY 249 -----DODLWG-----DVIVNGQWPF-LNVQP-----RKYRFP 278
DB 214 ADKGMAATVADRKMAMEMKINPTDLADVSGATYTLNGQAPRMNWTGLFRRGEKLRLEF 273
QY 279 LNAASRAULLLVKRTSSNRVRP----FOYASDAGLLQAPQVTSLLYLAVERVLIIL- 334
DB 274 INSGA---MTVF-----DIRIPGLKTVVASD-GQFVNPVEVDELRLAVAFETDIVE 322
QY 335 -----DFTNFAQGT-----LDLRNVAETNDVG----- 356
DB 323 PRAEATVFAQSDMRKTGYARGTLAVREGLVAYQPLDPRPLVTMDMGAGMDHGSMDGM 382
QY 357 -----DEDEYARTLEVMREVSSGTVEDNSQV-----P 384
DB 383 SGMDSCADDGMQMSMG--GDSMPAMDHSKMSMGMDHAGMGDMGMVMSHP 440
QY 385 STLRYVPF-----PPHK-EGP-----ADKHFEFSNGH----- 412
DB 441 ASBNDPLVDQAMSPJAKLNDPGLGRNKRKVLTAADLKSTFEEDPDREPSRTIELHL 500
QY 413 -----YLINDVGFADYNERVLAKEPGLTVEWELSSGMSHPVHILV----- 457
DB 501 TGHEKFAVSFDGKIRKADQPLLKXGE--RVRIVLVNDTM--MTRPHILHGMSDLDE 556
QY 458 --DFKILKRTGGRGVMPYESAGLKDVMLGREGTLTTEAHVQPTGAYMMHCHNLIHD 515
DB 557 DGNFRVRKHTID---MP---PGSK-----RSYRVTADE---LGRWAYHCHLLYHME 598
QY 516 NDKMAVFNTYAME 529
DB 599 --MGMFREVREE 609

```

RESULT 14
 LACS_TRAVE STANDARD: PRT: 527 AA.
 ID LACS_TRAVE
 AC Q12717;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Laccase 5 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
 GN (Irishiol oxidase) (diphenol oxidase) (Laccase IV).
 OS Trimetres versicolor (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphlophorales; Trimetres.
 OX NCBI_TaxID=5325;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=52J;
 RX MEDLINE=97464057; PubMed=9322748;
 RA Ong E., Pollock W.B., Smith M.;
 RT "Cloning and sequence analysis of two laccase complementary DNAs from
 RT the ligninolytic basidiomycete Trimetres versicolor.";
 RL Gene 196:113-119(1997).
 CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
 CC PRODUCTS (PROBABLE).
 CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenesemiquinone + 2
 CC H(2)O.
 CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
 CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
 CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.

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CC EMBL: U44431; AAC49829.1; -

DR HSSP: P37064; IAOZ.

DR InterPro: IPR001117; Cu-oxidase.

DR InterPro: IPR002355; Multicopper oxidase2.

DR Pfam: PF00394; Cu-oxidase; 3.

DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.

DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.

KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;

KW Ligand degradation; Multigene family.

FT SIGNAL 1 23

FT CHAIN 24 527

FT DOMAIN 25 150

FT DOMAIN 162 306

FT DOMAIN 373 488

FT METAL 87 87

FT METAL 89 89

FT METAL 132 132

FT METAL 134 134

FT METAL 425 425

FT METAL 428 428

FT METAL 430 430

FT METAL 480 480

FT METAL 481 481

FT METAL 482 482

FT METAL 486 486

FT METAL ? ?

FT CARBOHYD 74 74

FT CARBOHYD 77 77

FT CARBOHYD 156 156

FT CARBOHYD 209 209

FT CARBOHYD 233 233

FT CARBOHYD 242 242

FT CARBOHYD 276 276

FT CARBOHYD 317 317

FT CARBOHYD 358 358

FT CARBOHYD 366 366

FT CARBOHYD 393 393

FT CARBOHYD 402 402

FT CARBOHYD 464 464

FT SEQUENCE 527 AA; 56094 MW; D5957491F1F79825 CRC64;

Query Match 6.0%; Score 190; DB 1; Length 527;

Best Local Similarity 21.7%; Pred. No. 1.9e-06;

Matches 107; Conservative 61; Mismatches 206; Indels 118; Gaps 25;

QY 108 RPAATVGYGMSBPTFNVPRGTETVVRFINNATVE-----NSVHLGSPSRAPFDGMAE 162

DB 45 RAAVLNAG--GVPPGRLITGNKGFQINVIDNLNETMLKSTTIHMHGIFQAG--TNMAD 100

QY 163 DVTF-----PGEYKDYFPPNQSARLLMYHDMKRAENKYPQOAGAYIINDAEDEA 215

DB 101 GAATVNOCIATGNSFLYDFTPDQAGTWFYHSHLSTOYCD---GLRGGLVYVD--PDA 155

QY 216 LGLPSSYG--EPDIPLLTAAYYNAADTLRST--EGEDODLMGVDIVHNGOPWFLNV--- 269

DB 156 NA--SLYDVDDDTVTYTLADWHTAKLPAPAPAGDSVLINLGRSFGGATMLTYI 213

QY 270 ---QPKKYFRFLMAAVSAMLLYLVRTSSPNVRIF-----QVIASDAGLLAPVOTSM 322

DB 214 TVTQGRYFRFLVSI-----SCDPNTEFSIDGNHNMIIIVGVGNHFLALDVDSI 261

QY 323 YLAVEREYIIDFTNFAGOTLD-----LRNVAETNDVGDDEVFARTELVMF-----VY 372

DB 262 QIFAGGRYSFILN---AAQSIDNTWIRAIPTNGTDTTGGVNS-----ALIKYTAEEI 312

QY 373 SSGTVEDNSQVSTLRDVPFPHKEGSPADKH-----FKFRSRNGHYLINDVGA 421

DB 313 EPTTNTATSVILPTEFDLVPIDNPAPAGDPQVGVGLANSLSDFSGNS--FFINNETEV 370

QY 422 D-----VNERVLAKPELGTVEV--MELENSSC-----GMSHPVHIH 455

DB 371 PPTVPVLLQILSGAODASALLPNSGVYTLPSNSTIEISPIITTDGALNAPGAPHPFH 430

QY 456 LVDFKILKRTGRGQVWPYSEAGLKDVYMLGR--GELLTIEAHQOPT-----GAYMHCHN 510

DB 431 GHTFSVVRAG--STFENYANPVRRDTVTGSGDWVITR-----FTTDNPGFWPLHCH 483

QY 511 LIHEDNDMMNAVF 522

DB 484 DFLIDAGFAIVF 495

RESULT 15

LAC4_TRAVE

ID LAC4_TRAVE STANDARD; PRT; 520 AA.

AC 012719;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE Laccase 4 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)

DE (Urishiol oxidase) (Diphenol oxidase).

GN LC4 OR LC41.

OS Trameetes versicolor (White-rot fungus).

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OX Aphyllophorales; Trameetes.

OX NCBI_TaxID=5325;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PRL 572;

RA MEDLINE=95399443; PubMed-7669813;

RA Joensson L.J., Sjoestrom K., Haeggstrom I., Nyman P.O.;

RT Characterization of a laccase gene from the white-rot fungus

RT Trameetes versicolor and structural features of basidiomycete

RT laccases. "

RL Biochim. Biophys. Acta 1251:210-215(1995).

CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED

CC PRODUCTS (PROBABLE).

CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzoemiquinone + 2

CC H(2)O.

CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU

CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE

CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.

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CC or send an email to license@isb-sib.ch).

CC EMBL: X84683; CAA59161.1; -

DR HSSP: P37064; IAOZ.

DR InterPro: IPR001117; Cu-oxidase.

DR InterPro: IPR002355; Multicopper oxidase2.

DR Pfam: PF00394; Cu-oxidase; 3.

DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.

DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.

KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;

KW Ligand degradation; Multigene family.

FT SIGNAL 1 22

FT CHAIN 23 520

FT DOMAIN 24 149

FT DOMAIN 161 303

FT DOMAIN 370 491

FT DISULFID 107 509

FT DISULFID 139 227

FT METAL 86 86

FT METAL 88 88

FT METAL 131 131

FT METAL 133 133

PROBABLE.

COPPER (TYPE 2) (BY SIMILARITY).

COPPER (TYPE 3) (BY SIMILARITY).

COPPER (TYPE 3) (BY SIMILARITY).

COPPER (TYPE 3) (BY SIMILARITY).

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OM protein - protein search, using sw model

Run on: February 13, 2003, 05:12:13 ; Search time 74 Seconds
(without alignments)
1653.946 Million cell updates/sec

Title: US-09-218-702-2
Perfect score: 3199
Sequence: 1 MLFSWQLAAAGLLSGVLG.....AEQEPYNRLDEILDGIEE 594

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1705	53.5	602	Q9P8C3	Q9p8c3 acremonium
2	612.5	19.2	475	Q93M03	Q93m03 streptomyc
3	513	16.1	431	Q8RMC6	Q8rmc6 streptomyc
4	497.5	15.6	582	Q9AWU4	Q9awu4 oryza sativ
5	480	15.1	568	Q23123	Q23123 arabidopsi
6	465	14.6	581	Q949X9	Q949x9 arabidopsi
7	465	14.6	637	Q9FTS3	Q9fts3 oryza sativ
8	459	14.4	581	Q8W4N2	Q8w4n2 arabidopsi
9	450	14.1	591	Q9C9A4	Q9c9a4 arabidopsi
10	439.5	13.8	527	Q67206	Q67206 aquifex aeo
11	432	13.5	614	Q9FTS5	Q9fts5 oryza sativ
12	430.5	13.5	588	Q9FTS6	Q9fts6 oryza sativ
13	423.5	13.3	502	Q98FW8	Q98fw8 rhizobium
14	402	12.6	494	Q8YCF0	Q8ycf0 bruceila me
15	375.5	11.8	515	Q9CJ06	Q9cj06 pasteurella
16	375	11.8	477	Q8ZWA8	Q8zwa8 pyrobaculum

17	335.5	10.5	470	16	Q8XBS6	Q8xbs6 escherichia
18	315.5	9.9	513	16	Q9PMB8	Q9pmb8 campylobact
19	310	9.7	468	16	Q9CPE1	Q9cpe1 pasteurella
20	303	9.5	474	16	Q8Z141	Q8z141 yersinia pe
21	284	8.9	1662	2	P71431	P71431 leptothrix
22	236.5	7.4	460	2	Q9X3V2	Q9x3v2 pseudomonas
23	236	7.4	589	3	Q9C497	Q9c497 glomerella
24	235.5	7.4	717	16	Q8XPV6	Q8xpv6 ralstonia s
25	231.5	7.3	570	16	Q9A9L6	Q9a9l6 caulobacter
26	227.5	7.1	351	2	Q93F47	Q93f47 pseudomonas
27	223	7.0	500	16	Q9KB49	Q9kb49 bacillus ha
28	216.5	6.8	463	16	Q9HXW7	Q9hxm7 pseudomonas
29	215.5	6.8	611	16	Q9PH14	Q9phl4 xylella fas
30	214	6.7	721	16	Q9PA43	Q9pa43 xylella fas
31	213	6.7	675	2	Q9KJB8	Q9kjb8 marinomonas
32	209	6.6	561	3	Q96WN0	Q96wn0 botrytis ci
33	205.5	6.4	635	5	Q9NKK0	Q9nkk0 leishmania
34	203.5	6.4	520	3	Q59944	Q59944 cerioporios
35	203.5	6.4	591	10	Q9AU12	Q9aul2 pinus taeda
36	203	6.4	524	3	O13422	O13422 basidiomyc
37	202.5	6.3	565	10	Q9FLB5	Q9flb5 arabidopsi
38	202	6.3	518	3	O59896	O59896 pycnopus
39	201.5	6.3	567	10	Q941X2	Q941x2 oryza sativ
40	199.5	6.3	533	3	O60199	O60199 pleurotus o
41	199	6.2	464	16	Q92QV6	Q92qv6 rhizobium m
42	197	6.2	463	2	Q8RQE2	Q8rqe2 lactococcus
43	197	6.2	518	3	Q9HDS9	Q9hds9 polyporus c
44	197	6.2	605	16	O8XS25	O8xs25 ralstonia s
45	196	6.1	352	2	Q93F57	Q93f57 pseudomonas

ALIGNMENTS

RESULT 1

QSP8C3
ID Q9P8C3 PRELIMINARY; PRT; 602 AA.
AC Q9P8C3;
DC 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Polyphenol oxidase precursor.
DS PPOA.
OS Acremonium murorum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; mitosporic Hypocreaceae; Acremonium.
OX NCBI_TaxID=45278;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 157.72;
RX MEDLINE=21268855; PubMed=11375170;
RA Gouka R.J., van der Heiden M., Swarthoff T., Verrips C.T.;
RT "Cloning of a phenol oxidase gene from Acremonium murorum and its
expression in Aspergillus awamori.";
RL Appl. Environ. Microbiol. 67:2610-2616(2001).
DR EMBL; AJ271104; CAB75422.1; .
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 1.
KW Signal.
FT SIGNAL. 1 21 POTENTIAL.
FT CHAIN 62 602 POLYPHENOL OXIDASE.
SQ SEQUENCE 602 AA; 66920 MW; 0303D991405228A3 CRC64;

Query Match 53.5%; Score 1705; DB 3; Length 602;
Best Local Similarity 60.6%; Pred. No. 1.4e-122;
Matches 325; Conservative 72; Mismatches 129; Indels 10; Gaps 4;
QY 57 SPYNYLLRYNALPIPPVKOPKMIITNPVTGKDIWYIEIKPFQRIYPTLRPATLVGYD 116
||| |::: | ||||| |::: | ||||| |::: | |||||
DB 65 SPAYT-LFQAPLSIPVKEPFTVTNPNNGGIDYIEIKHFSQVFFDLGPADLVGYD 123
QY 117 GMSPGPTFNVRGTETVVRFINNATVENSVHLHSGSPSRAPFDGWAEDVTFPGKYDYFP 176
|:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |:|||||

```
Db 124 GISPGPTFQIEKGRSVVRFNKATVSESIHLHGSFSRAPWDMGWAEDVTNPGEYKDYYP 183
Qy 177 NYOSARLLWYHDHAPKTAENAYFCQAGAYIINDAEADALGPSYGEFIDPLILITAKY 236
Db 184 NAOAGRFSWYHDHAPKTAENAYNGOAGYIIHDAEDSLGPSYGEYDIPLIITSQY 243
Qy 237 NADGTLRSTEGEDQDLGWSDIVHVGQPPFLNVQPKRYFRFLNAAVSRRAWLLYLVRTSS 296
Db 244 NSDGLFTSKGETQSLGWSDIOVNGVPWPYFDVPRKYRFLRLDAAVSRFSFLYFVDAD 303
Qy 297 PNWRPFQVIASDAGLQAPVQTSNLYLAVAEYRIIIDFTNFAGQTLDLRNVAETNDVG 356
Db 304 EDRIPIPFQVIASDGLLEPVTSTKLVLISAERYEIIIDFSEFGKTIELRNEPVGGLG 363
Qy 357 DEDEVARTLEVMRFVYSSGTV--DNSQVPSLRLDVPPPHKEGPAKHKFERSNGHYL 414
Db 364 IEVNDYDDTKVMRFNVAEGLSPSTSVVPSLRLDVPPSPSTSTTIDHSFRFARTAGWS 423
Qy 415 INDVGFADYNERVLAKPELGTVEVWELENSGGWGHVPHIHLVDFKILKRTGG-----R 468
Db 424 INGVTFSDVENLLANVPLGTVOLQLNAAQGWTHPIHIHLVDFKILSRGTAATGATR 483
Qy 469 GQVMYESAGLKDVVWLRGETLITIAHYQVPTGAYMMHCHNLIHEDNDMMAVFNVTAME 528
Db 484 G-VEPYESAGLKDVVYLGKGETVWVVEAHYAPWPVGMFHECHNLIHEDNDMMAAFNVTVLP 542
Qy 529 EKGYLQEDFEDPMNPKWRAPVYNRDNDFHARAGNFSAESITARVOELAEQEPYNRLD 584
Db 543 DYGINSTALADPMQDEFRAPKPYVDNDVEVRENAFSTDEIEAQVQLMASYLPYDNPD 598

RESULT 2
Q93M03
ID Q93M03 PRELIMINARY; PRT; 475 AA.
AC Q93M03;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE Oxidoreductase-like protein.
GN AUR2f.
OS Streptomyces aureofaciens.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCM3239;
RA Kormanec J., Bistakova J., Novakova R., Homerova D., Rezuchova B.;
RT "Cloning and characterization of a new polyketide gene cluster in
Streptomyces aureofaciens CCM3239.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY033994; AAK61713.1; -.
SQ SEQUENCE 475 AA; 52602 MW; A2ED9A4CG38DD0C9 CRC64;
```

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Query Match 19.2%; Score 612.5; DB 2; Length 475;
Best Local Similarity 34.9%; Pred. No. 1.1e-38;
Matches 168; Conservative 62; Mismatches 188; Indels 64; Gaps 19;

Qy 64 YRNALDIPVVKPKMIITNPVTKDIWYIEIKPFQRIYTLRATLVGYDGMSPGPT 123
Db 39 FAHAMPPLPKNLPR---TSFTATSDL--VEIRMQAQVEIVKGLM-SKVRTYDGTFFPGPT 91
Qy 124 FNVPRGTETVVRFINNATVENSVHLHGSPRAPFFDQWAEADVTFPEYKDYFFPNQARL 183
Db 92 IRATOGREVVYVQINELQVNTAVHLGHAVLSEHDLGPMDTIVPGGERTYRYPNNQPAAS 151
Qy 184 LMYHDHAFMKTAEAYFGQAGAYIINDEAEDALGPSYGEFIDPLILITAKYINADGTLR 243
Db 152 LMYHDHMHLEAENVFMGLHGLYLLTDHNERLPLPS--GPYDVLVIRDAVEADGILL 209
Qy 244 STEGEDQDLWGDVH--VNGQWPFLNVQPKRYRFRFLNAAVSRRAWLLYLVRTSSPNVRI 301
Db 210 YTRP-----SDCPHMLVNGKERPYFQVAARKYRFRVYNACANRYVKLRFAD-----GI 257
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Qy 302 PFOVIASDAGLQAPVQTSNLYLAVAEYRIIIDFTNFAGQTLDLRNVAETNDVGD---- 357
Db 258 EFTQIGDGGFLETPTVQOSELLMGLGERADIVVDFSR-----KVGDSSVYL 303
Qy 358 EDEYARTL---EVMRFVYSSGTVEDNSQVPSLRLDVPPPHKEGPAKHKFERSNGHYL 414
Db 304 ENPGAQSIERPVEVMREDIVR-TAPDYSEVPGR--TTYPQOPTPVERDFEI-RTEPAMT 359
Qy 415 INDVGFADYNERVLAKPELGTVEVWELEN-----SSGG-----WSHPVHIHLVDFKILR 464
Db 360 INQOQY-DPN-RVDITAKLTGTEVTVTRVNEVAPAPGKPDFHLW-HSFHTLTYFRVLER 416
Qy 465 TGGRCQVMPYESAGLKDVVWLRGETLITIAHYQVPTGAYMMHCHNLIHEDNDMMAVFN 524
Db 417 ---NGRPAGTRDLGLKADVTVLGPGDTVKIAMTWGPTGOYLYHCHOLGHSSGGQGRIDI 473
Qy 525 TA 526
Db 474 VA 475

RESULT 3
Q8RMC6
ID Q8RMC6 PRELIMINARY; PRT; 431 AA.
AC Q8RMC6;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DE Jadz (Fragment).
GN JADZ.
OS Streptomyces venezuelae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=54571;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISP5230;
RX MEDLINE=21930291; PubMed=11932454;
RA Wang L., White R.L., Vining L.C.;
RT "Biosynthesis of the dideoxysugar component of jadomycin B: genes in
the jad cluster of Streptomyces venezuelae ISP5230 for L-digitoxose
assembly and transfer to the angucycline aglycone.";
RL Microbiology 148:1091-1103(2002).
DR EMBL: AY026363; AAL82808.1; -.
FT NON_TER 431 431
SQ SEQUENCE 431 AA; 47033 MW; 867152A032D1A300 CRC64;

Query Match 16.1%; Score 513; DB 2; Length 431;
Best Local Similarity 33.8%; Pred. No. 4.2e-31;
Matches 155; Conservative 53; Mismatches 195; Indels 56; Gaps 16;

Qy 11 ASGLLSGVLGIPMDTGSHPDIEAVDPEVTEVFADSLAAAGDDDDWESPYPNLLYNALDI 70
Db 21 ASGLLISRTSL-SDTRAGGPAGASPFAPVAAQAL-----APIVPTFTAMPI 68
Qy 71 PDVKQPKMIITNPVTKDIWYIEIKPFQRIYTLRATLVGYDGMSPGPTFNVPRCT 130
Db 69 PVPARVSVSTSTDT-----YSIPVQTQTAELIIPGVRTPLVT-YGGSPGPGTIRKASGR 121
Qy 131 ETVVRFINNATVENSVHLHGSPRAPFFDQWAEADVTFPEYKDYFFPNQARLLAWHDHA 190
Db 122 RVVVKQPNRIITGTSMHLLGAVVDANDGGPMDLITPGQRTTYTPNPQVATLWYHDHA 181
Qy 191 FMKTAENAYFGQAGAYIINDEAEDALGPSYGEFIDPLILITAKYINADGTL-----RSTE 246
Db 182 HHMEAEHYRVGSMGYLISDDNEDALPLPR--GTVDVPIVVRDIDLNPDTLFFDHNFTP 239
Qy 247 GEDQDLWGDVHVGQWPFLNVQPKRYRFRFLNAAVSRRAWLLYLVRTSSPNVRFQVI 306
Db 240 GRRS--WS-----TKGPQPYFQVAARKYRLRLILNGSNQRP---FEFRUSDG---EFTQI 286
Qy 307 ASDAGLQAPVQTSNLYLAVAEYRIIIDFTNF-AGQTLDLRNV--AETNDVGDEDEYAR 363
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[illegible]

Query Match 15.6%; Score 497.5; DB 10; Length 582;
Best Local Similarity 27.3%; Pred. NO. 1e-29;
Matches 171; Conservative 78; Mismatches 208; Indels 169; Gaps 26;

Qy	7	QLAAAGLLSGVLGIPMDTGSHPIEAVDEPVKTEVFADSLAAAGD-----DWESPP-----	59
Db	6	ELAVLLVLLGVGA-----AGTRPSSAPP-----VTEDTLQKVAGSLEMYVDELQPMKPI	55
Qy	60	YLLYRNALPIPPVKQPKMIITNPVTGKDIIWYIEIKFPQORIYPTLRPATLVGYDGM	119
Db	56	YGFSMRHGHSP-----IRLTIGMYQKK-WKFRDL-----PASTVVFVGT	96
Qy	120	-----PGPTFNVPVRGTETVVREIN-----NATVENSVHLHGSPS	153
Db	97	AATATFPGPTIEAAGVPLSVTQNYLPARHILPWPDTVPTAIPRRGGVPTVVHLHGGAH	156
Qy	154	RAPFDG-----WAEDVTFPGCEYKD-----YYPFNGOSARLLVYHDHAFKTAENAYF	200
Db	157	PPOSDCSAFAW-----FTAGFGETGANSTPYTYTNAQSPGVLYVYHDHIALGLTRANLLA	211
Qy	201	GQAGAYIINDEADA-LGLPSGYGEFDIPLILTAKYINADGTLRST-----EGEDQ	250
Db	212	GLLGAVYIRNPAAEPLPGCG--DEDFRVLMIADRSFYADGSTYMNMTGCIINIIHPOMQ	270

Qy	251	DLWGDVTHVNGQWPWFNLVQPKYRFRFLNNAVSRAMLLYLVRTSSPNVRIPQVFIASDA	310
Db	271	EYFGEAITVNGKAMPFLVAVARRRYRIITNSATYENFLSLTN-----GLPFTVVGSDT	324
Qy	311	GLLOAPVQTSNLXILAVAEYRIIITDFNFAQOTLDLNRVA-----ETNDVGDDEYA	362
Db	325	NYSKPVTAASLLVSAETFDVVVDFSQSTSSAEELVNTAPYPYDQAPNDLNG-----	379
Qy	363	RTLVMRFVSSGTVDNSQVPSFLRDVPPPHKKEGPADKH--FKFE-RSNG---HYLI	415
Db	380	--KVMKEVISPAKAKDTSRPAKLDDYVAVAEEAVQRRYIVMYEVEDAATGNPHTLYI	436
Qy	416	NDVGADVNERVLAKPELGTVEVWELENSGGWSHPVHIHLVDFKILKRTG-----	466
Db	437	NGKRLD---PATETPRPGTTEVWEVINLTPD-NHPLHLHLATFOATRVRLGVDEDAFKG	492
Qy	467	-----GRGVMPYESAGLKDQVVLGRGETLTI-----	493
Db	493	CMALKDAVRCNVSRRHVGEEVAPPEHEKGMKNVVKIAPGTMTTIVVYKFFWDSGRKPYF	552
Qy	494	EAHYQWPWTGAYMWHCHNLIHEDNDMM	519
Db	553	DATAEP---GVVYCHILHEDNAMI	575
RESULT 5			
Q23123	IC	023123	PRELIMINARY; PRT; 568 AA.
AD	AC	023123:	
DT	01-JAN-1998	(TReMBLrel. 05, Created)	
DT	01-JAN-1998	(TReMBLrel. 05, Last sequence update)	
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)	
DE	F19G10.5	protein.	
GN	F19G10.5		
OS	Arabidopsis thaliana	(Mouse-ear cross).	
OC	Eukaryota; Viridiplantae;	Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta;	eudicotyledons; core eudicots; Rosidae;	
OC	eucosids II; Brassicales;	Brassicaceae; Arabidopsis.	
OX	NCBI_TaxId=3702;		
RN	[1]		
RP	SEQUENCE FROM N. A.		
RC	STRAIN=CV. COLUMBIA;		
RA	Federspiel N.A.; Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,		
RA	Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y.,		
RA	Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vyotskaja V.,		
RA	Yu G., Ecker J., Theologis A., Davis R.W.;		
RL	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF000657; AA872167.1;		
DR	InterPro; IPR001117; Cu-oxidase.		
DR	Prfam; PF00394; Cu-oxidase; 1.		
DR	SEQUENCE 568 AA; 64355 MW; C4314C889576E35E CRC64;		

Query Match 15.1%; Score 480; DB 10; Length 568;
Best Local Similarity 28.0%; Pred. No. 2.2e-28;
Matches 146; Conservative 78; Mismatches 167; Indels 130; Gaps 20;

Qy	109	PATLVGYDGS-----PGPTFNVPRGTETVVRFIN--	-----AT-----V	142
Db	71	PATVFAYGTSRSKATVPGPTIETVGYDVTWRNLKSHILPMDPTISPAATPKGGI		130
Qy	143	ENSVHLHGSPRAPDGCWAEDVTFPGYKD-----YYEPNYQSARILLWLWHDIAFMK	-----	193
Db	131	PTVVHLGGTHIPTSQNA-DANFTAGFRTGPKWTKTTLHYENKQPGNNWT'HDHMGCL		189
Qy	194	TAENAYFCQAGAYIINDEA-EDALGSPGYGEFDIPILITAKYNNADGTL--RSTEGEDQD	-----	251
Db	190	TRVNLLAGLVGAYILRHHAVERSPQLPTG-DEFDRPLIIFDRSFRKDGSIYMATGNPS	-----	248
Qy	252	L-----WCDTVHNGQWPELNVQPKRYRREFLNAAVSRRAWLLYLVRTSSPNVRIPF	-----	303
Db	249	IHPQWPEYFGDVIVVINGKAPRLNVRRRRYFRRIIINAA'NSARFEKFF-----SNGLOF	-----	302
Qy	304	QVIASDAGLLQAPVQTSNLYLVAARVEYIIIDETNFAGOTLDRNVA-----ETNDVGDE	-----	358

DR	InterPro; IPR001117; Cu-oxidase.	KW	Cell division; Complete proteome.
DR	Pfam; PF00394; Cu-oxidase; 1.	SQ	SEQUENCE 527 AA; 59490 MW; F361BF791FF97355 CRC64;
KW	Coat protein.		
SQ	SEQUENCE 591 AA; 67358 MW; B0CE7B0E8F05AAF CRC64;		
	Query Match 14.1%; Score 450; DB 10; Length 591;		
	Best Local Similarity 27.4%; Pred. No. 4.8e-26;		
	Matches 142; Conservative 74; Mismatches 182; Indels 120; Gaps 18;		
QY	109 PATLVGVDGMS-----PGTFNVPRCTETVVRFIN-----NATV 142	QY	98 PFOORIYPTLRPATLVGYDGMSP-----GPTFNVPRGTETVVRFINNATVNSV 146
DB	86 PATPVFAIGTSKRSAVPGGTIEAVYGVDTVTWRNHLPLHLHLPDPTTSPALPKGGI 145	DB	58 PDGQVTSITAKTTEIPIPGKSTDMLVIEDNEYNPVIFLRKQGTFSADFVNSGDSII 117
QY	143 ENSVHLHGSPRAPFDGWAEDVTFPGYKD-----YFFPNYQARLLWHDHAFMK 193	QY	147 HLHGSPRAPF--DGWAEDVTFGEYKDYFNPY---QARLLWYHDHAFMKTAEANAYFG 201
DB	146 PTVVHLHGHIHEPTSDGNA--DSWFTAGFKETGSKWTKKTHYVKNQKPGNMYHDHAAGL 204	DB	118 HWHG--FRAPWKSDBGHYAVKQGE--TYSYDPDTIIDRSGTYFHPHPRGTGYQVYIG 173
QY	194 TAENAYFGQAGAYII-NDEADAIGLPSGYGEFDIPIILAKYINADGTL-RSTEGED-- 249	QY	202 QAGAYIINDEADAAL--GLPSGYGEFDIPIILITAKYINADGTLRSTEGEDQDLWDGDIHV 259
DB	205 TRVNLGAGLLGSYILRHSSVESPLRLPTG-REFDRPLVIFDRSFRKDGSIYMNATGNPT 263	DB	174 LAGMIITIEDEDEDNLKQALDLEYGVIDIPLIQDKTFDSSGQLYVNPNGHMGFWGDTILV 233
QY	250 -----QDLWCDVTHVNGQWPFNLVQPKYRPFNAVSRALLYLVRTSSPNVRIPF 303	QY	260 NGQWPFNLVQPKYRPFNAVSRALLYLVRTSSPNVRIPFQVFIASDAGLLQAPVQT 319
DB	264 IHPQWPEYFGDAIIVNGKAMPRLTVRRKYRFRITNASNARFFRF-----SNGLDF 317	DB	234 NLTPNPMYDMVERKTYRFRILLNGSNARPYRLALLR---GNORMFEWVIGVEGGLDTPREV 290
QY	304 QVIASDAGLLQAPVQTSNLYLAVAEYRIIIDFTNFAQTLDLRNVAETNDVDGDEYAR 363	QY	320 SNLYLAVAEYRIIIDFT-----NFAQTLDL-----RNAETN--- 353
DB	318 IVGSDSAYLAKPVSTKSVLLAPSEIVDVLVDFSKTSKTAILANNAPYPYPSGDPTVEE 377	DB	291 NEILVAFGERIDILVDFRDASVNDVIKLYNPNHLNIGMGTMRMGMERGMGMNGMN 350
QY	364 TLYMRFVSSGTVEDNSQVSTLRDVPFPHPKGGPADKHP--KFERSNG-----HYLIN 416	QY	354 -DVG--DEDEYARTLYMRFVSSGTVEDNSQVSTLRDVPFPHPKGGPADKHKFERSN 410
DB	378 NSKVMEFIINKSEVDSIIPKKLIEYP-PAHVSTSTRTRYIAMFEVSVSDEPHTLYIN 436	DB	351 MDMGMANDSEF-----EWFEVFTKDSAYDKS-IPQRLSEVT-PINTDGAQVQRLTGNRR 404
QY	417 DVGADVNERVLAPELGTVE-----VWELNSSGWSHPVHLVDFKILKRTG 466	QY	411 GHYLIN-----DVGFA---DVNE-RVLAKPELGTVEWLENSGWSHPVHLVDFKIL 462
DB	437 GLPY---NAPVETPKTGTSEFKSLMTIMKWVEVINLTED-NHPLHLHGLFKVLEQTA 492	DB	405 MVFTINGETWEDGVANQDINNPKVLFQONGVIIIEYVNTGMV-HPMHIHGFQFOVL 463
QY	467 -----GRQVMPYESAGLKDVV-----W 484	QY	463 KRTGGRGVMPYESA--GLKDVVWLGRGETLTIE---AHYQPTWGTAYMWHCHNLIHEDND 517
DB	493 LVKSEEFTECKTRNDKAVKCEISKYARGNKTAVTVHERGKNVFKMMPGHVTKILVRESY 552	DB	464 ERSUG-----PLRATDLGWKDTIVAPMETVRIADVMSHPYNEHQIYLLHCHILLEHDEG 518
QY	485 LGRGETTIEAHYQPTWGTAYMWHCHNLIHEDNDMAVF 522	QY	518 MMAVENVTA 526
DB	553 IHSNESYSFDAQTEP---GYVYHCHILHDHNMMPF 587	DB	519 MMVNYRVNA 527
	RESULT 10		
O67206	PRELIMINARY; PRT; 527 AA.		
AC	O67206;		
DT	01-AUG-1998 (TrEMBLrel. 07, Created)		
DT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	Periplasmic cell division protein (SUF1).		
GN	SUF1 OR AQ_1130.		
OS	Aquifex aeolicus.		
OC	Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.		
OX	NCBI_TaxID=63363;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=VF5;		
RX	MEDLINE=98196666; PubMed=9537320;		
RA	Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,		
RA	Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujaay M., Huber R.,		
RA	Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;		
RT	"The complete genome of the hyperthermophilic bacterium Aquifex		
RT	aeolicus.";		
RL	Nature 392:353-358(1998).		
DR	EMBL; AE000724; AAC07157.1; -		
DR	InterPro; IPR001117; Cu-oxidase.		
DR	InterPro; IPR002355; MultiCu_oxidase2.		
DR	Pfam; PF00394; Cu-oxidase; 1.		
DR	PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.		
	RESULT 11		
O9FTS5	PRELIMINARY; PRT; 614 AA.		
ID	O9FTS5		
AC	O9FTS5;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Putative spore coat protein-like protein.		
GN	P0409B08.12.		
OS	Oryza sativa (Rice).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzeae; Oryza.		
OX	NCBI_TaxID=4530;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV. NIPPONBARE;		
RA	Sasaki T., Matsumoto T., Yamamoto K.;		
RT	"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC		
RT	clone:P0409B08.";		
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AP002860; BAB18285.1; -		
DR	InterPro; IPR001117; Cu-oxidase.		
DR	InterPro; IPR002355; MultiCu_oxidase2.		
DR	Pfam; PF00394; Cu-oxidase; 1.		
DR	PROSITE; PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1.		
KW	Coat protein.		
SQ	SEQUENCE 614 AA; 68321 MW; 80C66EC856305193 CRC64;		

Query Match	13.58;	Score 432;	DB 10;	Length 614;
Best Local Similarity	28.6%;	Pred. No. 1.2e-24;		
Matches 165; Conservative	67;	Mismatches 172;	Indels 172;	Gaps 30;

Qy	69	PIPPVKPQKMIITNPVTG--KDIWYIEIKRPFORIRY-PTLRPATLVGYDGMSPGPt--	123
Db	79	PVP-----TNLTIGMYNKTWQHFRMDPPTPVFVYGSQLQTATF-----PGPIIV	122
Qy	124	--FNVP-----RGTEVVRFI--NNATVENSHVLHGSPRAPFDGWA----	161
Db	123	ARYNVPLVTVWENHLPOAHILPWPDPPTAIPKKAGGVPTVYHLHGAQAOPSDGDGHAFWF	182
Qy	162	-EDVTFGE---XKYDYFPNQY-SARLLWYHDHFMKTAENAYEQACAYIIN-DEAEDA	215
Db	183	TRDFAENGSTWTQTYTYPNVQPAAGNIWIYHDHALGLTRASULLAGLLAAAYIVENPELEMP	242
Qy	216	LGLPSGGEGEFDIPLITAKYYNADGTL-RSTEGE-----DODLMGDVIHVNGQPWF	266
Db	243	FNLPs---GEFDLHLVIADRKFNVDGTIFMDTVGAVPSVHPQWQPEYFCEVITVNGKAMPF	300
Qy	267	LNVPQRKYRRFLNAVSRAWLLYLVRTSSPNVR----IPQVITASDAGLIQAQVQTSNL	322
Db	301	QAVORRYRLRLNASNR---YL-----NIRFSNGLPFTVIASDATYLSRPVTVSNL	350
Qy	323	YLAVERVEIIIDFT-----NFAGOTLDLR-----NVAETNDV	355
Db	351	LLSPAEIFDVLDVDFSLVNPVNATIELLSAPYFPCTGPANATLDGKMVFNAVSAKVOV	410
Qy	356	GDEXYARTLEVRFVSSGSTVEDNSQVPSLTRDVPF-----PPHKEGPADKHFKFRS	409
Db	411	GDD-----MPMQEPENSTVVYPEI--GVPPFAKVTPPTMTKRIVLVLENMTS	455
Qy	410	NG-----HYLINDVGFADVERNVLAKPELGTVVEWELENSSGGWSHPVHIHLVDFK--	460
Db	456	NDPNTAKTMNLYINGLRLEDPPET--PTSGETLWHVINLTDP-NHPLHLHLAEFAQV	511
Qy	461	-----ILKRTG-----GRGVMPEYSAGLKDVVWLGRGETLTTETA	495
Db	512	QMLQLVDPTDKSCMLKHNDFACNLDOHAVGALQVPPEEKTKNVVKYIPPAYVTSVV	571
Qy	496	HYQ-----PW-----TGA--YMMHCNLIJHEDNM	519
Db	572	AFLRVHNNMPPFDATAAPGVYHYCHILDHEDNAM	607

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RESULT 12
Q9FTS6
ID Q9FTS6 PRELIMINARY; PRT; 588 AA.
AC O9FTS6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative spore coat protein-like protein.
GN P0409B08.11 OR P0044F08.29.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0409B08.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0044F08.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

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[illegible]

RESULT	13
Q98FW8	
ID	Q98FW8 PRELIMINARY; PRT; 502 AA.
AC	Q98FW8;
DT	01-OCT-2001 (TEMBRel. 18, Created)
DR	01-OCT-2001 (TEMBRel. 18, Last sequence update)
DE	01-JUN-2002 (TEMBRel. 21, Last annotation update)
DE	Putative periplasmic oxidoreductase..
CN	MLL3586.
OS	Rhizobium loti (Mesorhizobium loti).
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OX	Phyllobacteriaceae; Mesorhizobium.
CC	NCBI_TaxID=381;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MAFF303099;
RX	MEDLINE=21082930; PubMed=11214968;
RA	Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA	Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA	Kishida Y., Kiyoakawa C., Kohara M., Matsumoto M., Matsuno A.,
RA	Mochizuki Y., Nakayama S., Kakazaki N., Shimpo S., Sugimoto M.,
RA	Takeuchi C., Yamada M., Tabata S.;
RT	*Complete genome structure of the nitrogen-fixing symbiotic bacterium

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Pred. No. is the number of results predicted by chance to have a

RESULT 1
AR211554
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AR211554
Sequence 1 from patent US 6399329.
AR211554
AR211554.1 GI:21514906
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 3677)
Wang, H. and Bodie, E.A.
Phenol oxidizing enzymes
Patent: US 6399329-A 1 04-JUN-2002
Location/Qualifiers


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|||||
Db 2041 AGCATGGCCTTCTCTTAAGTCCAGCCCGCAAGTACCCTTTCGGATTCTCCAAGCGTG 2100
QY 2101 CCGTGTCTCGTGGTGGCTCCTTACCTCGTCAGGACCAAGCTCTCCCAACGTCAGAAATTC 2160
Db 2101 CCGTGTCTCGTGGTGGCTCCTTACCTCGTCAGGACCAAGCTCTCCCAACGTCAGAAATTC 2160
QY 2161 CTTTCCAAGTCATTTGGCTCTGATGTGGTCTCCTTCAAGCCCGGTTTCAGACCTCTTAACC 2220
Db 2161 CTTTCCAAGTCATTTGGCTCTGATGTGGTCTCCTTCAAGCCCGGTTTCAGACCTCTTAACC 2220
QY 2221 TCTACCTTCTGTGGCCGAGCGTTAGGAGATCATTTAGTATGGCTATGCCCTCCCTCTCAGCA 2280
Db 2221 TCTACCTTCTGTGGCCGAGCGTTAGGAGATCATTTAGTATGGCTATGCCCTCCCTCTCAGCA 2280
QY 2281 ATGAGTCAAGAATCTTAAGACTTAACACTTTGTAGACTTTCACCAACTTTTGCTGCCAGACTC 2340
Db 2281 ATGAGTCAAGAATCTTAAGACTTAACACTTTGTAGACTTTCACCAACTTTTGCTGCCAGACTC 2340
QY 2341 TTGACCTGGCCAAACGTTGTGAGACCAACGATGTGCGGACGAGGATGATGAGTACGCTCGCA 2400
Db 2341 TTGACCTGGCCAAACGTTGTGAGACCAACGATGTGCGGACGAGGATGATGAGTACGCTCGCA 2400
QY 2401 CTCTGAGGTGATGCGCTTCGTCGTCAGCTCTGGCACTTTGAGGACACACGCGAGGTCC 2460
Db 2401 CTCTGAGGTGATGCGCTTCGTCGTCAGCTCTGGCACTTTGAGGACACACGCGAGGTCC 2460
QY 2461 CTTCCACTCTCGTGACGTTCTTCCCTTCCTCAAGGAAGCCCGCCGCAACAGCACT 2520
Db 2461 CTTCCACTCTCGTGACGTTCTTCCCTTCCTCAAGGAAGCCCGCCGCAACAGCACT 2520
QY 2521 TCAAGTTTGAACGCGAGCAACGAGCACTACCTGATCAACGATTTGGCTTTGCCGATGCA 2580
Db 2521 TCAAGTTTGAACGCGAGCAACGAGCACTACCTGATCAACGATTTGGCTTTGCCGATGCA 2580
QY 2581 ATGAGCGTCTCTGGCCAGCCGAGCTCGGCACCGTTGAGCTCTGGGAGTCGAGAATC 2640
Db 2581 ATGAGCGTCTCTGGCCAGCCGAGCTCGGCACCGTTGAGCTCTGGGAGTCGAGAATC 2640
QY 2641 CCTCTGGAGGCTTGGAGCCACCCCGTCCACATTCACCTTTGTTGACTTCAAGATCCTCAAGC 2700
Db 2641 CCTCTGGAGGCTTGGAGCCACCCCGTCCACATTCACCTTTGTTGACTTCAAGATCCTCAAGC 2700
QY 2701 GAACGTGGTGGTCTGGCCAGGTGATGCCCTACGAGTCTGCTGGCTTTAAGGATGCTGCT 2760
Db 2701 GAACGTGGTGGTCTGGCCAGGTGATGCCCTACGAGTCTGCTGGCTTTAAGGATGCTGCT 2760
QY 2761 GGTGGGAGGGGTGAGACCTTGACCATCGAGGCCCACTACCAACCCCTGGAGCTGGAGCTT 2820
Db 2761 GGTGGGAGGGGTGAGACCTTGAGCCCTGAGCCATCGAGGCCCACTACCAACCCCTGGAGCTT 2820
QY 2821 ACATGTGGCACTGTGACAACTTCATTACAGAGGATAACGACATGATGGCTGTATTCAAGC 2880
Db 2821 ACATGTGGCACTGTGACAACTTCATTACAGAGGATAACGACATGATGGCTGTATTCAAGC 2880
QY 2881 TCACGCCCATGAGGAGAGGATATCTTCAAGGAGGACTTCGAGGACCCCACTGAACCCCA 2940
Db 2881 TCACGCCCATGAGGAGAGGATATCTTCAAGGAGGACTTCGAGGACCCCACTGAACCCCA 2940
QY 2941 AGTGGGCGCCCTTCTTACAAACCCGCAAGCACTTCCATGCTCGCCTGGAACTTCTCGG 3000
Db 2941 AGTGGGCGCCCTTCTTACAAACCCGCAAGCACTTCCATGCTCGCCTGGAACTTCTCGG 3000
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QY 3061 ATGAGATCCTGGAGGATCTTGGAAATCGAGGAGTAACACCCCGGACCAAGCTCTTACAATC 3120
Db 3061 ATGAGATCCTGGAGGATCTTGGAAATCGAGGAGTAACACCCCGGACCAAGCTCTTACAATC 3120
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RESULT 2
AR211556
LOCUS AR211556 1791 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from patent US 6399329.
ACCESSION AR211556
VERSION AR211556.1 GI:21514909
KEYWORDS .
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1791)
AUTHORS Wang, H. and Bodie, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 5 04-JUN-2002;
FEATURES Location/Qualifiers
source 1..1791
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BASE COUNT 380 a 551 c 451 g 409 t
ORIGIN

Query Match 40.1%; Score 1474; DB 6; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

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Db 181 CCATACAACTTGTCTTAC----- 198
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RESULT 3
AX384798
LOCUS AX384798 7259 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 3 from Patent WO0196543.
ACCESSION AX384798
VERSION AX384798.1 GI:19577933
KEYWORDS .
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1
AUTHORS Hood,E., Howard,J.A., Bailey,M., van Gastel,F.J., Ward,M., Wang,H. and Woodard,S.
TITLE Method of increasing recovery of heterologous active enzymes produced in plants

JOURNAL Patent: WO 0196543-A 3 20-DEC-2001;
Prodigene, Inc. (US) ; Genencor, Inc. (US)
FEATURES Location/Qualifiers
source 1..7259
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/note="Stachybotrys sp. n"

BASE COUNT 1928 a 1745 c 1583 g 1997 t 6 others
ORIGIN

Query Match 39.8%; Score 1462.6; DB 6; Length 7259;
Best Local Similarity 86.0%; Pred No. 0;
Matches 1806; Conservative 0; Mismatches 24; Indels 269; Gaps 6;

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QY 1330 TCTTTGATTTCTACGAAGCAACTCGGCCCGCAGCTAAATGATTTCTAGGATCATTTACCAAC 1389
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Q	y	2635	AGAACTCTCTGGAGCTGGAGCCACCCCGCTCCACATTCACCTTGTGACTTCAAGATCC	2694
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Q	y	2740	CTGGTCTTAAGATGCTCTGCTGGTGGCAGGGGTGAGACCTTGACCATCGAGGCCCACT	2799
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Q	y	2800	ACCAACCTCGAGCTGAGCTTACATGTGGCACTGTTCACAACTCATTTCCAGGAGTAACG	2859
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Q	y	2860	ACATGATGGCTGTATTCAACGTTCACCGCCATGGAGGAGAAGGATATCTTCAGGAGGACT	2919
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RESULT 5				
AR211555				
LOCUS	AR211555 2905 bp DNA linear PAT 20-JUN-2002			
DEFINITION	Sequence 3 from patent US 6399329.			
ACCESSION	AR211555			
VERSION	AR211555.1 GI:21514907			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 2905)			
AUTHORS	Wang, H. and Bodie, E.A.			
TITLE	Phenol oxidizing enzymes			
JOURNAL	Patent: US 6399329-A 3 04-JUN-2002;			
FEATURES	Location/Qualifiers			
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Best Local Similarity 59.3%; Pred. No. 8.8e-104;				
Matches 976; Conservative 0; Mismatches 537; Indels 133; Gaps 6;				
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Db	598	CCAGGGTGATCGCGAAAGCTCCATCCATCTCCACGGCTCCCGCTGCCCTTCGCTTTTGA	657
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Db	658	CGGATGGCTGATGATGATCATGATGAAGGGGAAATACAAAGGTACGATAGCGTGTGATTC	717
Qy	1710	-----GGATTACTACTTTGCC	1725
Db	718	TACGCATCAGAAAGCCCTATCATACTAACAGGACTTTCTCTCAGACTACTTACCCG	777
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Db	778	AACAACCAAGCTGCCAGATTTTGTGGTACCACGATCATGCTATGCATGTTGTAAGTCTT	837
Qy	1784	ACGAGCCCTTATCTTTCTTGGCTACCTTTGGCTAACCAACTTTCCTTTGTAAGTCTGTA	1843
Db	838	TACGCACTTTTATGTGTAGTGAACAGGAAGGATTAAGCTTAACATCTGTGCAGAACCGCAGA	897
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Db	898	AAATGCCATTTCCGCGAAGCGCGCCTACCTGATCACAGACCGCGCTGAGGATGCTCT	957
Qy	1904	CGGTCTCTTAGTGGGATGTGGGAGTTCGATATCCCTCTGTACTCTGACGGCCNAGTACTA	1963
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Db	1018	CAAGCGCGATGGAACCTTTAAGACCAGTCTGGGAGAAAGAGAGTGTGTGGGCGACAT	1077
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Qy	2204	CGTTTCAGACCTCTAACCTCTTACCTTCTCTGTCGGAGGGTTACGAGATCATTTATGGTAT	2263
Db	1258	GGTTCAACCTCAGATATGATGTTGCACCGCGAAGCGTACGAGAT-----	1305
Qy	2264	GCCTTCCCTCTCACGAATGAGTCAAGAACTCTTAAGACTTAACACTTTGATGCTTACCAA	2323
Db	1306	-----TGGTTCGATTTTCGCCCC	1323
Qy	2324	CTTTTGTGGCCAGACTTCTGACCTGGCGAAACGTTGCTGAGACCACGATGTGCGGGACGA	2383
Db	1324	CTATGGCGGCGAAACGTTGGATCTGGCGAACTTCGCAAGGGCAATGGTATCGGTACCGA	1383
Qy	2384	GGATGATACGCTCGCACTCTCGAGGTGATGCGTTTCGTCGTCAGCTCTGGCACTGTGTA	2443
Db	1384	CGAGGACTACGCAAAACACTGCAAGGTCAATGGTTTCCACGTTCACGCGCAACACGTGCT	1443
Qy	2444	GGACAACAGCAGGTCCTCCACTCTCCGTTGACGTTTCCCTTCCCTCTCAAGGAAGG	2503
Db	1444	CGATAACTCCGTGGTACCCGAGCAGCTATCTCAGATCCAGTTTCCCGCGGACA---AAAC	1500
Qy	2504	CCCCGGCGCAAGCACTTCAAGTTTGAACGCGACGAACAGGACACTTACCTGATCAACAGTGT	2563
Db	1501	CGACATAGACCATCACTTCGTTTCCATTCGTAACCAAGCGAGTGGCGCATCAACGCAT	1560

Query Match	12.5%;	Score 460.8;	DB 6;	Length 2905;
Best Local Similarity	59.3%;	Pred. No. 8.8e-104;		
Matches 976;	Conservative	0;	Mismatches 537;	Indels 133;

QY 1491 CTGACCCCTTTCAGATTACCCACCTTGGGCCCTGCCACTCTCGTCGGCTACGNTGGCAT 1550

QY 2564 TGGCTTTCCGATGTCAATGAGCGTGTCTCGCCAAAGCCCGAGCTCGCACCGTTGAGGT 2623
Db 1561 CGGGTTTCACAGCTCGAGAACCGTGTCTTGGCAAGGTACCGCGCGTACTGTCGAGCT 1620
QY 2624 CTGGAGCTCGAGAACTCCTCTGGAGGCTGGAGGACACCCCGTCCACATTTACCTTGTGTA 2683
Db 1621 TTGGAACTTGAGAACAGCTCCGGCGGCTGTCAACACCCCATCCAGCTCCACCTAGTAGA 1680
QY 2684 CTTCAAGATCTCAAGCAACTGG-----TGGTGTGGCCAGGTCATGCCCCCTACGAGTC 2737
Db 1681 CTTCCGAGTCTCGCACGCTACGGCGACGAAGGCACTCGCGCGCTCATGCCCTATGAGGC 1740
QY 2738 TGCTGGTCTTAAGGATGCTGCTGTGGCGAGGGTGAGACCCCTGACCATCGAGGCCCA 2797
Db 1741 CGCGGCTCTAAGGACGTGCTGTGGCTCGGCCGTACAGAGAGCGTCTCTGTCGAAGCACA 1800
QY 2798 CTACCAACCCCTGGAGTGTACATGTGGCACTGTCCACAACCTCATTTACAGAGATAA 2857
Db 1801 TTACGCCCATGGGACGGAGTCTACATGTTCCACTTGCACAACTCATCCAGRAAGACCA 1860
QY 2858 CGACATGATGGTGTATTCACGTCAACCGCATCGGAGAGAGGATATCTTCAGGAG-- 2915
Db 1861 AGACATGATGGCGCGCTTCGACGTGACTAAATCCAGAATTTTGGGTACAAACGAGACGAC 1920
QY 2916 -GACTTTCGAGGACCCATGAACCCCAAGTGGCGGCCGTCTCTTACAACCGCAACGACTT 2974
Db 1921 TGATTTCCACGATCTGAGGATCTTCGCTGGTGTCAAGAACTTTTACCGCGGGTGATCT 1980
QY 2975 CCATGCTCGCGTGGAAACTTCTCCCGCGAGTCCATCACTGCCGAGTGCGAGGCTGGC 3034
Db 1981 CACGCGCGATCGGGTATCTTTTCAGAGAATCCATCAGGCGCTAGAGTAATGATGTGGC 2040
QY 3035 CGAGCAGAGCGGTACAAACCGCCTCG 3060
Db 2041 GCTCGAGCAGCGCTTACAGCGAACTCG 2066

RESULT 6
AR211557
LOCUS AR211557 2063 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6399329.
ACCESSION AR211557
VERSION AR211557.1 GI:21514910
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2063)
AUTHORS Wang, H. and Bodie, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 6 04-JUN-2002;
FEATURES Location/Qualifiers
source 1..2063
BASE COUNT 501 a 604 c 510 g 448 t
ORIGIN

Query Match 12.4%; Score 455.6; DB 6; Length 2063;
Best Local Similarity 59.1%; Pred. No. 1.7e-102;
Matches 971; Conservative 0; Mismatches 544; Indels 129; Gaps 6;

QY 1501 CAGATTTACCCACCTTGGCGCCTGCCACTCTCGTCGGCTAGGATGGCATGAGCCCTGGT 1560
Db 376 CAGGCTATCCAAAGTCTACGTCCTGCTCGCTTGGTAGGCTATGATGGCATTTTCACGAGC 435
QY 1561 CCTACTTTCAATGTTCCCGAGAGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACC 1620
Db 436 CTTACGATCATCTGTCGCGAGAGAACAGACGCGTTGTACGATTCTGTAACACCGGTTGAT 495
QY 1621 GTGGAGAACTCGGTCATCTGCACGGCTCCCATCGCTGCCCTTTTCGATGGTGGGCT 1680
Db 496 CGCGAGAGTTTCGATTCATCTTTCATGTTCTCCCTCCCGTGGCCCTTTGACGGATGGGCT 555

QY 1681 GAAGATGTGACCTTCCCTGCGGAGGTACAAGAT----- 1713
Db 556 GAAGATTTGATATGAAAGGCCAATTTCARAGGTACACAGAACAAATCTTATGTCATCAGG 615
QY 1714 -----TACTACTTTTCCCACTACCAATCCG 1738
Db 616 TGCCTCTTTTATAACACGACGCTGTTCTTAGACTACTACTACCCGAAACAACAGGCTG 675
QY 1739 CCGCGCTTCTGTGTACCATGACACAGCT-TTCATGAAGGTATGTCAGAGCCTTTATCT 1797
Db 676 CCAGATTCCTGTGTGTACACGATCATGTCATGTTGTAAAGTCTTGCAGACTAATCAT 735
QY 1798 TTTCTGGCTACCTTTGGCTAACCAACTTCTTCCGTAGACTGCTGAGAAATGCTACTTTG 1857
Db 736 GGGAGCGAAAGCGGAAGATCGGGCTGACACTTATCGAGACTCGGAAATGCTATTTTG 795
QY 1858 GTCAGGCTGGCGCCTTACATTTATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTTAGTG 1917
Db 796 GACAGGCTGGCGCCTTACCTGATCAGACGCCAGCTGAGGACGCCCTCGGCTTCTCTCGG 855
QY 1918 GCTATGGCGAGTTGATATCCCTCTGATCTCTGACGCGGCAAGTACTATTAACGCCGATGTA 1977
Db 856 GTTACGGAATAATACGACATCCCACTGGTCTCAGTTTCCAAGTTCTTACAACAGTATGAA 915
QY 1978 CCCTGCGTTTCGACCGAGGCTGAGGACGAGGACTCTGTGGGAGATGTCATCCATGTCAAG 2037
Db 916 CTCCTCAAGCAGTGTGGGAGAAAGACAAAGTCTCTGGGCGAGCTATCCATGTCAAG 975
QY 2038 GACAGCCTAGCCTTTTCCCTTAACGTCACGCGCCCAAGTACCCTTTCCGATTTCTTCAAG 2097
Db 976 GTCAGCCTGGCCATTTCTCAAGCTTGAGCCTCGAAAGTATCGGCTTCGATTTCTTCAATG 1035
QY 2098 CTGCGCTGTCTGCTGTGGCTCTCTCTGCTGTCAGGACACGCTCTCCCAACGTCAGAA 2157
Db 1036 CGGCTGTTTCTCGGAACCTTTGCCCTCTATTTCGTCAAGCAACAAGCCACTGCTACTAGAC 1095
QY 2158 TTCTTTTCCAAAGTCAATGCTCTGATGCTGCTCTTCAAGCCCGCTTTCAGACTCTCTA 2217
Db 1096 TTCTTTTCCAGGTCAATGCTCTGATGAGGCTACTCAGGACCCCGGTCCAAACCTCAG 1155
QY 2218 ACCTCTACTCTTGTGTCGCGAGCTTACGAGATCATTTATGTTATGCCCTTCCCTCTCA 2277
Db 1156 ATATTTACGTGGCAGCAGCAGAGCGCTACGAGAT----- 1189
QY 2278 CGAATGAGTCAAGAATCTTAAGACTTAACACTTGTAGACTTCAACACTTTGCTGCCAGA 2337
Db 1190 -----TGATTTGACTTTTTCGCTTATGCGGCCAGA 1221
QY 2338 CTCCTGACTCGGCAACGTTGCTGAGACCAACGATGTGCGGCACGAGGATGATGCTC 2397
Db 1222 CGATAGATTTGCGTAACCTTTGCAAGGCCAATGGGCTGGGACCCATGACGATTATGCA 1281
QY 2398 GCACCTCTCAGGTGATGCGCTTCTGCTCAGCTCTGGCACTGTGAGGACAAACAGCCAGG 2457
Db 1282 ACACGTACAAGGTCAATGCGCTTCCATGTGAGCAGCAAGCAGTCTGCGATAATCTCGTGG 1341
QY 2458 TCCCTCTCACTCTCGGTGACGTTTCTTCCCTCTCAAGGAAGGCCCGCCGACAGC 2517
Db 1342 TACCCGCAAGCTATCTCAGATCCAGTTTCCCGCGCAGCA--AAACCGGCATTCGACCAC 1398
QY 2518 ACTTCAAGTTTCAACGACGACCAACGACACTACCTGATCAACGATGTTGGCTTTGCCGATG 2577
Db 1399 ACTTCGCTTCCATCGCAACACAGGATGGCGGATCAACGGCATCGGGTTTGAGAGC 1458
QY 2578 TCAATGAGCGTCTCTGGCCAAAGCCCGAGCTCGGACCGCTTGGAGGTCTGGGAGCTCGAGA 2637
Db 1459 TCCAGAACCGTATCTGGCCAAAGTACCGCGCGGACCTGTCGAGCTATGGGAACTCGAGA 1518
QY 2638 ACTCTCTGGAGGCTGGAGCCACCCCGCTCCACATTCACCTTGTGACTTCAAGATCTCA 2697
Db 1519 ACAGTCCCGCGGCTGGTGGCAGCCCACTCCAGCTCACTGCTGCTGACTTCCGAGTCGTCG 1578

QY 2698 AGGAACTGGTG-----GTCGTGGCCAGGTCATGCCCTACGAGTCTGCTGCTTTAAGG 2751
Db 1579 CACGCTACGGTACGAAACACTTCGGCGGTCATGCCCTACGAGTCGGCGCTCAAGG 1638
QY 2752 ATGTCGCTCTGGTGGCCAGGGTGAGACCTGACCATCGAGGCCCACTACCAACCTCGA 2811
Db 1639 AGTCTGTGGTCTGGCCGCCAGAGACGGTCTCGTCGAACACACTACGCCCTCGG 1698
QY 2812 CTGGAGCTTACATGTGGCACTCTCAACCTCATTCACGAGGATACGACATGATGGTG 2871
Db 1699 AGGAGTCTACATGTGTCCACTGCCAACCTGATCCACGAACCAAGACATGATGGCG 1758
QY 2872 TATTAACCTCACCCCATCGGAGGAGGATATCTTCA---GGAGGACTTCGAGGACC 2928
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QY 2929 CCATGAACCCCAAGTGGCGCGCTTCCATTACACCGCAACGACTTCCATGCTCGCGTG 2988
Db 1819 CGAAGATTCTCGCTGGTCTGCAAGACCTTCAACCGCGCTCACTTGACGGCGGATCGG 1878
QY 2989 GAACTTCTCCCGGAGTCCATCACTGCCCCGAGTGCAGGAGTGGCCGAGCAGGCGCT 3048
Db 1879 GTATCTTCTCAGAACGATCCATCAGGCTAGAGTGAACGAGTTGGCGCTGGAACAGCCGT 1938
QY 3049 ACAACCGCTCGATGATCTTGG 3072
Db 1939 ACAGCGAACTGGCACAGGTACCGG 1962

RESULT 7
MYRBOR MYRBOR 1942 bp mRNA linear PLN 01-FEB-2000
LOCUS M. verrucaria mRNA for bilirubin oxidase, complete cds.
DEFINITION D12579.1 GI:456711
ACCESSION D12579.1
VERSION D12579.1
KEYWORDS Myrothecium verrucaria (strain:MT-1) cDNA to mRNA.
SOURCE Myrothecium verrucaria
ORGANISM Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.
REFERENCE 1 (bases 1 to 1942)
AUTHORS Koikeda,S., Ando,K., Kaji,H., Inoue,T., Murao,S., Takeuchi,K. and Samejima,T.
TITLE Molecular cloning of the gene for bilirubin oxidase from Myrothecium verrucaria and its expression in yeast
JOURNAL J. Biol. Chem. 268 (25), 18801-18809 (1993)
MEDLINE 93366794
REFERENCE 2 (bases 1 to 1942)
AUTHORS Ando,K
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1992) Kelichi Ando, Amano Pharmaceutical Co., Ltd., Tsukuba Research Laboratories; 22 Miyukigaoka, Tsukuba, Ibaragi 305, Japan (Tel:0298-56-5026, Fax:0298-56-5012)
COMMENT On Feb 26, 1994 this sequence version replaced gi:436235.
Submitted (07-JUL-1992) to DDBJ by:
Kelichi Ando
Tsukuba Research Laboratories
Amano Pharmaceutical Co., Ltd.
22 Miyukigaoka
Tsukuba
Ibaragi 305
Japan
Phone: 0298-56-5026
Fax: 0298-56-5012.
Location/Qualifiers
1. 1942
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/strain="MT-1"
/db_xref="taxon:5532"
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MSPGPTFOVPRGVETVFRINNAEAPNSVHLHGSEAFADGWLADITPEGSFKDYY
PNROSARTLWHDHAMHITAENAYRQAGLYMLTDPADALNLPSCYGEFDPMLLTLS
KOYTANGNLVTNGLNSFWGDV IHVNGQPPFKVPRKYRFRDLDAVRSFGLYF
ADTAIDTRLPFKVFIASDGLLEHPADTSLTYISMAERTVEVDFSDTAGKTIEURLN
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mat_peptide 180. .1781
/product="bilirubin oxidase"
polyA_signal 1832. .1837
polyA_site 1942
BASE COUNT 440 a 549 c 436 g 517 t
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Query Match 10.4%; Score 382.6; DB 8; Length 1942;
Best Local Similarity 57.5%; Pred. No. 2.9e-84;
Matches 907; Conservative 0; Mismatches 539; Indels 131; Gaps 7;
QY 1501 CAGATTTACCCACCTTGGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGT 1560
Db 324 CAGGTTTACCTTGACCTTGGATCCGCTGATCGTGGGTATGATGAATGTCTCCTGGC 383
QY 1561 CCTACTTTCAATGTTCCAGAGAGACAGACTGTAGTTAGGTTCATCAACATGCCACC 1620
Db 384 CTAATTTCCAGGTTTCCCTCGTGGAGTTGAACAGTTGTCCGCTTCATTAAACATGCTGAG 443
QY 1621 GTGGAGAACTCGGTCCATCTGCACGGCTCCCGCTCGCCCTTTTCGATGGTTGGGCT 1680
Db 444 GCTCTTAACCTCGTTCACCTGCACGGATCATCTCTCGTGGCCCTTTGACGGATGGCA 503
QY 1681 GAAGATGACCTTCCCTGGCGAGTACAAGATTACTATTTCCCAACTACCAATCCGCC 1740
Db 504 GAGGACATCACCGAGCTGGCAGCTTCAAAGACTATTACTACCCAATAGACAGTCTGCT 563
QY 1741 CGCCTTCTGTGTACCATCACCGCTTTCATGAGGTATGTACGAGCCTTTATCTTTC 1800
Db 564 CTAACCTATGATGATACCATCATGCTATGCATA----- 597
QY 1801 TTGGTACCTTTGGGTAACCAACTTCTTTCGTAGACTGCTGAGATGCTACTTTGGTC 1860
Db 598 -----TCACTGCTGAGACGCTACCGTGGCC 624
QY 1861 AGGCTGGCCCTTACATTAACAACGAGGCTGAGGATGCTCTGGTCTTCTTAGTGGCT 1920
Db 625 AGGCTGGTCTTACATGCTCACTGACCCAGCGAAGACGCTCTCAACTTTGCCAAGTGGAT 684
QY 1921 ATGGCGAGTTCGATATCCCTCTGATCCTCACGGCCAACTACTATACGCGGATGGTACC 1980
Db 685 ATGGCGAGTTCGATATTCCAATGATCCTCACGTCGAAGCAATATACGCAACGCGCACT 744
QY 1981 TGGCTTTCGACCGAGGCTGAGGACGAGGCTGTGGGGAGATGTCAATCCATGTCAACGGAC 2040
Db 745 TGGTCACCACTAATGGAGAGCTGAACCTATTCTGGGCTGATGTAATTCAGTGAACGGTC 804
QY 2041 AGCCATGGCCCTTTCCTTAACGTCCAGCCCGCGAAGTACCGTTTCCGATTTCCCAACGCTG 2100
Db 805 AACCCCTGGCCCTTCAAGAACGTTGAGCCCTCGCAAAATATCGATTCCGCTTCTCGATGCC 864
QY 2101 CCGTGTCTGCTGCTTGGCTCTTACCTCGTCAGGACGAGCTCTCCACAGCTCAGAAATTC 2160
Db 865 CAGTTTCTGCTGCTTTCGGCCCTTACTTTGCTGATACCTGATGCTATCGACACTCGCTTGC 924
QY 2161 CTTTCCAAGTCACTGCTGCTGATGCTGCTCTTCTTCAAGCCCGCTTTCAGACACTCTAACC 2220
Db 925 CTTTCAAGGTTATTGCCCTCCGATTCTGGTCTTCTTGAACACCCCTCGCGGATACCACTTGC 984
QY 2221 TCTACCTTGTCTGTGCCGAGCGTTACGAGATCATTTATGTTGATGCCCTCCCTCTCAACA 2280

Db	985	TGTACATTTCATGCCGAGGTTACGAAGTGTGTTT-----	1022
Qy	2281	ATGAGTCAAGAACTCTAAGACTAACACTTTGAGACTTCACCAACTTTGCTGGCCAGACTC	2340
Db	1023	-----GACTTTCGCGACTATGCTGGCAAGACTA	1050
Qy	2341	TTGACTCGCAAGCTTGCTCGAGACCA---ACGATGTCGGGAGCAGGAGTGAATGACGCTC	2397
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Qy	2398	GCACCTCTCGAGGTGATGGCTTCGTCGACCTCTGGCACTGTTGAG---GACAACAGCC	2454
Db	1111	ACACGACAAGTCTATGGTTTCGTGGTAGCAGACACAACTCAGCCAGATACCTCAG	1170
Qy	2455	AGGTCCCTCCACACTCCGTCGAGGTTTCCTTCCTCCTCAAGAAGGCCCGCCGACA	2514
Db	1171	TTGTTCCCTGCCTAACCTTCGTATGTTCCCTTCCCTCTCCACCAACAACCC---CC	1227
Qy	2515	AGCACTTCAAGTTTGAACGCAAGCAACGGACACTACCTGATCAACGATGTTGGCTTTGCCG	2574
Db	1228	GACAGTTCCGCTTTGGTCGCACGGGCTCTACTCTGAGCTATTAAATGGTGTGTTTGGTG	1287
Qy	2575	ATGTCAATGAGCGTCTCTGGCCAGCCGAGCTCGGCACCGTTGAGGTCTGGGAGCTCG	2634
Db	1288	ATGTTCAAAACCGTCTGCTTGCAACAGTACCCGTTGGTACTGTGCGAGCGTTGGGAGCTCA	1347
Qy	2635	AGAACTCTCTGGAGGTGGAGCCACCCGTCACATTCACCTTGTTCGACTTCAAGATCC	2694
Db	1348	TCAACCGCGGTAAACGTTGGAGCGCACCTATTTCACATCCATCTTTCTCGACTTCAAGGTGA	1407
Qy	2695	TCAACGCAAGTGGTGGTCGTG-----GCCAGGTCTATGCCCTACGAGTCTGCTGGTCTTA	2748
Db	1408	TTTCTCGTACTTCCGGCAACAACGCGCGGACAGTCAATGCCATACAGT---CCGTCCTCA	1464
Qy	2749	AGGATGCTGCTGGTTGGCAGGGTGAGACCTTGACCATTGAGCGCCCACTACCAACCT	2808
Db	1465	AAGACGTTGCTCGGCTTGCTGCGCCGTGAACCTGTGGTTGTTGAGGCTCATTCACGCGCTT	1524
Qy	2809	GGACTGGAGCTTACATGCGCACTGTCACACCTCATTCACAGAGTACAGCATATGATGG	2868
Db	1525	TCCCTGGGTATACATGTTTCCATTGCCAATTTGATTCACAGGATCAGGATATGATGG	1584
Qy	2869	CTGTATTCAACCTCACCGCATCGGAGGAGAGGATATCTTCAGGAGGACTTTCGAGGACC	2928
Db	1585	CTGCCTTTAACGCCACCGTCTCGCAGATTATGGCTATATCCCACTGTTTCTGTTGACC	1644
Qy	2929	CCATGAACCCCAAGTGGCGCGCTTTCCTTACACCGCAACGACTTCCATGCTCGCGGTG	2988
Db	1645	CTATGGAAGAGCTTTGGCAGGCTCGCTTATATGAACCTCGCGAGTTCACAGGCTCAGAGTG	1704
Qy	2989	GAACCTTCTCCCGGAGTCCATCACTGCGCCGAGTGCAGAGCTGGCCGAGCAGGAGCGCT	3048
Db	1705	GCCAGTTACGCGTTTCAAGCTGTTTACTGATGAGCGTATTACAGACTATGGCTGAATACAGACCTT	1764
Qy	3049	ACAAACGCGCTCGATGAG	3065
Db	1765	ACGCCGCACTGACGAG	1781
RESULT 8			
LOCUS	E05283	Bilirubin oxidase gene.	
DEFINITION	E05283		
ACCESSION	E05283		
VERSION	E05283.1	GI:2173473	
KEYWORDS	JP 1993199882-A/1.		
SOURCE	Myrothecium verrucaria.		
ORGANISM	Myrothecium verrucaria		
REFERENCE	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.		
AUTHORS	Ando,K., Koikeda,S. and Samejima,T.		
TITLE	PRODUCTION OF BILIRUBIN OXIDASE		

JOURNAL	Patent: JP 1993199882-A 1 10-AUG-1993;		
COMMENT	AMANO PHARMACEUT CO LTD		
	OS Myrothecium verrucaria		
PN	JP 1993199882-A/1		
PD	10-AUG-1993		
PF	24-JAN-1992 JP 1992034126		
PI	ANDO KEIICHI, KOIKEDA SATOSHI, SAMEJIMA TATSUYA PC		
	C12N15/53,C12N1/19,C12N9/06,(C12N15/53,C12N1:645); CC		
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CC	topology: Linear;		
CC	*source: strain=MT-1;		
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FT	CDS	66..1784	
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BASE COUNT	457 a 549 c 436 g 517 t		
ORIGIN			
	Query Match 10.4%; Score 382.6; DB 6; Length 1959;		
	Best Local Similarity 57.5%; Pred. No. 2.9e-84;		
	Matches 907; Conservative 0; Mismatches 539; Indels 131; Gaps 7;		
Qy	1501	CAGATTTACCCACACCTTGGCGCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGCT	1560
Db	324	CAGGTTTACCTTGACCTTGGATCCGCTGATCGTGGGTATGATGGATGCTCCTGGC	383
Qy	1561	CCTACTTTCAATGTTCCAGAGGAACAGAGCTGTAGTTAGTTTCATCAACAATGCCACC	1620
Db	384	CCTACTTTCCAGTTCTCTGGAGTTGAAACAGTTGCCGCTTCATTAAACAATGCTGAG	443
Qy	1621	GTGGAACACTCGGTCCATCTGCACGGCTCCCATCGGTGCCCCCTTTCGATGGTTGGGCT	1680
Db	444	GCTCTAACTCGGTTCACTGTCACGGATCATCTCTCGTCGCGCCTTTGACGGATGGCA	503
Qy	1681	GAAGATGTACCTCCCTGGCGAGTACAGGATTACTACTTTCCCAACTACCAATCCGCG	1740
Db	504	GAGGACATCACCGCTGGCAGCTTCAAAGACTATTACTACCCAAATAGACAGTCTGCT	563
Qy	1741	CGCCTTGTGTAGCATGACCACGCTTTTCATGAAGTATGCTACGAGCCTTTATCTTTTC	1800
Db	564	CGTACCCATGATGATACCGATCATGCTATGCATA-----	597
Qy	1801	TTGGCTACCTTTGGCTAACCAACTTCCTTCGTAGACTGCTGAGATGCTACTTTGGTC	1860
Db	598	-----TCACTGCTGAGAAGCGCTACCGTGGCC	624
Qy	1861	AGGCTGGCGCTACATATTCAACGAGAGGCTGAGGATGCTCTCGGTCTTCCTAGTGGCT	1920
Db	625	AGGCTGGCTCTACATGCTCACTGACCCAGCGAAGACGCTCTCAACTTGCCAAAGTGGAT	684
Qy	1921	ATGGCGAGTTTCGATATCCCTCTGATCCTGACGCGCAAGTACTATAACGCGGATGTAACC	1980
Db	685	ATGGCGAGTTTCGATATTCGAATGATCTCACGTCCCAAGCAATATACCGCAAGCGCACT	744
Qy	1981	TGCGTTTCAGCAGGCTGAGGACCGAGGAGGAGGATGTCATCCATGTCACGGAC	2040
Db	745	TGTCACCACTAATGAGAGCTGAATCATCTCTGGGTGATGTAATTCACGTGAACGGTC	804
Qy	2041	AGCCATGGCGCTTTCCTTAACGTTCCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTG	2100
Db	805	AACCCCTGGCTTTCAAGAAGCTTGAGCCTCGCAAAATATGATTTCCCGCTTCCCTCGATGCCG	864
Qy	2101	CGGTGCTGCTGCTTGGCTCTCTACCTCGTCAGGACCAAGCTCTCCCAAGCTCAGAAATTC	2160
Db	865	CAGTTTCTCGCTTTTCGGCGCTTTACTTGTGCTACTGATGCTATGACACTCGCTGCTGC	924
Qy	2161	CTTTCCAAGTCAATGCTCTGATGCTGGTCTCCTTCAAGCCCCCGCTTCAGACCTCTAACCC	2220

Db	1097	GCTGGAGGTTGTTATC-----	1113
Qy	2302	TAAACATTGTAGACTCTACCAACACTTTGCTGGCCAGACTCTTGACCTGGCCAACTGTCGT	2361
Db	1114	-----GACTTCTCCACCTTCGCTGGCCAGTCCATCGATATCGGCAACCTTCCTG	1162
Qy	2362	AGACCAACGATGTCGGGACGAGGATGAGTACGCTCGCAGTCTCTCGAGGTGATGCGCTTCG	2421
Db	1163	GTGCTGACGGTCTCGGTGTTGAGCTGAGTTGATAACACTGACAAAGTATCATGCGATTTCG	1222
Qy	2422	TCGTCAGCTCTGGCAGCTGTTGAG---GACAACACCGAGGTCCCTCCACTCTCCGTGACG	2478
Db	1223	TCGTTGATGAAGTCTCTGAGTCGCCGACACTTCTGAGTGCCCTGCCAACCTCCGAGATG	1282
Qy	2479	TTCCCTTTCCCTCTACAAGAGGCCCCGCCGACAAGCAC-----ATCA	2523
Db	1283	TTCCCTTTCCCGAGGGCGGAACCTGGGACCCCGCAACCCCACTGATGACGAGACTTTCA	1342
Qy	2524	AGTTTGAACGCGAGCAACGAGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCATG	2583
Db	1343	CTTTCGGCCGTCGTAATGACAGTGGACAATCAACGGAGTTACCTTCTCGGATGTCGAGA	1402
Qy	2584	AGCGTCTCTGGCCAGCCCCGAGCTGGCACCCTTGAGGTCTGGGAGTCTCGAGACTCCT	2643
Db	1403	ACCCTCTCTCCGCAATGTGCCCGCGACACTGTGTAGATCTGGCGACTTGAGAACAACT	1462
Qy	2644	CTGGAGGCTGGAGCCACCCGTCACATTCACCTTGTGACTTCAAGATCTCCTCAAGCGAA	2703
Db	1463	CAACGGTTGAGCTCACCTGTTTCACTTCACTCTGTTGACTTCCGAGTCTCTTCGTT	1522
Qy	2704	CTGTTGTCGTGGCCAGTCAATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCGTCGTT	2763
Db	1523	CCACTGCCCGTGG---AGTCGAGCCTTATGAGGCTGCTGGTCTCAAGGATGTTGTCGGC	1579
Qy	2764	TGGGAGGGGTGAGACCTGACCATCGAGGCCCACTACCAACCCCTGGAC-----	2812
Db	1580	TGGCTCGTGTGAGTGTGTTATGTTGAGGCCCACTACGCTCTTTCCTCCGTAAGTTCG	1639
Qy	2813	-----TGGAGCTTACATGTGCA	2830
Db	1640	CCTTTTACTTAACCTGTTTCACTCATGCTACATCTACAAGTGTGTCTACATGTTGA	1699
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AX101096			
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Stachybotrys chartarum.			
ORGANISM			
Stachybotrys chartarum			
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.			
REFERENCE			
Wang, H.			
Stachybotrys phenol oxidizing enzyme			
Patent: WO 0121809-A 1 29-MAR-2001;			
JOURNAL			

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		Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;	
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DEFINITION Sequence 1 from Patent WO0121748.
ACCESSION AX108672
VERSION AX108672.1 GI:13923900
KEYWORDS
SOURCE Stachybotrys chartarum.
ORGANISM Stachybotrys chartarum
REFERENCE Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.
AUTHORS 1 (bases 1 to 1958)
TITLES Convents,D.U., Doornink,M.U., de Vries,C.H. and Wang,H.
JOURNAL Detergent compositions comprising phenol oxidizing enzymes
PATENT: WO 0121748-A 1 29-MAR-2001;
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BASE COUNT 394 a 593 c 490 g 481 t
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Best Local Similarity 55.2%; Pred. No. 9.6e-64;
Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;
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DEFINITION Sequence 1 from Patent WO0220711.
ACCESSION AX456852
VERSION AX456852.1 GI:21715723
KEYWORDS stachybotrys chartarum.
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ORGANISM Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.
REFERENCE 1
AUTHORS Aehle,W., Convents,D., Doornink,M., van Gastel,F., Rodriguez,A.M., Topozada,A., de Vries,C.H. and Wang,H.
TITLE Detergent compositions comprising phenol oxidizing enzymes
JOURNAL Patent: WO 0220711-A 1 14-MAR-2002;
UNILEVER PLC (GB); LEVER HINDUSTAN LTD (IN); UNILEVER NV (NL)
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VERSION	ARL122997.1 GI:14107963			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
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AUTHORS	Wang, H.			
TITLE	Phenol oxidizing enzymes			
JOURNAL	Patent: US 6168936-A 3 02-JAN-2001;			
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Best Local Similarity	55.2%; Pred. No. 9.6e-64;			
Matches 957; Conservative	0; Mismatches 501; Indels 276; Gaps 8;			

Qy	2524	AGTTTGAACGAGCAACGGACACTACCTGATCAACGATGTGGCTTTCGGATGTCAAATG	2583
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DEFINITION	Sequence 3 from Patent WO0121748.		
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KEYWORDS	Stachybotrys chartarum.		
SOURCE	Stachybotrys chartarum.		
ORGANISM	Eukaryota; Fungi, Ascomycota; mitosporic Ascomycota; Stachybotr		
REFERENCE	1 (bases 1 to 2095)		
AUTHORS	Convent, D.U., Doornink, M.U., de Vries, C.H. and Wang, H.		
TITLE	Detergent compositions comprising phenol oxidizing enzymes		
JOURNAL	Patent: WO 0121748-A 3 29-MAR-2001;		
FEATURES	Location/Qualifiers		
source	1..2095		
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BASE COUNT	437 a 618 c 510 g 530 t		
ORIGIN			
Query Match	8.2%;	Score 300.4;	DB 6; Length 2095;
Best Local Similarity	55.2%;	Pred. No. 9.6e-64;	
Matches	957; Conservative	0; Mismatches 501;	Indels 276; Gaps
Qy	1491	CTGACCCCTTTTCAGATTATACCCACCTTGGCGCCCTGCCACTCTCGCGGCTACGATGGCAT	1550
Db	380	CTTCTCCCACCATCTACCTTGATCTGGAGCGCGCCCAACATGGTTGGATACGATGGCAT	439
Qy	1551	GAGCCCTGTGCTTACTTTTCAATGTTTCCCCAGAGAACAGAGACTGTAGTTAGTTTCATCAA	1610

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Qy 2644 CTGGAGGCTGAGCGACCCCTCCACATTCACCTTTGTGTGACTTCAAGATCCTCAAGCGAA 2703
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Qy 2704 CTGCTGCTGTCGGCCAGGTCATGCCCTACGAGTCTGCTGGTCTTAAAGGATGTCGCTCGGT 2763
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Qy 2813 -----TGAGCTTACATGTGGCA 2830
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 17:04:56 ; Search time 720.875 Seconds
(without alignments)
11486.872 Million cell updates/sec

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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3676.6	100.0	3677	21	AA550018
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3	3676.6	100.0	3677	24	AA47582
4	3675.8	100.0	3677	20	AA227602
5	3664.6	99.7	3676	20	AA225728
6	2054.6	55.9	2067	20	AA225735
7	2054	55.9	2067	20	AA227609
8	1474.6	40.1	7248	24	ABA92911
9	1474	40.1	1791	20	AA227601

10	1474	40.1	1791	21	AA550019	Stachybotrys chart
11	1474	40.1	1791	21	AA551314	Stachybotrys chart
12	1474	40.1	1791	24	AA47584	S chartarum phenol
13	1469.2	40.0	1791	20	AA225727	Stachybotrys chart
14	507.6	13.8	2110	21	AA261243	DNA encoding a phe
15	460.8	12.5	2905	21	AA550020	Bipolaris spicife
16	460.8	12.5	2905	21	AA551315	Bipolaris spicifer
17	460.8	12.5	2905	24	AA47583	B spicifera phenol
18	455.6	12.4	2063	21	AA550021	Curvularia pallesc
19	455.6	12.4	2063	21	AA551316	Curvularia pallesc
20	455.6	12.4	2063	24	AA47585	C pallescens pheno
21	382.6	10.4	1959	14	AAQ47790	Bilirubin oxidase
22	300.4	8.2	1958	22	AAF30028	Stachybotrys chart
23	300.4	8.2	1958	24	ABK50918	DNA encoding pheno
24	300.4	8.2	1958	24	ABL53881	Stachybotrys chart
25	300.4	8.2	2095	22	AAF82586	Stachybotrys chart
26	300.4	8.2	2095	22	AAF30029	Stachybotrys chart
27	300.4	8.2	2095	24	ABK50919	DNA encoding pheno
28	300.4	8.2	2095	24	ABL53882	Stachybotrys chart
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31	150	4.1	858	21	AA551317	A atrum phenol oxl
32	150	4.1	858	24	AA47586	C glutamicum codin
33	60	1.6	1533	22	AAH66018	Corynebacterium gl
34	60	1.6	1614	22	AAF71220	C glutamicum codin
35	54.6	1.5	3446	23	ABL50557	Micromonospora car
36	46.4	1.3	14041	22	AAH48024	Internal control B
37	46.4	1.3	14041	22	AAH48024	Bacillus lichenifo
38	44.6	1.2	1470	24	ABK74913	Micromonospora DNA
39	44.6	1.2	109519	22	AA508693	EST clone CB15. H
40	43.2	1.2	426	20	AAV89078	Human tumour suppr
41	43.2	1.2	5468	21	AA58907	Human tumour suppr
42	43.2	1.2	5477	21	AA58911	Human tumour suppr
43	43.2	1.2	5564	21	AAC58908	Human tumour suppr
44	43.2	1.2	5573	21	AAC58912	Human tumour suppr
45	42.8	1.2	1082	24	AA582581	cDNA sequence #368

ALIGNMENTS

RESULT 1
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ID AAA50018 standard; DNA; 3677 BP.
XX AC AAA50018;
XX AC
XX 10-OCF-2000 (first entry)
XX DE Stachybotrys chartarum phenol oxidising enzyme gene.
XX KW Phenol oxidising enzyme; detergent; bleaching; ds.
XX OS Stachybotrys chartarum.
XX FH Key Location/Qualifiers
FT CDS 1044..3095
FT FT /*tag= a
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FT FT 1044..1237
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RESULT 2
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XX Stachybotrys chartarum phenol oxidizing enzyme genomic DNA.
XX Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
XX pulp; paper bleaching; ds.
XX Stachybotrys chartarum.
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XX Key Location/Qualifiers
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XX PR 23-JUN-1999; 99US-0338723.
XX XX
XX PA (GENM) GENENCOR INT INC.
XX Wang H, Bodle EA;
XX WPI; 2000-452191/39.
XX DR

DR P-PSDB; AAY96761.
XX
XX New phenol oxidizing enzyme for modifying colors associated with dyes
PT or colored compounds, is obtained from fungus and is encoded by a
PT nucleic acid comprising a specific nucleotide sequence
XX
XX Claim 10; Fig 1A-B; 45pp; English.
XX
XX This genomic DNA encodes Stachybotrys chartarum phenol oxidizing enzyme.
CC Phenol oxidizing enzymes encoded by nucleic acid sequences which
CC hybridize to this DNA are claimed, as long as the enzyme is capable of
CC modifying the colour associated with dyes or coloured compounds. The
CC enzymes are useful in detergent compositions and for modifying colors
CC associated with dyes or colored compounds which occur in stains in a
CC sample. The enzymes are also useful for pulp and paper bleaching,
CC anti-dye transfer in detergent and other textile applications.
XX
XX SQ Sequence 3677 BP; 822 A; 1057 C; 849 G; 948 T; 1 other;
XX

Query Match 100.0%; Score 3676.6; DB 21; Length 3677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 841 TGGCTAAATTTGGCTATCTCTATGCGGTAGCAGCGCTGTGGCTACAACCTGCTGCCATG 900
QY 901 GCTGAAGCATCGTGAGATCATATAAAGTCTCCGAATCTCCGTGAAGTCAGAAATCGTCTC 960
Db 901 GCTGAAGCATCGTGAGATCATATAAAGTCTCCGAATCTCCGTGAAGTCAGAAATCGTCTC 960
QY 961 TCCACACAGTCAACAACAAGCTTTCTTCTCTTACAGCTTAGCCCTGAGCAGACATTCACAGA 1020
Db 961 TCCACACAGTCAACAACAAGCTTTCTTCTCTTACAGCTTAGCCCTGAGCAGACATTCACAGA 1020
QY 1021 ACTCTTCCCTTCTTTTCGTCAATATGCTGTTCAAGTCATGGCAACTGGCAGCAGCTCCG 1080
Db 1021 ACTCTTCCCTTCTTTTCGTCAATATGCTGTTCAAGTCATGGCAACTGGCAGCAGCTCCG 1080
QY 1081 GGCTCTGCTGTGGAGTCTCGGCATCCCGATGGACACGGCAGCCACCCATTGAGGCTG 1140
Db 1081 GGCTCTGCTGTGGAGTCTCGGCATCCCGATGGACACGGCAGCCACCCATTGAGGCTG 1140
QY 1141 TTGATCCCGAAGTGAAGACTGAGGCTTTGGCTGACTCCCTTCTGTCAGCAGCGCATG 1200
Db 1141 TTGATCCCGAAGTGAAGACTGAGGCTTTGGCTGACTCCCTTCTGTCAGCAGCGCATG 1200
QY 1201 AGGACTGGGAGTCACTTCCATCAACTTGTCTTTACAGGTGAGACACCTGTCCACCTGTT 1260
Db 1201 AGGACTGGGAGTCACTTCCATCAACTTGTCTTTACAGGTGAGACACCTGTCCACCTGTT 1260
QY 1261 TTTCCTTCGATAACTAATCTTATAGGAATGCCCTGCCAATTCACCTGTGCAAGCAGCCCA 1320
Db 1261 TTTCCTTCGATAACTAATCTTATAGGAATGCCCTGCCAATTCACCTGTGCAAGCAGCCCA 1320
QY 1321 AGATGATGCTTTTGAATTTTACGAAGCACTCGGCCCGGCACTAATGATTTCTAGGATC 1380
Db 1321 AGATGATGCTTTTGAATTTTACGAAGCACTCGGCCCGGCACTAATGATTTCTAGGATC 1380
QY 1381 ATTACCAACCTGTACCGGCAAGACATTTGGTACTATGAGATCGAGATCAAGCCATTT 1440
Db 1381 ATTACCAACCTGTACCGGCAAGACATTTGGTACTATGAGATCGAGATCAAGCCATTT 1440
QY 1441 CAGCAAAGGGTGAGTTTGTCTCAAAACCTTGTGTAATTAATCATTTTACTGACCCCTT 1500
Db 1441 CAGCAAAGGGTGAGTTTGTCTCAAAACCTTGTGTAATTAATCATTTTACTGACCCCTT 1500
QY 1501 CAGATTTACCCACCTTGGCCCTGCCACTCTCGTGGCTACGATGGCATGAGCCCTGGT 1560
Db 1501 CAGATTTACCCACCTTGGCCCTGCCACTCTCGTGGCTACGATGGCATGAGCCCTGGT 1560
QY 1561 CCTACTTTCATGTTCCAGAGAACAGAGACTGTAGTTAGTTTCAATCAACAAATGCCACC 1620
Db 1561 CCTACTTTCATGTTCCAGAGAACAGAGACTGTAGTTAGTTTCAATCAACAAATGCCACC 1620
QY 1621 GTGGAGAACTCGGTCCATCTGCACGGCTCCCATCGCTGCCCTTCGATGGTTGGCT 1680
Db 1621 GTGGAGAACTCGGTCCATCTGCACGGCTCCCATCGCTGCCCTTCGATGGTTGGCT 1680
QY 1681 GAAGATGTGACCTTCCCTGGCGAGTACAAGGATTAATCTTTTCCCAACTTACCAATCCGCC 1740
Db 1681 GAAGATGTGACCTTCCCTGGCGAGTACAAGGATTAATCTTTCCCAACTTACCAATCCGCC 1740
QY 1741 CGCCTTCTGTGTATCATGACACCGCTTTTCAATGAAGGATAGTACGAGCCTTTATCTTTC 1800
Db 1741 CGCCTTCTGTGTATCATGACACCGCTTTTCAATGAAGGATAGTACGAGCCTTTATCTTTC 1800
QY 1801 TTGGCTACTTTTGGCTAACCAACTTCCCTTCTGTAAGTCTGAGAAATGCCTACTTTGGTC 1860
Db 1801 TTGGCTACTTTTGGCTAACCAACTTCCCTTCTGTAAGTCTGAGAAATGCCTACTTTGGTC 1860

QY 1861 AGGCTGGCGCCTACATATTATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCT 1920
Db 1861 AGGCTGGCGCCTACATATTATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCT 1920
QY 1921 ATGGCGAGTTCCATATCCCTCTGATCCTACGGCCAAAGTACTATACGGCGGATGTTACCC 1980
Db 1921 ATGGCGAGTTCCATATCCCTCTGATCCTACGGCCAAAGTACTATACGGCGGATGTTACCC 1980
QY 1981 TCCGTTTCGACCCAGGCTGAGGACGAGGACTGTGGGAGATGTATCCATGTCAACGGAC 2040
Db 1981 TCCGTTTCGACCCAGGCTGAGGACGAGGACTGTGGGAGATGTATCCATGTCAACGGAC 2040
QY 2041 AGCCATGCGCTTTTCCCTTAACGTCCAGCCCGCAAGTACCGTTTCCGATTTCTCAACGCTG 2100
Db 2041 AGCCATGCGCTTTTCCCTTAACGTCCAGCCCGCAAGTACCGTTTCCGATTTCTCAACGCTG 2100
QY 2101 CCGTGTCTCGTCTTGGCTCTTACCTCGTCAGGACGAGCTCTCCCAACGTCAGAAATTC 2160
Db 2101 CCGTGTCTCGTCTTGGCTCTTACCTCGTCAGGACGAGCTCTCCCAACGTCAGAAATTC 2160
QY 2161 CTTTCCAAAGTCAATGCTCTGATGCTGCTTCAAGCCCGGTTCAAGACTCTTAACC 2220
Db 2161 CTTTCCAAAGTCAATGCTCTGATGCTGCTTCAAGCCCGGTTCAAGACTCTTAACC 2220
QY 2221 TCTACTCTTGTCTGCCGAGCGTTACGAGATCATTTATGTTGATGCCCCCTCTCAACGA 2280
Db 2221 TCTACTCTTGTCTGCCGAGCGTTACGAGATCATTTATGTTGATGCCCCCTCTCAACGA 2280
QY 2281 ATGAGTCAAGAATCTTAAGACTTAACACTTTGTAGACTTTCACCAACTTTGTCGCCAGACTC 2340
Db 2281 ATGAGTCAAGAATCTTAAGACTTAACACTTTGTAGACTTTCACCAACTTTGTCGCCAGACTC 2340
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Db 2341 TTGACTCTGGCAACCTTGTCTGAGACCAAGATGTGCGGCACGAGGATGATGCTCGCA 2400
QY 2401 CTCTCGAGGTGATGCGCTTCTGCTGAGCTGTGGCACTGTGAGGACAAACAGCCAGTCC 2460
Db 2401 CTCTCGAGGTGATGCGCTTCTGCTGAGCTGTGGCACTGTGAGGACAAACAGCCAGTCC 2460
QY 2461 CCTCCACTCTCGTGACGTTCTCTTCCCTCTCAACAAGGAAGCCCGCCGCAACAGCACT 2520
Db 2461 CCTCCACTCTCGTGACGTTCTCTTCCCTCTCAACAAGGAAGCCCGCCGCAACAGCACT 2520
QY 2521 TCAAGTTTGAACGCAAGCAACGACACTACTGATCAACCATGTTGGCTTTGCGGATGTCA 2580
Db 2521 TCAAGTTTGAACGCAAGCAACGACACTACTGATCAACCATGTTGGCTTTGCGGATGTCA 2580
QY 2581 ATGAGCGTGTCTTGCCCAAGCCCGAGCTCGGCACCGTTGAGGTCTGGGAGCTCGAGAATC 2640
Db 2581 ATGAGCGTGTCTTGCCCAAGCCCGAGCTCGGCACCGTTGAGGTCTGGGAGCTCGAGAATC 2640
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Db 2641 CCTCTGGAGGCTGAGACACACCCCTGACATTCAGTTGTTGACTTCAAGATCTCAAGC 2700
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Db 2701 GAACTGGTGGTCTGCGCAGGTCATGCCCTACGAGTCTGCTGCTTAAAGGATGCTGCT 2760
QY 2761 GGTGGGAGGGGTGAGACCCCTGACATTCGAGGCCCACTTACCAACCCCTGGACTGGAGCTT 2820
Db 2761 GGTGGGAGGGGTGAGACCCCTGACATTCGAGGCCCACTTACCAACCCCTGGACTGGAGCTT 2820
QY 2821 ACATGTGGACTGTCAACACCTCTATTCAGGAGATAACGACATGATGGCTGTATTCAAGC 2880
Db 2821 ACATGTGGACTGTCAACACCTCTATTCAGGAGATAACGACATGATGGCTGTATTCAAGC 2880
QY 2881 TCACGCCCATGAGGAGAGGATATCTTCAGGAGACTTTCAGGACCCCATCAACCCCA 2940
Db 2881 TCACGCCCATGAGGAGAGGATATCTTCAGGAGACTTTCAGGACCCCATCAACCCCA 2940

Qy 541 TCTCTTCGGCATCAGCCTCTATGCCGACGACACACACCTCATTTGGCCCGGACCACTTTG 600
Db 541 TCTCTTCGGCATCAGCCTCTATGCCGACGACACACACCTCATTTGGCCCGGACCACTTTG 600
Qy 601 AGCGCGCACGCACTTCGCGCGGAAGAGTTGATAAACACCCCTTCACCCCTGCCCAATGCAT 660
Db 601 AGCGCGCACGCACTTCGCGCGGAAGAGTTGATAAACACCCCTTCACCCCTGCCCAATGCAT 660
Qy 661 GGAGTTTGGTCTATTGTCTATGATCACTTACCTTACATGATCAGGATCCTTGAAGA 720
Db 661 GGAGTTTGGTCTATTGTCTATGATCACTTACCTTACATGATCAGGATCCTTGAAGA 720
Qy 721 GGGTGTGGAAGCCAGACAGCTTGTCCCTGTCTTGCAGACTCAGGTCTCTAGCGG 780
Db 721 GGGTGTGGAAGCCAGACAGCTTGTCCCTGTCTTGCAGACTCAGGTCTCTAGCGG 780
Qy 781 CTATCACAGCTCAGGATTTATCAAGTCCCGTAAAGTCCAGACCCCTTTTCATTGTATGATGC 840
Db 781 CTATCACAGCTCAGGATTTATCAAGTCCCGTAAAGTCCAGACCCCTTTTCATTGTATGATGC 840
Qy 841 TGCCTAATTTCCGCTATCTCTATCCGCTAGCAGCCGCTTTGGCTACAACTGGCTGCCATG 900
Db 841 TGCCTAATTTCCGCTATCTCTATCCGCTAGCAGCCGCTTTGGCTACAACTGGCTGCCATG 900
Qy 901 GCTGAAGCATCGTGAGATCTATAAAGTCTCCGAATCCTCGGTGAAGTCAGAATCGTCTC 960
Db 901 GCTGAAGCATCGTGAGATCTATAAAGTCTCCGAATCCTCGGTGAAGTCAGAATCGTCTC 960
Qy 961 TCCACACCACTCAACAACAGCTTTCTTCTTACAGCTTAGCCTGAGCACATTCACAGA 1020
Db 961 TCCACACCACTCAACAACAGCTTTCTTCTTACAGCTTAGCCTGAGCACATTCACAGA 1020
Qy 1021 ACTCTTCCCTCTTTTGGTCAATATGCTTGTCAAGTCAATGSCAACTGSCAGCAGCCCTCG 1080
Db 1021 ACTCTTCCCTCTTTTGGTCAATATGCTTGTCAAGTCAATGSCAACTGSCAGCAGCCCTCG 1080
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Db 1081 GGCTCCTGTCTGGAGTCTCCGGATCCGGATGGACACGGGAGCCACCCCATTTGAGGCTG 1140
Qy 1141 TTGATCCGGAAGTGAAGACTCAGGTCTTCGCTGACTCCCTCTTGTGTCAGCAGCGCATG 1200
Db 1141 TTGATCCGGAAGTGAAGACTCAGGTCTTCGCTGACTCCCTCTTGTGTCAGCAGCGCATG 1200
Qy 1201 ACGACTGGGAGTCACTCCATACAACTTGTCTTACAGGTGAGACACCTGTCCCACTGTT 1260
Db 1201 ACGACTGGGAGTCACTCCATACAACTTGTCTTACAGGTGAGACACCTGTCCCACTGTT 1260
Qy 1261 TTCCCTCGATAACTTACTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCA 1320
Db 1261 TTCCCTCGATAACTTACTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCA 1320
Qy 1321 AGATGTATGCTTTTGTATTTCTACGAAGCAACTCGGCCCGGACCTAAATGTATTCTAGGATC 1380
Db 1321 AGATGTATGCTTTTGTATTTCTACGAAGCAACTCGGCCCGGACCTAAATGTATTCTAGGATC 1380
Qy 1381 ATTACCAACCCCTGTACCGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTT 1440
Db 1381 ATTACCAACCCCTGTACCGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTT 1440
Qy 1441 CAGCAAGGGTGTAGTTTGTCTCAGAACTTGTGGTAAATTAATCATTTGTACTGACCCCTT 1500
Db 1441 CAGCAAGGGTGTAGTTTGTCTCAGAACTTGTGGTAAATTAATCATTTGTACTGACCCCTT 1500
Qy 1501 CAGATTTTACCCACCTTGTGCGCCCTGCCACTCTCTCGGCTACGATGCGATGAGCCCTGGT 1560
Db 1501 CAGATTTTACCCACCTTGTGCGCCCTGCCACTCTCTCGGCTACGATGCGATGAGCCCTGGT 1560
Qy 1561 CCTACTTTCAATGTTTCCAGAGGAACAGAGACTGTAGTTAGTTTCAATCAACAATGCCACC 1620
Db 1561 CCTACTTTCAATGTTTCCAGAGGAACAGAGACTGTAGTTAGTTTCAATCAACAATGCCACC 1620
Qy 1621 GTGGAGAACTCGGTCCATCTGCACGGCTCCCCATCGCGTGGCCCTTTTCGGATGGTGGCT 1680

Db 1621 GTGGAGAACTCGGTCCATCTGCACGGCTCCCATCGCGTGGCCCTTTTCGGATGGTGGGCT 1680
Qy 1681 GAAGATGTGACCTTCCCTGGCGAGTACAAGATTACTACTTTCCCAACTACCAATCCGCC 1740
Db 1681 GAAGATGTGACCTTCCCTGGCGAGTACAAGATTACTACTTTCCCAACTACCAATCCGCC 1740
Qy 1741 CGCCTTCTGTGGTACCATGACACGCTTTTCATGAAGTATGCTACGAGCCCTTATCTTTTC 1800
Db 1741 CGCCTTCTGTGGTACCATGACACGCTTTTCATGAAGTATGCTACGAGCCCTTATCTTTTC 1800
Qy 1801 TTGGCTACCTTTGGCTAACCAACTTCTTTCGTAGACTGCTGAGAACTGCTACTTTGGTC 1860
Db 1801 TTGGCTACCTTTGGCTAACCAACTTCTTTCGTAGACTGCTGAGAACTGCTACTTTGGTC 1860
Qy 1861 AGGTGGCGCCTACATTTATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCT 1920
Db 1861 AGGTGGCGCCTACATTTATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCT 1920
Qy 1921 ATGGCGAGTTTCGATATCCCTCTGATCTCTGACGGCAAGTACTATTAACCGGATGGTACCC 1980
Db 1921 ATGGCGAGTTTCGATATCCCTCTGATCTCTGACGGCAAGTACTATTAACCGGATGGTACCC 1980
Qy 1981 TGCCTTCGACCGAGGGTGAGACCAAGGACCTTGTGGGAGATGTCATCCATGTCAACGGAC 2040
Db 1981 TGCCTTCGACCGAGGGTGAGACCAAGGACCTTGTGGGAGATGTCATCCATGTCAACGGAC 2040
Qy 2041 AGCCATGGCCTTCTTAAACGTCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGGTG 2100
Db 2041 AGCCATGGCCTTCTTAAACGTCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGGTG 2100
Qy 2101 CCGTGTCTCGTGTGGCTCTCTACCTCTGTCAGGACAGCTCTCCCAACGTCAGAATTC 2160
Db 2101 CCGTGTCTCGTGTGGCTCTCTACCTCTGTCAGGACAGCTCTCCCAACGTCAGAATTC 2160
Qy 2161 CTTTCCAAAGTCAATTCGCTCTGATGCTGGTCTCCCTTCAAGCCCCCGTTTCAGACCTTAACC 2220
Db 2161 CTTTCCAAAGTCAATTCGCTCTGATGCTGGTCTCCCTTCAAGCCCCCGTTTCAGACCTTAACC 2220
Qy 2221 TCTACCTTGTCTTGGCGAGGCTTACGAGATCATTTTGGTATGCCCCCTCCCTCTCAAGA 2280
Db 2221 TCTACCTTGTCTTGGCGAGGCTTACGAGATCATTTTGGTATGCCCCCTCCCTCTCAAGA 2280
Qy 2281 ATGAGTCAAGAACTCTAAGACTAACACTTGTAGACTTCCACCAACTTTGCTGGCCAGACTC 2340
Db 2281 ATGAGTCAAGAACTCTAAGACTAACACTTGTAGACTTCCACCAACTTTGCTGGCCAGACTC 2340
Qy 2341 TTGACCTGCGCAACGTTCTGAGACCAACGATGTCGGCGAGGAGATGAGTACGCTCGCA 2400
Db 2341 TTGACCTGCGCAACGTTCTGAGACCAACGATGTCGGCGAGGAGATGAGTACGCTCGCA 2400
Qy 2401 CTCTCGAGGTGATGGCTTCTCGTCTGAGTCTGGGACCTGTTTGGAGTCTGGGAGTCTG 2460
Db 2401 CTCTCGAGGTGATGGCTTCTCGTCTGAGTCTGGGACCTGTTTGGAGTCTGGGAGTCTG 2460
Qy 2461 CCTCCACTCTCCGTGAGCTTCTTCCCTCTCAAGGAAGGCCCCCGGACCAAGCACT 2520
Db 2461 CCTCCACTCTCCGTGAGCTTCTTCCCTCTCAAGGAAGGCCCCCGGACCAAGCACT 2520
Qy 2521 TCAAGTTTGAACGAGCAACCGACACTACCTTACCTGATCAAGGATGTTGGCTTTGCCGATGCA 2580
Db 2521 TCAAGTTTGAACGAGCAACCGACACTACCTTACCTGATCAAGGATGTTGGCTTTGCCGATGCA 2580
Qy 2581 ATGAGCGTCTCTGGCCAAAGCCGAGCTCGGACGCTTGGAGTCTGGGAGTCTCGAGAAT 2640
Db 2581 ATGAGCGTCTCTGGCCAAAGCCGAGCTCGGACGCTTGGAGTCTGGGAGTCTCGAGAAT 2640
Qy 2641 CCTCTGGAGGCTGGAGCCACCCCGTCCACATTCACCTTTGTTGACTTCAAGATCTCTCAAGC 2700
Db 2641 CCTCTGGAGGCTGGAGCCACCCCGTCCACATTCACCTTTGTTGACTTCAAGATCTCTCAAGC 2700
Qy 2701 GAACTGGTGTGGTGGCAGGTCATGCCCTACGAGTCTGCTGGTCTTAAAGATGTCGTCT 2760

Db	2701	GA	CTGGTGGTCTGGCCGAGGCTATGCCCTACGAGCTCTGCTGGTCTTAAGGATGTCGTCT	2760
Qy	2761	GG	TGGCAGGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCTGGACTGGAGCTT	2820
Db	2761	GG	TGGCAGGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCTGGACTGGAGCTT	2820
Qy	2821	AC	ATGTGGCACTGTCAACAACCTTATTCAGGAGGATAACGACATGATGGCTGTATTCAAAG	2880
Db	2821	AC	ATGTGGCACTGTCAACAACCTTATTCAGGAGGATAACGACATGATGGCTGTATTCAAAG	2880
Qy	2881	TC	ACGCCCATGTGAGGAGAGGAGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCA	2940
Db	2881	TC	ACGCCCATGTGAGGAGAGGAGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCA	2940
Qy	2941	AG	TGGCGCGCGTCTCTTACAACCCAAACGACTTCATGCTCGCGCTGGAACTTCTCCG	3000
Db	2941	AG	TGGCGCGCGTCTCTTACAACCCAAACGACTTCATGCTCGCGCTGGAACTTCTCCG	3000
Qy	3001	CC	GAGTCCATCACTGCCCGAGTGCAGGAGCTTGGCGGAGCAGGAGCGGTACAAACCGCTCG	3060
Db	3001	CC	GAGTCCATCACTGCCCGAGTGCAGGAGCTTGGCGGAGCAGGAGCGGTACAAACCGCTCG	3060
Qy	3061	AT	GAGATCTCTGGAGGATCTTGAATCGAGGAGTAACCCGAGCCACAAGCTCTACAACTC	3120
Db	3061	AT	GAGATCTCTGGAGGATCTTGAATCGAGGAGTAACCCGAGCCACAAGCTCTACAACTC	3120
Qy	3121	GT	TTTGAGTCTTAAGACGAGGCTCTTGGTGGCTATTCTTTCTTCCCTACGGGGAACCTC	3180
Db	3121	GT	TTTGAGTCTTAAGACGAGGCTCTTGGTGGCTATTCTTTCTTCCCTACGGGGAACCTC	3180
Qy	3181	GT	TGTCACCTGCGATGTGAAGGACCATCACAAAGCAACGTAATATTTGGACTCACCACTG	3240
Db	3181	GT	TGTCACCTGCGATGTGAAGGACCATCACAAAGCAACGTAATATTTGGACTCACCACTG	3240
Qy	3241	TC	ATTACCGCCCACTGTACCTATTTCGATCTCTGTTCACAACTTTCTAGTCGAGAGTGT	3300
Db	3241	TC	ATTACCGCCCACTGTACCTATTTCGATCTCTGTTCACAACTTTCTAGTCGAGAGTGT	3300
Qy	3301	CC	ATAGTCAAGNAACGCCCATAGGCGTATCGCTCAAACTGAACTATTGTGTGCTCTGTA	3360
Db	3301	CC	ATAGTCAAGNAACGCCCATAGGCGTATCGCTCAAACTGAACTATTGTGTGCTCTGTA	3360
Qy	3361	CG	TGGAGTAGATGTCAATTGTGATGAGACACAGTAATACCGTATATCTTTTCTTAGGAC	3420
Db	3361	CG	TGGAGTAGATGTCAATTGTGATGAGACACAGTAATACCGTATATCTTTTCTTAGGAC	3420
Qy	3421	T	ACAGGATCAGTTTCTCATGAGATTACATCCGCTCTAATGTTGTCCATGAGAGTCTAGCT	3480
Db	3421	T	ACAGGATCAGTTTCTCATGAGATTACATCCGCTCTAATGTTGTCCATGAGAGTCTAGCT	3480
Qy	3481	A	AGGTTGAGAAATGATPAGACAGGAATCAATTTGATGCTCTCAGCTCGTATTACCGATGTA	3540
Db	3481	A	AGGTTGAGAAATGATPAGACAGGAATCAATTTGATGCTCTCAGCTCGTATTACCGATGTA	3540
Qy	3541	G	ACAAGTTAGGTAAGTTTGGTATCCGAAATGACTCAGGCTCCCTCATTAGGTTGCA	3600
Db	3541	G	ACAAGTTAGGTAAGTTTGGTATCCGAAATGACTCAGGCTCCCTCATTAGGTTGCA	3600
Qy	3601	T	GTAACACTCTCAGCAACTCATGCGTGTGGGACCAATCATCCATACCTGATTTTTGAT	3660
Db	3601	T	GTAACACTCTCAGCAACTCATGCGTGTGGGACCAATCATCCATACCTGATTTTTGAT	3660
Qy	3661	AA	CTGACCTGGGTCAAT 3677	
Db	3661	AA	CTGACCTGGGTCAAT 3677	

RESULT 5
AAZ25728
ID AAZ25728 standard; DNA; 3676 BP.
XX
XX AAZ25728;
XX

DT	XX	05-JAN-2000	(first entry)
DE	XX	Stachybotrys chartarum phenol oxidising enzyme genomic DNA.	
XX	XX	Stachybotrys chartarum; phenol oxidising enzyme; colour: dye;	
KW	XX	detergent; anti-dye transfer; stain removal; bleaching; ds.	
OS	XX	Stachybotrys chartarum.	
XX	PN	WO9949010-A2.	
PD	XX	30-SEP-1999.	
XX	XX	23-MAR-1999; 99WO-EP02042.	
PR	XX	24-MAR-1998; 98US-0046969.	
PR	XX	22-DEC-1998; 98US-0218702.	
PA	XX	(UNIL) UNILEVER NV.	
PA	XX	(UNIL) UNILEVER PLC.	
PI	XX	Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;	
PI	XX	Wang C;	
DR	XX	WPI; 1999-601211/51.	
DR	XX	P-PSDB; AAY45222.	
XX	XX	Detergent composition containing phenol oxidase from Stachybotrys, used	
PT	XX	to bleach stains and prevent dye transfer -	
XX	XX	Example 14; Fig 6; 56pp; English.	
CC	XX	The present invention describes a detergent composition containing a	
CC	XX	purified phenol oxidising enzyme derived from Stachybotrys. The present	
CC	XX	sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The	
CC	XX	enzyme can be used to modify the colour of dyes and other coloured	
CC	XX	compounds (e.g. for use in pulp and paper bleaching also for removing	
CC	XX	stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye	
CC	XX	transfer during fabric washing.	
XX	XX	Sequence 3676 BP; 822 A; 1056 G; 849 G; 948 T; 1 other;	
QY	XX	Query Match 99.7%; Score 3664.6; DB 20; Length 3676;	
Db	XX	Best Local Similarity 100.0%; Pred. No. 0;	
XX	XX	Matches 3676; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
QY	1	CTGGGTACGCTCACTTGGTAGACAGCCCTCAGAGCCTCAGTGCGTGGGGTGCAGAAAGGCC 60	
Db	1	CTGGGTACGCTCACTTGGTAGACAGCCCTCAGAGCCTCAGTGCGTGGGGTGCAGAAAGGCC 60	
QY	61	AGTCAATATCTTTGGTCACCTGAATAGTTCCTTGTACGCGCAAAAAGCTCTTCCCGAA 120	
Db	61	AGTCAATATCTTTGGTCACCTGAATAGTTCCTTGTACGCGCAAAAAGCTCTTTCGCCGAA 120	
QY	121	GGGCGACAGACTCAAGTGAGACATATAGATGCATGCTCTTCATAGCCACAGTTAGGG 180	
Db	121	GGGCGACAGACTCAAGTGAGACATATAGATGCATGCTCTTCATAGCCACAGTTAGGG 180	
QY	181	TGGTGACCTACTCGAAGAGGCCCGCATTTGCATGCATACGACATGTCGCTTCCATGCAAC 240	
Db	181	TGGTGACCTACTCGAAGAGGCCCGCATTTGCATGCATACGACATGTCGCTTCCATGCAAC 240	
QY	241	ATGTATGGGCACATCGGGGATCAGGCACCCTTCGATCGAATAAGACCCCCCTGGTTT 300	
Db	241	ATGTATGGGCACATCGGGGATCAGGCACCCTTCGATCGAATAAGACCCCCCTGGTTT 300	
QY	301	CCTTTTGGTTCTTTTCCCTTCTCAACGACGCGTGAGCGTGGTTTAATTGACAAGGCCGA 360	
Db	301	CCTTTTGGTTCTTTTCCCTTCTCAACGACGCGTGAGCGTGGTTTAATTGACAAGGCCGA 360	
QY	361	TGGTGCTCTTTCACGAGGTTACATCGAACTCTCTTCTTTTCCCAATCATGACCTGCCCCC 420	
Db	361	TGGTGCTCTTTCACGAGGTTACATCGAACTCTCTTCTTTTCCCAATCATGACCTGCCCCC 420	

Qy 421 GAGTTTAGCCCCCATCAGGGCTGTGAATCCACTTCGATATCCTAGCCTAGTCTACTC 480
Db 421 GAGTTTAGCCCCCATCAGGGCTGTGAATCCACTTCGATATCCTAGCCTAGTCTACTC 480
Qy 481 TTCATAGTTGCTCCTGATGGGCACATTGGTCACATTGGCTTGGTTCTCCTACCTCGT 540
Db 481 TTCATAGTTGCTCCTGATGGGCACATTGGTCACATTGGCTTGGTTCTCCTACCTCGT 540
Qy 541 TCTCTTCCGCATCAAGCCTCTATGCCGACGACACACCTCATTTGGCCGGACCACTTTG 600
Db 541 TCTCTTCCGCATCAAGCCTCTATGCCGACGACACACCTCATTTGGCCGGACCACTTTG 600
Qy 601 AGCGGCACGCACCTTCGCGCCGAAGAGTTGATAACACCCTTCACCCCTTGGCCCAATGAT 660
Db 601 AGCGGCACGCACCTTCGCGCCGAAGAGTTGATAACACCCTTCACCCCTTGGCCCAATGAT 660
Qy 661 GGAGTTTGGTCTATTGTGATGATCACCTCACATTCACATGATCAGGATCCCTGGGAAGA 720
Db 661 GGAGTTTGGTCTATTGTGATGATCACCTCACATTCACATGATCAGGATCCCTGGGAAGA 720
Qy 721 GGGTGTGGAAGCCAGACAGCTTGTCCCTGTTCTTGCAGACTCAGGTCAGCTCCTAGCGG 780
Db 721 GGGTGTGGAAGCCAGACAGCTTGTCCCTGTTCTTGCAGACTCAGGTCAGCTCCTAGCGG 780
Qy 781 CTATCACAGCTCAGGATTTCAAGTCCCGTAAAGTCCAGACCCCTTTCATTTGATGATGC 840
Db 781 CTATCACAGCTCAGGATTTCAAGTCCCGTAAAGTCCAGACCCCTTTCATTTGATGATGC 840
Qy 841 TGCCTAATTTGGCTATCTCTATGCCGTAGCAGCGGTCTTGGCTACAACTGGCTGCCATG 900
Db 841 TGCCTAATTTGGCTATCTCTATGCCGTAGCAGCGGTCTTGGCTACAACTGGCTGCCATG 900
Qy 901 GCTGAAGCATCGTGAGATCTATAAAGTCTCCGAATCCCTCGGTGAAGTCAAGTCCGTCTC 960
Db 901 GCTGAAGCATCGTGAGATCTATAAAGTCTCCGAATCCCTCGGTGAAGTCAAGTCCGTCTC 960
Qy 961 TCCACACCAGTCAACAACAGCTTCTTCTCTTACAGTTCAGCTGAGCACATTCACAGA 1020
Db 961 TCCACACCAGTCAACAACAGCTTCTTCTCTTACAGTTCAGCTGAGCACATTCACAGA 1020
Qy 1021 ACTCTTCCCTTCTTTTGGTCAATATGCTGTTCAAGTCATGCAACTGGCAGCAGCCTCCG 1080
Db 1021 ACTCTTCCCTTCTTTTGGTCAATATGCTGTTCAAGTCATGCAACTGGCAGCAGCCTCCG 1080
Qy 1081 GGCTCCTGTCTGGAGTCTCTCGGCATCCCGATGGACACCGGCAGCACCCCAATTGAGGCTG 1140
Db 1081 GGCTCCTGTCTGGAGTCTCTCGGCATCCCGATGGACACCGGCAGCACCCCAATTGAGGCTG 1140
Qy 1141 TTGATCCGGAAGTGAAGACTGAGGTCTTTCGTGCTGACTCCCTCTTGTGCTGACGAGCGGATG 1200
Db 1141 TTGATCCGGAAGTGAAGACTGAGGTCTTTCGTGCTGACTCCCTCTTGTGCTGACGAGCGGATG 1200
Qy 1201 ACGACTGGAGTCACTCCATACAACTTGCCTTACAGGTGAGACACCTGTCCCACTGTT 1260
Db 1201 ACGACTGGAGTCACTCCATACAACTTGCCTTACAGGTGAGACACCTGTCCCACTGTT 1260
Qy 1261 TTCCTCGATAAATAACTCTTTATAGGAATGCCCTGCCAAATTCACCTGTCAAGCAGCCCA 1320
Db 1261 TTCCTCGATAAATAACTCTTTATAGGAATGCCCTGCCAAATTCACCTGTCAAGCAGCCCA 1320
Qy 1321 AGATGATGCTTTGATTTTCTACGAAGCAACTCGGCCCCCGACTTAATGATTTCTAGGATC 1380
Db 1321 AGATGATGCTTTGATTTTCTACGAAGCAACTCGGCCCCCGACTTAATGATTTCTAGGATC 1380
Qy 1381 ATTACCAACCTGTCCACGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTT 1440
Db 1381 ATTACCAACCTGTCCACGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTT 1440
Qy 1441 CAGCAAGGGTGAGTTTCTCAGAAACCTTCTGGTAAATTAATCATTTTACTGACCCCTTT 1500
Db 1441 CAGCAAGGGTGAGTTTCTCAGAAACCTTCTGGTAAATTAATCATTTTACTGACCCCTTT 1500

Qy 1501 CAGATTTACCACCACCTTCGCGCCCTGCCCACCTCTCTGTCGGCTACGATGGCATGAGCCCTGGT 1560
Db 1501 CAGATTTACCACCACCTTCGCGCCCTGCCCACCTCTCTGTCGGCTACGATGGCATGAGCCCTGGT 1560
Qy 1561 CCTACTTTCAATGTTTCCAGAGGACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACC 1620
Db 1561 CCTACTTTCAATGTTTCCAGAGGAAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACC 1620
Qy 1621 GTGAGAACTCGGTCCATCTCTGCACGGCTCCCATCGCCTGCCCCCTTTTCGATGTTGGGCT 1680
Db 1621 GTGAGAACTCGGTCCATCTCTGCACGGCTCCCATCGCCTGCCCCCTTTTCGATGTTGGGCT 1680
Qy 1681 GAAGATGAGACTTCCTCTGGCGAGTACAAGGATTACTACTTTTCCCAACTACCAATCCGCC 1740
Db 1681 GAAGATGAGACTTCCTCTGGCGAGTACAAGGATTACTACTTTTCCCAACTACCAATCCGCC 1740
Qy 1741 CGCCTTCGTGGTACCATGACCACGCTTTTCATGAAGGTATGCTACGAGCCTTTATCTTTC 1800
Db 1741 CGCCTTCGTGGTACCATGACCACGCTTTTCATGAAGGTATGCTACGAGCCTTTATCTTTC 1800
Qy 1801 TTGGCTACTTTTGGCTAACCAACTTCTCTTTCGTAGACTGCTGAGAAATGCCTACTTTGGTTC 1860
Db 1801 TTGGCTACTTTTGGCTAACCAACTTCTCTTTCGTAGACTGCTGAGAAATGCCTACTTTGGTTC 1860
Qy 1861 AGGCTGGGCCCTACATTAACAGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCT 1920
Db 1861 AGGCTGGGCCCTACATTAACAGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCT 1920
Qy 1921 ATGGCGAGTTCGATATCCCTCTGATCCTGAGCGCCCAAGTACTATAACGCCGATGTACCC 1980
Db 1921 ATGGCGAGTTCGATATCCCTCTGATCCTGAGCGCCCAAGTACTATAACGCCGATGTACCC 1980
Qy 1981 TGGCTTCACCGAGGGTGAGGACCAGGACCTGTGGGAGAGTGTATCCATGATGTCAACGGAC 2040
Db 1981 TGGCTTCACCGAGGGTGAGGACCAGGACCTGTGGGAGAGTGTATCCATGATGTCAACGGAC 2040
Qy 2041 AGCATGGCCCTTCTTAACGTCCAGCCCCGCAAGTACCGTTTCCGATTTCTCTCAAGCTG 2100
Db 2041 AGCATGGCCCTTCTTAACGTCCAGCCCCGCAAGTACCGTTTCCGATTTCTCTCAAGCTG 2100
Qy 2101 CCGTGTCTGCTGCTTGGCTCTCTACCTCTGTCAGGACCAGCTCTCCCAACGTCAGAAATTC 2160
Db 2101 CCGTGTCTGCTGCTTGGCTCTCTACCTCTGTCAGGACCAGCTCTCCCAACGTCAGAAATTC 2160
Qy 2161 CTTTCCAAAGTCATTGGCTCTGATGCTGCTCTCTTCAAGCCCCCGTTTCAGACCTCTAACC 2220
Db 2161 CTTTCCAAAGTCATTGGCTCTGATGCTGCTCTCTTCAAGCCCCCGTTTCAGACCTCTAACC 2220
Qy 2221 TCTACCTTGTCTTGGCCGAGGTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCAGCA 2280
Db 2221 TCTACCTTGTCTTGGCCGAGGTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCAGCA 2280
Qy 2281 ATGAGTCAAGAACTCTAAGACTTAACACTTTAGACTTCCACCAACTTTGCTGGCCAGACTC 2340
Db 2281 ATGAGTCAAGAACTCTAAGACTTAACACTTTAGACTTCCACCAACTTTGCTGGCCAGACTC 2340
Qy 2341 TTGACCTCGCAACGTTTCTGAGACCAACGATGTGGGAGCAGGAGTGAAGTACGGTTCGCA 2400
Db 2341 TTGACCTCGCAACGTTTCTGAGACCAACGATGTGGGAGCAGGAGTGAAGTACGGTTCGCA 2400
Qy 2401 CTCGAGGATGATGGCTTCGTCGACCTCTGGGACCTTGGGACCTTGTGAGGACAAACGCCAGTCC 2460
Db 2401 CTCGAGGATGATGGCTTCGTCGACCTCTGGGACCTTGTGAGGACAAACGCCAGTCC 2460
Qy 2461 CCTCCACTCTCCGTGACCTTCTTTCCTCTCAAGAAAGGCCCCCGCCGACAAAGCACT 2520
Db 2461 CCTCCACTCTCCGTGACCTTCTTTCCTCTCAAGAAAGGCCCCCGCCGACAAAGCACT 2520
Qy 2521 TCAAGTTTGAACGACGACAAACGACACTACCTGATCAACGATGTTGGCTTGGCCGATGTCA 2580
Db 2521 TCAAGTTTGAACGACGACAAACGACACTACCTGATCAACGATGTTGGCTTGGCCGATGTCA 2580
Qy 2581 ATGAGCGTGTCTCTGGCCAAAGCCCCGAGCTCGGACACCGTTGAGGTCTGGGAGCTCGAGA 2640

|||||
Db 2581 ATGAGCGTGTCTTGCCAAAGCCCGAGCTGCGCACCGTTGAGGTCTGGAGCTCGAGAACT 2640
Qy CCTCTGAGGCGTGAGGACACCCCGTGCACATTCCACCTTGTGTGACCTTCAAGATCCTCAAGC 2700
Db CCTCTGAGGCGTGAGGACACCCCGTGCACATTCCACCTTGTGTGACCTTCAAGATCCTCAAGC 2700
Qy GAACTGGTGGTGGCGCAGGTGATGCCCTACGAGTGTGCTGGTCTTTAAGGATGCTCGTCT 2760
Db GAACTGGTGGTGGCGCAGGTGATGCCCTACGAGTGTGCTGGTCTTTAAGGATGCTCGTCT 2760
Qy GGTGGGAGGGGTGAGACCTTACCATTCGAGGCCCACTACCAACCCCTGGAGCTG 2820
Db GGTGGGAGGGGTGAGACCTTACCATTCGAGGCCCACTACCAACCCCTGGAGCTG 2820
Qy ACATGTGGCACTGTCAACAACCTCATTCACGAGGATACGACATGATGGCTGTATTCAACG 2880
Db ACATGTGGCACTGTCAACAACCTCATTCACGAGGATACGACATGATGGCTGTATTCAACG 2880
Qy TCACCGGCATGGAGGAGGAGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCA 2940
Db TCACCGGCATGGAGGAGGAGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCA 2940
Qy AGTGGCGCGGTTCTTTACAAACCGCAACGACTTCCATGCTCGCGCTGGAACTTCTCCG 3000
Db AGTGGCGCGGTTCTTTACAAACCGCAACGACTTCCATGCTCGCGCTGGAACTTCTCCG 3000
Qy CCGAGTCCATCACTGCCGAGTGAGGAGTGGCGGAGCGAGGAGCGCTACAAACCGCGCTCG 3060
Db CCGAGTCCATCACTGCCGAGTGAGGAGTGGCGGAGCGAGGAGCGCTACAAACCGCGCTCG 3060
Qy ATGAGATCCTGGAGGATCTTGGAAATCAGAGAGTAACACCCCGAGGACCAAGCTCTACAATC 3120
Db ATGAGATCCTGGAGGATCTTGGAAATCAGAGAGTAACACCCCGAGGACCAAGCTCTACAATC 3119
Qy GTTTTGTAGCTTTAAGAGAGGCTCTTGGTGGGTATCTTTTCTTCCCTACCGGGAATCTC 3180
Db GTTTTGTAGCTTTAAGAGAGGCTCTTGGTGGGTATCTTTTCTTCCCTACCGGGAATCTC 3179
Qy GCTGTCCACTCGGATGTGAAGGACCATCACAAAGCAAGTATATATGGACTCACCACTG 3240
Db GCTGTCCACTCGGATGTGAAGGACCATCACAAAGCAAGTATATATGGACTCACCACTG 3239
Qy TCATTACCGCCCACTGTGTACCTATTTCGATCTTCTGTTCAAACTTTTCTAGTCGAGAGTGT 3300
Db TCATTACCGCCCACTGTGTACCTATTTCGATCTTCTGTTCAAACTTTTCTAGTCGAGAGTGT 3299
Qy CCATAGTCAAGAAAGCCCATAGGCGTATCGTCTAAACTGAACATATGTGTGGTCTGTGA 3360
Db CCATAGTCAAGAAAGCCCATAGGCGTATCGTCTAAACTGAACATATGTGTGGTCTGTGA 3359
Qy CGTGGAGTAGATGTCAATTGTGTGATGAGACACAGTAATAACGGTATATCTTTTCTTAGGAC 3420
Db CGTGGAGTAGATGTCAATTGTGTGATGAGACACAGTAATAACGGTATATCTTTTCTTAGGAC 3419
Qy TACAGGATCAGTTTCTCATGAGATTATACCTCGTCTAATGTGTGTGTCATGAGAGTCTAGCT 3480
Db TACAGGATCAGTTTCTCATGAGATTATACCTCGTCTAATGTGTGTGTCATGAGAGTCTAGCT 3479
Qy AAGGTTGAGAAATGATCAGACGGAAATCATTTGTAGTGTCTCAGCTCGTATATACCGATGTAA 3540
Db AAGGTTGAGAAATGATCAGACGGAAATCATTTGTAGTGTCTCAGCTCGTATATACCGATGTAA 3539
Qy GACAAGTTAGGTAAAGTGTGTTGTTATCCGAAATACACTCAGGCTCCCTCATTTAGGTTGCA 3600
Db GACAAGTTAGGTAAAGTGTGTTGTTATCCGAAATAGACTCAGGCTCCCTCATTTAGGTTGCA 3599
Qy TGTGAAAACCTTTCAGCAACTCATGGGTGTTGGGACCAAAATCATCATACCTGATTTTGTAT 3660
Db TGTGAAAACCTTTCAGCAACTCATGGGTGTTGGGACCAAAATCATCATACCTGATTTTGTAT 3659
Qy AACTGACCTGGGTCAAT 3677
|||||

Db 3660 AACTGACCTGGGTCAAT 3676
RESULT 6
AAZ25735
ID AAZ25735 standard; DNA; 2067 BP.
XX
XX AAZ25735;
XX AC
XX 05-JAN-2000 (first entry)
XX
XX Stachybotrys chartarum phenol oxidising enzyme PCR fragment.
DE Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
XX Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
KW detergent; anti-dye transfer; stain removal; bleaching; PCR primer; ss.
XX
XX Synthetic.
OS Stachybotrys chartarum.
XX
XX WO9949010-A2.
XX
XX 30-SEP-1999.
XX
XX 23-MAR-1999; 99WO-EP02042.
PF
XX 24-MAR-1998; 98US-0046969.
PR
XX 22-DEC-1998; 98US-0218702.
PR
XX (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
XX
XX Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;
PI Wang C;
PI
XX WPI; 1999-601211/51.
DR
XX Detergent composition containing phenol oxidase from Stachybotrys, used
PT to bleach stains and prevent dye transfer -
PT
XX
XX Example 17; Fig 9; 56pp; English.
PS
XX The present invention describes a detergent composition containing a
CC purified phenol oxidising enzyme derived from stachybotrys. The present
CC sequence represents a PCR fragment of stachybotrys chartarum phenol
CC oxidising enzyme. The enzyme can be used to modify the colour of dyes
CC and other coloured compounds (e.g. for use in pulp and paper bleaching
CC also for removing stains, e.g. food, tea, blood etc., from fabrics) and
CC for preventing dye transfer during fabric washing.
XX
XX Sequence 2067 BP; 445 A; 621 C; 500 G; 501 T; 0 other;
Qy 1041 AATATGCTGTTCAAGTCATGCAACTGGCAGCAGCTCCGGGCTCCTGTCTGGAGTCCCT 1100
Db 7 AATATGCTGTTCAAGTCATGCAACTGGCAGCAGCTCCGGGCTCCTGTCTGGAGTCCCT 66
Qy 1101 GGCATCCCGATGGACACCGGAGCCACCCCATTTGAGGCTGTTGATCCCGAAGTGAAGACT 1160
Db 67 GGCATCCCGATGGACACCGGAGCCACCCCATTTGAGGCTGTTGATCCCGAAGTGAAGACT 126
Qy 1161 GAGGCTTCGCTGACTCCCTCTTCTGCTCAGCAGCGATGACGACTGGAGTCACTCCA 1220
Db 127 GAGGCTTCGCTGACTCCCTCTTCTGCTCAGCAGCGATGACGACTGGAGTCACTCCA 186
Qy 1221 TACAACCTTGCCTTTTACAGGTGAGACACCTGTCCCACTGTTTCCCTCGATAAATCTCT 1280
Db 187 TACAACCTTGCCTTTTACAGGTGAGACACCTGTCCCACTGTTTCCCTCGATAAATCTCT 246
Qy 1281 TATAGGAATGCCCTGCCCAATTTCCACCTCTCAAGCAGCCCAAGATGTATGTCTTTGATTTT 1340
|||||

Db 247 TATAGGAATGCCCTGCCAAATTCACCTCTCAAGCAGCCCAAGATGATGCTGTTGATTTT 306
Qy 1341 CTACGAACAACCTCGGCCCGGCACTAATATCTTAGGATCATTTACCAACCCCTGTCACCGG 1400
Db 307 CTACGAACAACCTCGGCCCGGCACTAATATCTTAGGATCATTTACCAACCCCTGTCACCGG 366
Qy 1401 CAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAGGGTGAGTTGCT 1460
Db 367 CAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAGGGTGAGTTGCT 426
Qy 1461 CAGAAACCTTGTGGTAAATTAATCATTTGTTACTGACCCCTTTTCAGATTTTACCCACCTTCGG 1520
Db 427 CAGAAACCTTGTGGTAAATTAATCATTTGTTACTGACCCCTTTTCAGATTTTACCCACCTTCGG 486
Qy 1521 CCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGTCTCTACTTTTCAATGTTTCCAG 1580
Db 487 CCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGTCTCTACTTTTCAATGTTTCCAG 546
Qy 1581 AGGAACAGAGACTGTAGTTAGTTAGTTTCATCAACAATGCCACCTGGAGAACTCGGTCCTATCT 1640
Db 547 AGGAACAGAGACTGTAGTTAGTTAGTTTCATCAACAATGCCACCTGGAGAACTCGGTCCTATCT 606
Qy 1641 GCACGGCTCCCATCGCTGCGCCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCCTGG 1700
Db 607 GCACGGCTCCCATCGCTGCGCCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCCTGG 666
Qy 1701 CGAGTACAAGGATTACTACTTTTCCCACTACCAATFCCCGCCGCTTCTGTGTACCATGA 1760
Db 667 CGAGTACAAGGATTACTACTTTTCCCACTACCAATFCCCGCCGCTTCTGTGTACCATGA 726
Qy 1761 CCAGCTTTTCATGAAAGTATGCTACGAGCCCTTATCTTCTTGGCTACCTTTTGGCTAAC 1820
Db 727 CCAGCTTTTCATGAAAGTATGCTACGAGCCCTTATCTTCTTGGCTACCTTTTGGCTAAC 786
Qy 1821 AACTTCCCTTTCGTAGACTGCTGAGATGCCCTACTTGTGAGGCTGGCGCTACATATC 1880
Db 787 AACTTCCCTTTCGTAGACTGCTGAGATGCCCTACTTGTGAGGCTGGCGCTACATATC 846
Qy 1881 AACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGCTATGCGAGTTTCGATATCCCT 1940
Db 847 AACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGCTATGCGAGTTTCGATATCCCT 906
Qy 1941 CTGATCTGAGCGCAAGTACTATAACCCGATGATACCCCTGCGTTTCGACGAGGGTGAG 2000
Db 907 CTGATCTGAGCGCAAGTACTATAACCCGATGATACCCCTGCGTTTCGACGAGGGTGAG 966
Qy 2001 GACCAGGACCTGTGGGAGATGTCATCCATGTCACGACAGCCATGGCTTCTCTTAAC 2060
Db 967 GACCAGGACCTGTGGGAGATGTCATCCATGTCACGACAGCCATGGCTTCTCTTAAC 1026
Qy 2061 GTCCAGCCCGCAAGTACCGTTTCCGATTCTCAACGCTGCCGTCTCTGCTGGCTC 2120
Db 1027 GTCCAGCCCGCAAGTACCGTTTCCGATTCTCAACGCTGCCGTCTCTGCTGGCTC 1086
Qy 2121 CTCACCTCTGTCAGGACAGCTCTCCCAAGCTCAGAAATTCCTTTCCAAAGTCAATTCCTCT 2180
Db 1087 CTCACCTCTGTCAGGACAGCTCTCCCAAGCTCAGAAATTCCTTTCCAAAGTCAATTCCTCT 1146
Qy 2181 GATGCTGTCTCTTCAAGCCCGGTTTCAGACCTCTAACCTCTACCTTCGTTGGCCGAG 2240
Db 1147 GATGCTGTCTCTTCAAGCCCGGTTTCAGACCTCTAACCTCTACCTTCGTTGGCCGAG 1206
Qy 2241 CGTTACGAGATCATTTATGTTATGCCCTCCCTCTCAGGAATGAGTCAAGAACTCTAAGA 2300
Db 1207 CGTTACGAGATCATTTATGTTATGCCCTCCCTCTCAGGAATGAGTCAAGAACTCTAAGA 1266
Qy 2301 CTAACACTTGTAGACTTCACCAACTTTTGTGGCCAGACTTTGTACCTGCGCAAGCTTGTCT 2360
Db 1267 CTAACACTTGTAGACTTCACCAACTTTTGTGGCCAGACTTTGTACCTGCGCAAGCTTGTCT 1326
Qy 2361 GAGACCAACGATGTGGGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATCGGCTTC 2420
Db 1327 GAGACCAACGATGTGGGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATCGGCTTC 1386

Qy 2421 GTCGTCAGCTCTGCACTGTTTGAGSACAACAGCCAGGTCCTCTCCACTCTCCGTGACGTT 2480
Db 1387 GTCGTCAGCTCTGCACTGTTTGAGSACAACAGCCAGGTCCTCTCCACTCTCCGTGACGTT 1446
Qy 2481 CTTTCCCTCTCTACAGAAGAGGCCCGCCGACAGCACTTCAAGTTTGAACGCCAGCAAC 2540
Db 1447 CTTTCCCTCTCTACAGAAGAGGCCCGCCGACAGCACTTCAAGTTTGAACGCCAGCAAC 1506
Qy 2541 GGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCATGACGCTGCTCTGCGCCAG 2600
Db 1507 GGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCATGACGCTGCTCTGCGCCAG 1566
Qy 2601 CCCGAGCTCGCACCGTTGAGGCTCTGGAGCTCGGAGAACTCCTCTGAGGCTTGGAGCCAC 2660
Db 1567 CCCGAGCTCGCACCGTTGAGGCTCTGGAGCTCGGAGAACTCCTCTGAGGCTTGGAGCCAC 1626
Qy 2661 CCCGTCACATTCACCTTGTGACTTCAAGATCTCAAGCGAACTGGTGGTGGCCAG 2720
Db 1627 CCCGTCACATTCACCTTGTGACTTCAAGATCTCAAGCGAACTGGTGGTGGCCAG 1686
Qy 2721 GTCATGCCCTACGAGTCTGCTTAAAGGATGTCGCTGGTTGGCAGGGGTCAGACC 2780
Db 1687 GTCATGCCCTACGAGTCTGCTTAAAGGATGTCGCTGGTTGGCAGGGGTCAGACC 1746
Qy 2781 CTGACCATCGAGGCCCACTACCAACCCCTGGACTTGAGGCTTACATGTGGCACTGTCAACAAC 2840
Db 1747 CTGACCATCGAGGCCCACTACCAACCCCTGGACTTGAGGCTTACATGTGGCACTGTCAACAAC 1806
Qy 2841 CTCATTACAGGAGTAACGACATGATGGCTGTATTCAAGCTACCGCCATGGAGGAGAG 2900
Db 1807 CTCATTACAGGAGTAACGACATGATGGCTGTATTCAAGCTACCGCCATGGAGGAGAG 1866
Qy 2901 GGATATCTTCAGGAGGACTTCGAGACCCCAAGTGAACCCCAAGTGGCGCGCTTCCCTTAC 2960
Db 1867 GGATATCTTCAGGAGGACTTCGAGACCCCAAGTGAACCCCAAGTGGCGCGCTTCCCTTAC 1926
Qy 2961 AACCGCAACGACTTCCATGCTCGGCTGGAACCTTCTCCGCGAGTCCATCACTGCCCGA 3020
Db 1927 AACCGCAACGACTTCCATGCTCGGCTGGAACCTTCTCCGCGAGTCCATCACTGCCCGA 1986
Qy 3021 GTGAGGAGCTGGCGGAGCAGGACCGGTACACCCCTCGATGAGATCCTGAGGATCTT 3080
Db 1987 GTGAGGAGCTGGCGGAGCAGGACCGGTACACCCCTCGATGAGATCCTGAGGATCTT 2046
Qy 3081 GGAATCGAGGAGTA 3094
Db 2047 GGAATCGAGGAGTA 2060

RESULT 7

AAZ27609

ID AAZ27609 standard; DNA; 2067 BP.

XX

AC

AC

DF

XX

XX

XX

DE

KW

KW

KW

KW

OS

XX

PN

PD

PF

XX

XX

PR

PR

Stachybotrys phenol oxidase coding sequence.

Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
fabric washing; stain bleaching; anti-dye transfer; detergent; ss.

Stachybotrys chartarum.

WO9949020-A2.

30-SEP-1999.

23-MAR-1999; 99WO-US06327.

24-MAR-1998; 98US-0046969.

22-DEC-1998; 98US-0218702.

PR 22-MAR-1999; 99US-0273957.
XX (GEMV) GENENCOR INT INC.
XX
XX Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;
XX WPI; 1999-591088/50.
XX Novel enzyme for modifying coloured compounds used to prevent
XX dye-transfer -
XX
XX Example 17; Fig 9; 64pp; English.
XX This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
XX of the invention. The invention is used to modify a coloured compound and
XX prevent dye transfer during fabric washing, or for stain bleaching or
XX anti-dye transfer. It is useful in the detergent, paper and pulp, textile
XX and food industries.
XX
XX Sequence 2067 BP; 445 A; 621 C; 500 G; 501 T; 0 other;
SQ
Query Match 55.9%; Score 2054; DB 20; Length 2067;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1041 AATATGCTGTTCAAGTCATGGCAACTGGCAGCAGCCCTCCGGGCTCCTGTCTGGAGTCCTC 1100
Db 7 AATATGCTGTTCAAGTCATGGCAACTGGCAGCAGCCCTCCGGGCTCCTGTCTGGAGTCCTC 66
Qy 1101 GGCATCCGGATGGACACGGGAGCCACCCCATTTGAGGCTGTTGATCCGGAAGTGAAGACT 1160
Db 67 GGCATCCGGATGGACACGGGAGCCACCCCATTTGAGGCTGTTGATCCGGAAGTGAAGACT 126
Qy 1161 GAGGCTTCGCTGACTCCCTCCTTGGCTGACGAGCGGATGACGACTGGGAGTCACTCCCA 1220
Db 127 GAGGCTTCGCTGACTCCCTCCTTGGCTGACGAGCGGATGACGACTGGGAGTCACTCCCA 186
Qy 1221 TACAACCTTGCTTTACAGGTGAGACACCTGTCCACCTGTTTTCCTCGATAAATCTCT 1280
Db 187 TACAACCTTGCTTTACAGGTGAGACACCTGTCCACCTGTTTTCCTCGATAAATCTCT 246
Qy 1281 TATAGGAATGCCCTGGCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTTTGATTTT 1340
Db 247 TATAGGAATGCCCTGGCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTTTGATTTT 306
Qy 1341 CTAGGAAGCAACTCGGCCCGGACTAAATGTATTCTAGGATCATTTACCAACCTGTCAACCGG 1400
Db 307 CTAGGAAGCAACTCGGCCCGGACTAAATGTATTCTAGGATCATTTACCAACCTGTCAACCGG 366
Qy 1401 CAAGGACATTTGGTACTATGATCGAGATCAAGCCATTTTCAGCAAAAGGGTGAGTTTGCT 1460
Db 367 CAAGGACATTTGGTACTATGATCGAGATCAAGCCATTTTCAGCAAAAGGGTGAGTTTGCT 426
Qy 1461 CAGAAACCTTGTTGGTAATTAATCATTTGTTACTGACCCCTTCAGATTTACCCACCTTGCG 1520
Db 427 CAGAAACCTTGTTGGTAATTAATCATTTGTTACTGACCCCTTCAGATTTACCCACCTTGCG 486
Qy 1521 CCCTGCCACTCTCGCTGCTACGATGGCATGCGCTGGCTCTACTTTCAATGTTCCACG 1580
Db 487 CCCTGCCACTCTCGCTGCTACGATGGCATGCGCTGGCTCTACTTTCAATGTTCCACG 546
Qy 1581 AGGAACAGAGACTAGTTAGTTTTCATCAACAATGCCACCGTGAGAACTCGGTCCTCATCT 1640
Db 547 AGGAACAGAGACTAGTTAGTTTTCATCAACAATGCCACCGTGAGAACTCGGTCCTCATCT 606
Qy 1641 GCAGGCTTCCCATCGGCTGCCCTTTGATGTTGGCTGAAGATGACCTTCCCTG 1700
Db 607 GCAGGCTTCCCATCGGCTGCCCTTTGATGTTGGCTGAAGATGACCTTCCCTG 666
Qy 1701 CGAGTACAGGATTACTACTTTCCCAACTACCAATCCGCCGCTTCTGTGGTACCATGA 1760
Db 667 CGAGTACAGGATTACTACTTTCCCAACTACCAATCCGCCGCTTCTGTGGTACCATGA 726

Qy 1761 CCACGCTTTCATGAAGGTATGCTACGAGCCCTTATCTTTCTTGGCTACCTTTGGCTAAACC 1820
Db 727 CCACGCTTTCATGAAGGTATGCTACGAGCCCTTATCTTTCTTGGCTACCTTTGGCTAAACC 786
Qy 1821 AACTTCCTTTGCTAGACTGCTGAGAATGCTACTTTGCTCAGGCTGGCGCTACATTATC 1880
Db 787 AACTTCCTTTGCTAGACTGCTGAGAATGCTACTTTGCTCAGGCTGGCGCTACATTATC 846
Qy 1881 AACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTCCGATATCCCT 1940
Db 847 AACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTCCGATATCCCT 906
Qy 1941 CTGATCTGACGGCCAAAGTACTATAACGCCGATGGTACCCCTGCTTCGACGAGGGTGAG 2000
Db 907 CTGATCTGACGGCCAAAGTACTATAACGCCGATGGTACCCCTGCTTCGACGAGGGTGAG 966
Qy 2001 GACCAGACCTGTGGGAGATGTCATCCATGTCACGACAGACCATGGCCCTTTCCTTAAC 2060
Db 967 GACCAGACCTGTGGGAGATGTCATCCATGTCACGACAGACCATGGCCCTTTCCTTAAC 1026
Qy 2061 GTCCAGCCCGCAAGTACCCTGTTCCGATTTCTCAACGCTGCCGTGCTGCTGCTTGGCTC 2120
Db 1027 GTCCAGCCCGCAAGTACCCTGTTCCGATTTCTCAACGCTGCCGTGCTGCTGCTTGGCTC 1086
Qy 2121 CTCCTACCTGTCAGACACAGCTCTCCCAACGTCAGAAATTCCTTTCCAAAGTCATTTGCCCT 2180
Db 1087 CTCCTACCTGTCAGACACAGCTCTCCCAACGTCAGAAATTCCTTTCCAAAGTCATTTGCCCT 1146
Qy 2181 GATGCTGCTCTCCTCAAGCCCGCTTCAGACCTCTACCTCTACCTGCTGCTGCTGCTGCTG 2240
Db 1147 GATGCTGCTCTCCTCAAGCCCGCTTCAGACCTCTACCTCTACCTGCTGCTGCTGCTGCTG 1206
Qy 2241 CGTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCAGAAATGAGTCAAGAACTCTAAGA 2300
Db 1207 CGTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCAGAAATGAGTCAAGAACTCTAAGA 1266
Qy 2301 CTAACTCTGTAGACTTCAACCACTTTGCTGGCAGACTCTTGACCTGCGCAAGCTTGCT 2360
Db 1267 CTAACTCTGTAGACTTCAACCACTTTGCTGGCAGACTCTTGACCTGCGCAAGCTTGCT 1326
Qy 2361 GAGACCAAGATGTCGGGACGAGGATGAGTACGCTCGACTCTCGAGGTGATGGCTTC 2420
Db 1327 GAGACCAAGATGTCGGGACGAGGATGAGTACGCTCGACTCTCGAGGTGATGGCTTC 1386
Qy 2421 GTCGTCAGCTCTGGCACTGTTTGAGGCAACAGCCAGGTGCCCTCCACTCTCCGTCGACTT 2480
Db 1387 GTCGTCAGCTCTGGCACTGTTTGAGGCAACAGCCAGGTGCCCTCCACTCTCCGTCGACTT 1446
Qy 2481 CCTTTCCCTCTCAAGGAAGGCCCGCCGACAAAGCACTTCAAGTTTGAACGACGCAAC 2540
Db 1447 CCTTTCCCTCTCAAGGAAGGCCCGCCGACAAAGCACTTCAAGTTTGAACGACGCAAC 1506
Qy 2541 GGACACTACCTGATCAAGGATGTTGGCTTTGCCGATGTCATAGCGTGTCTTGCCCAAG 2600
Db 1507 GGACACTACCTGATCAAGGATGTTGGCTTTGCCGATGTCATAGCGTGTCTTGCCCAAG 1566
Qy 2601 CCCGAGCTCGCACCGTTGAGGTCTGGGAGCTCGAGAACTCCTCTGGAGGTGAGGCCAC 2660
Db 1567 CCCGAGCTCGCACCGTTGAGGTCTGGGAGCTCGAGAACTCCTCTGGAGGTGAGGCCAC 1626
Qy 2661 CCCGTCCCACTTACCTTGTGACTTCAAGATCCTCAAGCGAACTGGTGGTGGCCAG 2720
Db 1627 CCCGTCCCACTTACCTTGTGACTTCAAGATCCTCAAGCGAACTGGTGGTGGCCAG 1686
Qy 2721 GTCATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCGCTTGGTGGGAGGGTGAGACC 2780
Db 1687 GTCATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCGCTTGGTGGGAGGGTGAGACC 1746
Qy 2781 CTGACCATCGAGGCCCACTACCAACCTTGAGCTGGAGCTTACATGTGCACCTGTGCACAC 2840
Db 1747 CTGACCATCGAGGCCCACTACCAACCTTGAGCTGGAGCTTACATGTGCACCTGTGCACAC 1806
Qy 2841 CTCATTACGAGGATACGACATGATGGCTGTATTTCACGCTACCGCCATGGAGGAGAAG 2900

|||||
Db 1807 CTCATTACGAGGATACGACATGATGGCTGATTCAACGTCACCGCCATGGAGGAG 1866
Qy 2901 GGATATCTTCAGGAGACTTCGAGGACCCCATGAACCCCAAGTGGCGCCCTTCTTAC 2960
Db 1867 GGATATCTTCAGGAGACTTCGAGGACCCCATGAACCCCAAGTGGCGCCCTTCTTAC 1926
Qy 2961 AACCGACGACTTCATGCTCGCGCTCGGAACTTCTCCGCGAGTGCATCACTGCCGA 3020
Db 1927 AACCGCAACGACTTCATGCTCGCGCTCGGAACTTCTCCGCGAGTGCATCACTGCCGA 1986
Qy 3021 GTGCGAGGAGTGGCGAGCAGGAGCCGTACACCGCTCGATGAGATCCTGGAGATCTT 3080
Db 1987 GTGCGAGGAGTGGCGAGCAGGAGCCGTACACCGCTCGATGAGATCCTGGAGATCTT 2046
Qy 3081 GGAATCGAGGAGTA 3094
Db 2047 GGAATCGAGGAGTA 2060

RESULT 8
ABA92911
ID ABA92911 standard; DNA; 7248 BP.
XX
AC ABA92911;
DT
DE
DE
XX Stachybotrys chartarum laccase gene.
KW Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;
KW copper; metal cofactor; gene; plant; ds.
XX
OS Stachybotrys chartarum.
PN WO200196543-A2.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US19174.
XX
PR 15-JUN-2000; 2000US-211732P.
XX
PA (PROD-) PRODIGENE INC.
PA (GENM) GENENCOR INC.
XX
XX
PI Hood E, Howard JA, Bailey M, Van Gastel FJC, Ward M, Wang H;
PI Woodward S;
XX
XX WPI; 2002-090204/12.
XX
XX Improving recovery of active enzyme e.g. laccase, which requires
PT transitional metal cofactor e.g. copper for activity, from a plant, by
PT introducing plant nucleotide sequences encoding the enzyme and exposing
PT it to cofactor -
XX
XX Example 5; Fig 16A-E; 81pp; English.
XX
XX The present invention describes a method for improving the recovery of
CC an active enzyme from a plant where the enzyme requires a transitional
CC metal cofactor for activity. The method comprises introducing into the
CC plant nucleotide sequences encoding the enzyme and exposing the enzyme
CC to the metal cofactor. The method is useful for improving recovery of
CC active enzyme which requires a transitional metal cofactor for activity,
CC preferably for improving recovery of active laccase which requires
CC copper for activity. The method can be used for improving recovery of
CC active organophosphate hydrolase (OPH, E.C. 3.1.8.1) which requires
CC zinc, nickel, cobalt or manganese for activity, where the method further
CC comprises adding bicarbonate ion salt. The present sequence encodes the
CC fungal Stachybotrys chartarum laccase enzyme. Laccases are also called
CC blue copper oxidases and use copper to accept and donate electrons in
CC the oxidation and reduction of substrates.
XX

SQ Sequence 7248 BP; 1928 A; 1744 C; 1579 G; 1997 T; 0 other;

Query Match 40.1%; Score 1474.6; DB 24; Length 7248;
Best Local Similarity 86.1%; Pred. No. 0;
Matches 1806; Conservative 0; Mismatches 24; Indels 267; Gaps 5;

Qy 1030 TTCCTTTTTCGTCATATGCTTCAAGTCAATGCGACACTGCGACGAGCCTCCGGCTCCTGT 1089
Db 5184 TTCGGCTTTGTCATATGCTTCAAGTCAATGCGACACTGCGACGAGCCTCCGGCTCCTGT 5243
Qy 1090 CTGGAGTCTCTCGGCATCCGATGGACACCGCGAGCCACCCATTGAGGCTGTGATCCCG 1149
Db 5244 CTGGAGTCTCTCGGCATCCGATGGACACCGCGAGCCACCCATTGAGGCTGTGATCCCG 5303
Qy 1150 AAGTGAAGACTGAGGTCTTCGCTGACTCCCTCTTGTCTGCTGACGAGCGATGACGACTGG 1209
Db 5304 AAGTGAAGACTGAGGTCTTCGCTGACTCCCTCTTGTCTGCTGACGAGCGATGACGACTGG 5363
Qy 1210 AGTCACCTCCATACAACTTTCAGGTGAGACACCTGTCCACCTGTTTTCCTCGA 1269
Db 5364 AGTCACCTCCATACAACTTTCAGGTGAGACACCTGTCCACCTGTTTTCCTCGA 1269
Qy 1270 TAACTAACTCTTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGATG 1329
Db 5390 -----AGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGAT----- 5430
Qy 1330 TCCTTTGATTTTCTACGAAAGCAACTCGGCCCGCGACTAATATTCTAGGATCAATACCAAC 1389
Db 5431 -----GATCATTACCAAC 5443
Qy 1390 CCGTGCACCGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAGG 1449
Db 5444 CCTGTACCGCGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAG- 5502
Qy 1450 GTGAGTTTGTCTCAGAAACCTTTGTGGTAATTAATCATTGTTACTGACCCCTTCAGATTAC 1509
Db 5503 -----GATTTAC 5509
Qy 1510 CCCACCTTGGCGCCCTGCCACTCTCGTGGCTACGATGGCATGAGCCCTGGTCTCTACTTTC 1569
Db 5510 CCCACCTTGGCGCCCTGCCACTCTCGTGGCTACGATGGCATGAGCCCTGGTCTCTACTTTC 5569
Qy 1570 AATGTTCCAGAGGAACAGAGACTGTAGTTAGTTTCATCAACAATGCCACCGTGGAGAAC 1629
Db 5570 AATGTTCCAGAGGAACAGAGACTGTAGTTAGTTTCATCAACAATGCCACCGTGGAGAAC 5629
Qy 1630 TCGGTCCATCTGCACGGCTCCCATCGCTGCCCTTCGATGTTGGCTGNAGATGTG 1689
Db 5630 TCGGTCCATCTGCACGGCTCCCATCGCTGCCCTTCGATGTTGGCTGNAGATGTG 5689
Qy 1690 ACCTTCCCTGGCGAGTACAAGGATTACTACTTTCCAACTACCAATCCGCCCGCTTCTG 1749
Db 5690 ACCTTCCCTGGCGAGTACAAGGATTACTACTTTCCAACTACCAATCCGCCCGCTTCTG 5749
Qy 1750 TGGTACCATGACCCAGCTTTTCATGAAGGTATGCTACGAGCCCTTATCTTTTCTTGGCTACC 1809
Db 5750 TGGTACCATGACCCAGCTTTTCATGA-----GATTTAC 5774
Qy 1810 TTTGGCTAACCAACTTCCTTTCTAGACTGCTGAGATGCCCTACTTTGGCTGAGCTGGCG 1869
Db 5775 -----AGACTGCTGAGAAATGCCCTACTTTGGCTGAGCTGGCG 5810
Qy 1870 CCTACATTATCAACACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCTATGCGGAGT 1929
Db 5811 CCTACATTATCAACACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCTATGCGGAGT 5870
Qy 1930 TCGATATCCCTCTGATCCTCGAGCGCAAGTACTATAACCCCGATGTAACCTTCCTCGA 1989
Db 5871 TCGATATCCCTCTGATCCTCGAGCGCAAGTACTATAACCCCGATGTAACCTTCCTCGA 5930
Qy 1990 CCGAGGGTGAGGACACGAGACCTGTGGGAGATGTCATCCATGTCAACGAGACGACATGCC 2049
Db 5931 CCGAGGGTGAGGACACGAGACCTGTGGGAGATGTCATCCATGTCAACGAGACGACATGCC 5990

Qy 2050 CTTTCTTAAGCTCCAGCCCGCAAGTACCCTTTCCGATTCTTCAACGCTCCCGTGTCTC 2109
Db 5991 CTTTCTTAAGCTCCAGCCCGCAAGTACCCTTTCCGATTCTTCAACGCTCCCGTGTCTC 6050
Qy 2110 GTGCTTGGCTCCTTACCTCTGTCAGGACCAGCTCTCCCAAGTCAGAAATTCCTTTCCAA 2169
Db 6051 GTGCTTGGCTCCTTACCTCTGTCAGGACCAGCTCTCCCAAGTCAGAAATTCCTTTCCAA 6110
Qy 2170 TCATTGGCTCTGATGCTGCTCTTCAAGCCCGGTTGACAGCTCTAACCTCTACCTTACCTTG 2229
Db 6111 TCATTGGCTCTGATGCTGCTCTTCAAGCCCGGTTGACAGCTCTAACCTCTACCTTACCTTG 6170
Qy 2230 CTGTTGGCGAGCGTTACGAGATCATTTATTGGTATGCCCTCCCTCTCACGAATGAGTCAA 2289
Db 6171 CTGTTGGCGAGCGTTACGAGATCATTT----- 6199
Qy 2290 GAACCTTAAGACTTAACACTTGTAGACTTACCAACTTTGCTGGCCAGACTCTTGAACCTGC 2349
Db 6200 -----GACTTACCAACTTTGCTGGCCAGACTCTTGAACCTGC 6236
Qy 2350 GCAAGTTGCTGAGACCAACGATGTCGGCGACGAGGATGAGTCGCACTCTCGAGG 2409
Db 6237 GCAAGTTGCTGAGACCAACGATGTCGGCGACGAGGATGAGTCGCACTCTCGAGG 6296
Qy 2410 TGATGCGCTTCTGCTCAGCTCTGSCACTGTTGAGGACAACAGCCAGGTCCCTCCACTC 2469
Db 6297 TGATGCGCTTCTGCTCAGCTCTGSCACTGTTGAGGACAACAGCCAGGTCCCTCCACTC 6356
Qy 2470 TCCGTGAGCTTCTTTCCCTCTCTACAAGGAAGGCCCGCGCAAGCAACTTCAAGTTTG 2529
Db 6357 TCCGTGAGCTTCTTTCCCTCTCTACAAGGAAGGCCCGCGCAAGCAACTTCAAGTTTG 6416
Qy 2530 AACGAGCAAGCGACACTACCTGATCAAGATGTTGGCTTTGCCGATGTCATGAGCGTG 2589
Db 6417 AACGAGCAAGCGACACTACCTGATCAAGATGTTGGCTTTGCCGATGTCATGAGCGTG 6476
Qy 2590 TCCTGGCCAAAGCCGAGCTCGGCACCGTTGAGGTCTGGAGCTCGAGAACTCCTCTGGAG 2649
Db 6477 TCCTGGCCAAAGCCGAGCTCGGCACCGTTGAGGTCTGGAGCTCGAGAACTCCTCTGGAG 6536
Qy 2650 GGTGAGCCACCCGTCACATTCACCTTTGAGTTCGAAGATCTCAAGGCAACTGGTG 2709
Db 6537 GGTGAGCCACCCGTCACATTCACCTTTGAGTTCGAAGATCTCAAGGCAACTGGTG 6596
Qy 2710 GTCGTGGCCAGTCAATGCCCTACGAGTCTGCTGGCTTTAAGGATGTCGCTGGTTGGCA 2769
Db 6597 GTCGTGGCCAGTCAATGCCCTACGAGTCTGCTGGCTTTAAGGATGTCGCTGGTTGGCA 6656
Qy 2770 GGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTTACATGTGGC 2829
Db 6657 GGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTTACATGTGGC 6716
Qy 2830 ACTGTCAACCTCATTCACGAGGATACGACATGATGGCTGTATTCAACGTCACCGCA 2889
Db 6717 ACTGTCAACCTCATTCACGAGGATACGACATGATGGCTGTATTCAACGTCACCGCA 6776
Qy 2890 TGGAGGAGAGGATATCTTCAGGAGGACTTCGAGAGCCCATGAACCCCAAGTGGCGCG 2949
Db 6777 TGGAGGAGAGGATATCTTCAGGAGGACTTCGAGAGCCCATGAACCCCAAGTGGCGCG 6836
Qy 2950 CCGTTTCTTACAACCGCAACGACTTCTCCATGCTCGCGCTGGAAACTTCTCCCGCGAGTCCA 3009
Db 6837 CCGTTTCTTACAACCGCAACGACTTCTCCATGCTCGCGCTGGAAACTTCTCCCGCGAGTCCA 6896
Qy 3010 TCACGTCCCGAGTCAGGAGTGGCCGAGGAGCGGTACACCCGCTCGATGAGATCC 3069
Db 6897 TCACGTCCCGAGTCAGGAGTGGCCGAGGAGCGGTACACCCGCTCGATGAGATCC 6956
Qy 3070 TGGAGATCTTGGATCGAGGATTAACCCCGAGCCACAAGCTCTACAATCGTTTG 3126
Db 6957 TGGAGATCTTGGATCGAGGATTAACCCCGAGCCACAAGCTCTACAATCGTTTG 7013

RESULT 9
AAZ27601
ID AAZ27601 standard; DNA; 1791 BP.
XX
AC AAZ27601;
XX
DT 16-DEC-1999 (first entry)
XX
DE Stachybotrys phenol oxidase coding sequence.
XX
KW Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
KW fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
XX
OS Stachybotrys chartarum.
XX
PN WO9949020-A2.
XX
FD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-US06327.
XX
PR 24-MAR-1998; 98US-0046969.
PR 22-DEC-1998; 98US-0218702.
PR 22-MAR-1999; 99US-0273957.
XX
PA (GEMV) GENENCOR INT INC.
XX
PI Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;
XX
DR WPI; 1999-591088/50.
DR P-PSDB; AAY39992.
XX
PT Novel enzyme for modifying coloured compounds used to prevent
PT dye-transfer -
XX
PS Claim 21; Fig 5; 64pp; English.
XX
CC This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
CC of the invention. The invention is used to modify a coloured compound and
CC prevent dye transfer during fabric washing, or for stain bleaching or
CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC and food industries.
XX
SQ Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;
Query Match 40.1%; Score 1474; DB 20; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
Qy 1038 GTCATATGCTGTTCAAGTCAATGCGCACTGGCAGCAGCTCCGGGCTCCTGCTGGAGTC 1097
Db 1 GTCATATGCTGTTCAAGTCAATGCGCACTGGCAGCAGCTCCGGGCTCCTGCTGGAGTC 60
Qy 1098 CTCGCAATCCCGATGGACACCGGACGCCACCCATTGAGGCTGTTGATCCCGAAGTGAAG 1157
Db 61 CTCGCAATCCCGATGGACACCGGACGCCACCCATTGAGGCTGTTGATCCCGAAGTGAAG 120
Qy 1158 ACTGAGGCTTCGCTGACTCCCTCCTTCTGTCAGCAGGCGATGACACTGGGAGTCACCT 1217
Db 121 ACTGAGGCTTCGCTGACTCCCTCCTTCTGTCAGCAGGCGATGACACTGGGAGTCACCT 180
Qy 1218 CCATACAACTTCTTTACAGGTGAGACACCTGTCCACCTGTTTCCCTCGATAACTAAC 1277
Db 181 CCATACAACTTCTTTAC----- 198
Qy 1278 TCTTTAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGATGCTTTGAT 1337
Db 199 -----AGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGAT----- 239
Qy 1338 TTTCTACGAGCAACTCGGCCCGGACTAATGATTTCTAGGATCATTACCAACCTGTAC 1397
Db 240 -----GATCATTACCAACCTGTAC 260

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Qy 1398 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTGAGCAAAAGGTGAGTTT 1457
Db 261 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTGAGCAAAAG----- 311
Qy 1458 GCTCAGAACCTTGTGGTAAATTAATCATTTGTTACTGACCCCTTTTCAGATTTACCCACACCTT 1517
Db 312 -----GATTTACCCACACCTT 326
Qy 1518 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGTCTACTTTCAATGTTTCC 1577
Db 327 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGTCTACTTTCAATGTTTCC 386
Qy 1578 CAGAGGAACAGAGACTGAGTTAGTTAGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 1637
Db 387 CAGAGGAACAGAGACTGAGTTAGTTAGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 446
Qy 1638 TCTGCACGGCTCCCATCGCTCGCCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCC 1697
Db 447 TCTGCACGGCTCCCATCGCTCGCCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCC 506
Qy 1698 TGGCGAGTACAAGGATTAATACTTTCCCACTACCAATCCCGCCGCTCTGTGGTACCA 1757
Db 507 TGGCGAGTACAAGGATTAATACTTTCCCACTACCAATCCCGCCGCTCTGTGGTACCA 566
Qy 1758 TGACCACGCTTTCATGAAAGGTATGCTACGAGCCCTTATCTTTTCTTGGCTACCTTTGGCTA 1817
Db 567 TGACCACGCTTTCATGA----- 583
Qy 1818 ACCAATCTCTTTCGTAGACTGCTGAGAAATGCCTACTTTTGGTCAGGCTGGCGCCTACATT 1877
Db 584 -----AGACTGCTGAGAAATGCCTACTTTTGGTCAGGCTGGCGCCTACATT 627
Qy 1878 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTGCGATATC 1937
Db 628 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTGCGATATC 687
Qy 1938 CCTCTGATCTTCAGCGGCCAAATGACTATTAACCGCGATGTAACCCCTGCGTTCGACCGAGGTT 1997
Db 688 CCTCTGATCTTCAGCGGCCAAATGACTATTAACCGCGATGTAACCCCTGCGTTCGACCGAGGTT 747
Qy 1998 GAGGACGAGGACCTTGGGGAGATGCTATCCATGCTCAACGACGACCCATGGCCTTCCCTT 2057
Db 748 GAGGACGAGGACCTTGGGGAGATGCTATCCATGCTCAACGACGACCCATGGCCTTCCCTT 807
Qy 2058 AACGTCCAGCCCGCAAGTACCGCTTTCCGATTTCCATACGCTGCGGTCTCTCGTCTTGG 2117
Db 808 AACGTCCAGCCCGCAAGTACCGCTTTCCGATTTCCATACGCTGCGGTCTCTCGTCTTGG 867
Qy 2118 CTCCTCTACCTCGTCAGGACGAGCTCTCCCAACGCTCAGAATTCCTTTCCAAAGTCATTGCC 2177
Db 868 CTCCTCTACCTCGTCAGGACGAGCTCTCCCAACGCTCAGAATTCCTTTCCAAAGTCATTGCC 927
Qy 2178 TCTGATGTGCTGCTCTTCAAGCCCGCTTCAAGACCTTAACCTCTACCTTGTGCTTCC 2237
Db 928 TCTGATGTGCTGCTCTTCAAGCCCGCTTCAAGACCTTAACCTCTACCTTGTGCTTCC 987
Qy 2238 GAGCGTTACGAGATCATTTATTTGGTATGCCCTCTCAGCAATGAGTCAAGAATCTA 2297
Db 988 GAGCGTTACGAGATCATTTATTT----- 1008
Qy 2298 AGACTTAACACTTTGTAGACTTCCACCACTTTGCTGGCCAGACTCTTGACCTCGCAACGTT 2357
Db 1009 -----GACTTCCACCAACTTTGCTGGCCAGACTCTTGACCTCGCAACGTT 1053
Qy 2358 GCTGAGACCAACGATGTCGGGACGAGAGATGAGTACGCTCGCACTCTCGAGGTGATGCC 2417
Db 1054 GCTGAGACCAACGATGTCGGGACGAGAGATGAGTACGCTCGCACTCTCGAGGTGATGCC 1113
Qy 2418 TTCGTGCTGAGCTCTGGCACTGTTGAGGACAAACGACGAGTCCCTCCACATCTCCGTGAC 2477
Db 1114 TTCGTGCTGAGCTCTGGCACTGTTGAGGACAAACGACGAGTCCCTCCACATCTCCGTGAC 1173
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Qy 2478 GTTCCTTTTCCCTCCTCAAGAAGAGGCCCGCCGACAGCACTTCAAGTTTGAACGCAGC 2537
Db 1174 GTTCCTTTTCCCTCCTCACAAGAAGAGGCCCGCCGACAGCACTTCAAGTTTGAACGCAGC 1233
Qy 2538 AACGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCAATGACGCTGCTCGTGCC 2597
Db 1234 AACGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCAATGACGCTGCTCGTGCC 1293
Qy 2598 AAGCCCGAGCTCGGCACCGTTGAGTCTGGAGCTCGAGAACTCCCTCTGGAGGCTGGAGC 2657
Db 1294 AAGCCCGAGCTCGGCACCGTTGAGTCTGGAGCTCGAGAACTCCCTCTGGAGGCTGGAGC 1353
Qy 2658 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCTCAAGCGAACTGGTGGTGGTGGC 2717
Db 1354 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCTCAAGCGAACTGGTGGTGGTGGC 1413
Qy 2718 CAGGTCAATGCGCTACGAGTCTGCTGCTTAAGGATGCTGCTGGCAAGGCTGAG 2777
Db 1414 CAGGTCAATGCGCTACGAGTCTGCTGCTTAAGGATGCTGCTGGCAAGGCTGAG 1473
Qy 2778 ACCCTGACCATCGAGGCCCACTTACCAACCCCTGGACTGGAGCTTACATGTGGCACTGTGCAC 2837
Db 1474 ACCCTGACCATCGAGGCCCACTTACCAACCCCTGGACTGGAGCTTACATGTGGCACTGTGCAC 1533
Qy 2838 AACCTCATTCACGAGGATAACGACATGATGCTGTATTCAAGTCAACGCCCATGGAGGAG 2897
Db 1534 AACCTCATTCACGAGGATAACGACATGATGCTGTATTCAAGTCAACGCCCATGGAGGAG 1593
Qy 2898 AAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCCCTTCCCT 2957
Db 1594 AAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCCCTTCCCT 1653
Qy 2958 TACAACCCCAACGACTTCCATGCTCGCGCTGGAACCTTCTCCGCCGAGTCCATCACTGCC 3017
Db 1654 TACAACCCCAACGACTTCCATGCTCGCGCTGGAACCTTCTCCGCCGAGTCCATCACTGCC 1713
Qy 3018 CGAGTGCAGGAGCTGGCCGACGAGGACCGGTACAACGCCCTCGATGAGATCCTCGAGGAT 3077
Db 1714 CGAGTGCAGGAGCTGGCCGACGAGGACCGGTACAACGCCCTCGATGAGATCCTCGAGGAT 1773
Qy 3078 CTGGAATCGAGGAGTAA 3095
Db 1774 CTGGAATCGAGGAGTAA 1791

RESULT 10
AAA50019
ID AAA50019 standard; DNA; 1791 BP.
XX
AC AAA50019;
XX AC
XX AC
DT 10-Oct-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidising enzyme cDNA.
XX
KW Phenol oxidising enzyme; detergent; bleach; ss.
XX OS
XX Stachybotrys chartarum.
XX
FH Key
FT CDS Location/Qualifiers
FT 7..1791
FT /*tag= a
PN WO200039306-A2.
XX
PD 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-EP10287.
XX
PR 23-DEC-1998; 98US-0220871.
XX
PR 23-JUN-1999; 99US-0338723.
XX
PA (UNIL ) UNILEVER NV.
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PA (UNIL) UNILEVER PLC.
XX (HIND-) HINDUSTAN LEVER LTD.
PI Bodie EA, Van Der Velden S, De Vries CH, Wang H;
XX WPI: 2000-514528/46.
DR P-PSDB; AAY95537.
XX Detergent composition comprising novel phenol oxidising enzyme obtained
PT from fungus or bacteria, useful for pulp and paper bleaching, bleaching
PT color of stains on fabric and for anti-dye redeposition
XX Disclosure; Fig 5A-B; 45pp; English.
XX
CC The present sequence is that of the Stachybotrys chartarum MUCL 38898
CC cDNA encoding a phenol oxidising enzyme (see AAY95537). The invention
CC relates to detergent compositions comprising novel phenol oxidising
CC enzymes that are encoded by nucleic acids capable of hybridising to
CC the S. chartarum phenol oxidising enzyme gene (see AAA50018), provided
CC the enzymes are capable of modifying the colour associated with dyes
CC or coloured compounds, and are produced from a bacterium, yeast or
CC fungus (see AAY95538-40). The phenol oxidising enzymes can be used
CC for pulp and paper bleaching, for bleaching the colour of stains on
CC fabric and for anti-dye transfer in detergent and textile
CC applications. They may also be capable of modifying the colour in
CC the absence or presence of an enhancer. Expression vectors and host
CC cells comprising a nucleic acid encoding a phenol oxidising enzyme,
CC methods for producing the phenol oxidising enzyme, and methods for
CC constructing expression hosts are provided.
XX
SQ Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

Query Match 40.1%; Score 1474; DB 21; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

Qy 1038 GTCATATGCTGTTCAAGTCATGCGCACTGGCAGCAGCCTCCGGCTCCTGCTGGAGTC 1097
Db 1 GTCATATGCTGTTCAAGTCATGCGCACTGGCAGCAGCCTCCGGCTCCTGCTGGAGTC 60

Qy 1098 CTCGGCATCCGATGGACACCGGAGCCACCCCATTTGAGGCTGTGATCCCGAAGTGAAG 1157
Db 61 CTCGGCATCCGATGGACACCGGAGCCACCCCATTTGAGGCTGTGATCCCGAAGTGAAG 120

Qy 1158 ACTGAGGCTTCGCTGACTCCCTCCTGCTGCAGCAGCGATGACGACTGGGAGTCACTT 1217
Db 121 ACTGAGGCTTCGCTGACTCCCTCCTGCTGCAGCAGCGATGACGACTGGGAGTCACTT 180

Qy 1218 CCATACAACTTGCTTTACAGGTGAGACACCTGTCCCACTGTTTCCCTCGATAACTAAC 1277
Db 181 CCATACAACTTGCTTTAC----- 198

Qy 1278 TCTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTTTGAT 1337
Db 199 -----AGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGAT----- 239

Qy 1338 TTTCTACGAAGCAACTCGGCCCCGACTAATGTTCTTAGGATCATTAACCAACCTGTCCAC 1397
Db 240 -----GATCATTAACCAACCTGTCCAC 260

Qy 1398 CGGAAGGACATTTGGTACTATGATGCGAGATCAAGCCATTTTCAGAAAGGGTGAGTTT 1457
Db 261 CGGAAGGACATTTGGTACTATGATGCGAGATCAAGCCATTTTCAGAAAG----- 311

Qy 1458 GCTCAGAAACCTTGTGGTAATTAATCATGTTACTGACCCCTTTTCAGATTTACCCACCTT 1517
Db 312 -----GATTTACCCACCTT 326

Qy 1518 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGCTACTCTTCAATGTTC 1577
Db 327 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGCTACTCTTCAATGTTC 386

Qy 1578 CAGAGGAACAGAGACTGTAGTTAGTTTCATCAACAATGCCACCCTGGGAACTCGGTCCA 1637

Db 387 CAGAGGAACAGAGACTGTAGTTAGTTTCATCAACAATGCCACCCTGGAGAACTCGGTCCA 446
Qy 1638 TCTGCACGGCTCCCATCGCTGCCCTTTTCGATGGTTGGGCTGAAGATGTGACTTCCC 1697
Db 447 TCTGCACGGCTCCCATCGCTGCCCTTTTCGATGGTTGGGCTGAAGATGTGACTTCCC 506
Qy 1698 TGGCGAGCTACAGGATTAATACTTTTCCCACTACCAATCCCGCCGCTTCTGTGTGATACA 1757
Db 507 TGGCGAGTACAGGATTAATACTTTTCCCACTACCAATCCCGCCGCTTCTGTGTGATACA 566
Qy 1758 TGACCAAGCTTTTCATGAAGGATGCTACGAGCCCTTATCTTTCTTGGCTACTCTTGGCTA 1817
Db 567 TGACCAAGCTTTTCATGA----- 583
Qy 1818 ACCAACTTCCTTTTCGTAGCTGCTGAGAATGCCCTACTTTTGGTCAAGCTGGCGCCTACATT 1877
Db 584 -----AGACTGCTGAGAATGCCCTACTTTTGGTCAAGCTGGCGCCTACATT 627
Qy 1878 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTGGATATC 1937
Db 628 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTGGATATC 687
Qy 1938 CCTCTGATCTGAGCGCAAGTACTATAACCCGATGGTACCCTGCGTTTCGACGAGGGT 1997
Db 688 CCTCTGATCTCTGAGCGCAAGTACTATAACCCGATGGTACCCTGCGTTTCGACGAGGGT 747
Qy 1998 GAGGACGAGGACCTGTGGGAGATGTCATCCATGTCACGCGACAGCCATGGCTTTCCTT 2057
Db 748 GAGGACGAGGACCTGTGGGAGATGTCATCCATGTCACGCGACAGCCATGGCTTTCCTT 807
Qy 2058 AACGTCCAGCCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCGGTGCTCTGCTTGG 2117
Db 808 AACGTCCAGCCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCGGTGCTCTGCTTGG 867
Qy 2118 CTCCTCTACCTGTCGACGACAGCTCTCCCAACGTCAGAAATTCCTTTCGAAGTCAATTGCC 2177
Db 868 CTCCTCTACCTGTCGACGACAGCTCTCCCAACGTCAGAAATTCCTTTCGAAGTCAATTGCC 927
Qy 2178 TCTGATGCTGCTCTCTCAAGCCCCCGTTTCAGACCTCTAACCTCTACCTTGTGTTGCC 2237
Db 928 TCTGATGCTGCTCTCTCTCAAGCCCCCGTTTCAGACCTCTAACCTCTACCTTGTGTTGCC 987
Qy 2238 GAGGCTTACGAGATCAATTATTGGTATGCCCCCTCTCTACGAAATGAGTCAAGAATCTA 2297
Db 988 GAGGCTTACGAGATCAATTAT----- 1008
Qy 2298 AGACTAACCTTTGATAGCTTCACCAACTTTTGTCTGGCCAGACTCTTGACCTCGCAACGTT 2357
Db 1009 -----GACTTCACCAACTTTTGTCTGGCCAGACTCTTGACCTCGCAACGTT 1053
Qy 2358 GCTGAGACCAACGATGTCCGGCAGGAGATGAGTACGCTCCACTCTCGAGGTGATGCCG 2417
Db 1054 GCTGAGACCAACGATGTCCGGCAGGAGATGAGTACGCTCCACTCTCGAGGTGATGCCG 1113
Qy 2418 TTCGTGCTGACGCTCTGACACTGTTGAGGACAAACGAGGTCCTCCACTCTCCGCTGAC 2477
Db 1114 TTCGTGCTGACGCTCTGACACTGTTGAGGACAAACGAGGTCCTCCACTCTCCGCTGAC 1173
Qy 2478 GTTCCTTTCCCTCTCTCAAGGAAGGGCCCCCGCCGACAAAGCACTTCAAGTTTGAACGACG 2537
Db 1174 GTTCCTTTCCCTCTCTCAAGGAAGGGCCCCCGCCGACAAAGCACTTCAAGTTTGAACGACG 1233
Qy 2538 AACGGACACTACCTTGATCAACGATGTTGGGCTTTGCGGATGTCAATGAGCGTGTCTGGCC 2597
Db 1234 AACGGACACTACCTTGATCAACGATGTTGGGCTTTGCGGATGTCAATGAGCGTGTCTGGCC 1293
Qy 2598 AAGCCCGAGCTCGGACGCTTGGAGTCTGGGAGTCCGAGAACTCCTCTGGAGGCTGGAGC 2657
Db 1294 AAGCCCGAGCTCGGACGCTTGGAGTCTGGGAGTCCGAGAACTCCTCTGGAGGCTGGAGC 1353
Qy 2658 CACCCCGTCCACATTCACCTTGTGTTGACTTCAAGATTCCTCAAGCGAACTGSGTGGCTGGC 2717
Db 1353 CACCCCGTCCACATTCACCTTGTGTTGACTTCAAGATTCCTCAAGCGAACTGSGTGGCTGGC 2717

Db 1354 CACCCGTCACATTCACCTTGTGACTTCAAGATCCTCAACGGAACCTGGTGGTGGC 1413
Qy 2718 CAGGTATGCCCTACGAGTCTGCTGGTCTTAAGGATGCTGCTGGTGGCAGGGGTGAG 2777
Db 1414 CAGGTATGCCCTACGAGTCTGCTGGTCTTAAGGATGCTGCTGGTGGCAGGGGTGAG 1473
Qy 2778 ACCCTGACCATCGAGGCCGACACTACCAACCGCTGGACTGAGCTTACATGTGGCACTGTAC 2837
Db 1474 ACCCTGACCATCGAGGCCGACACTACCAACCGCTGGACTGAGCTTACATGTGGCACTGTAC 1533
Qy 2838 AACCTCATTCACGAGGATTAACGACATGATGGCTGTATTCAAGCTCACCGCCATGGAGGAG 2897
Db 1534 AACCTCATTCACGAGGATTAACGACATGATGGCTGTATTCAAGCTCACCGCCATGGAGGAG 1593
Qy 2898 AAGGATATCTTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCCCTTCTCT 2957
Db 1594 AAGGATATCTTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCCCTTCTCT 1653
Qy 2958 TACAACCGCAACGACTTCCATGCTCGCGTGGAACTTCTCGCGCGAGTCCATCACTGCC 3017
Db 1654 TACAACCGCAACGACTTCCATGCTCGCGTGGAACTTCTCGCGCGAGTCCATCACTGCC 1713
Qy 3018 CGAGTGCAGGAGCTGGCGGAGCAGGCGGTACAACCGCTCGATGAGATCCTGGAGGAT 3077
Db 1714 CGAGTGCAGGAGCTGGCGGAGCAGGCGGTACAACCGCTCGATGAGATCCTGGAGGAT 1773
Qy 3078 CTTGGAATCGAGGAGTAA 3095
Db 1774 CTTGGAATCGAGGAGTAA 1791

RESULT 11
ID AAA51314 standard; DNA; 1791 BP.
XX
AC AAA51314;
XX
DT 09-OCT-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidizing enzyme cDNA.
XX
KW Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
KW pulp; paper bleaching; ss.
XX
OS Stachybotrys chartarum.
XX Key Location/Qualifiers
FH CDS 7..1791
FT /*tag= a
FT /product= phenol_Oxidizing_Enzyme
XX
XX WO200037654-A2.
PN 29-JUN-2000.
XX
XX 20-DEC-1999; 99WO-US31009.
XX
XX 23-DEC-1998; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.
XX
XX (GENW) GENENCOR INT INC.
XX
XX Wang H, Bodie EA;
XX WPI: 2000-452191/39.
DR P-PSDB; AAY96761.
XX
XX New phenol oxidizing enzyme for modifying colors associated with dyes
XX or colored compounds, is obtained from fungus and is encoded by a
XX nucleic acid comprising a specific nucleotide sequence
XX
XX Disclosure; Fig 5A-B; 45pp; English.

CC This cDNA encodes Stachybotrys chartarum phenol oxidizing enzyme.
CC Phenol oxidizing enzymes encoded by nucleic acid sequences which
CC hybridize to this DNA are claimed, as long as the enzyme is capable of
CC modifying the colour associated with dyes or coloured compounds. The
CC enzymes are useful in detergent compositions and for modifying colors
CC associated with dyes or colored compounds which occur in stains in a
CC sample. The enzymes are also useful for pulp and paper bleaching,
CC anti-dye transfer in detergent and other textile applications.
XX
SQ Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

Query Match 40.1%; Score 1474; DB 21; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

Qy 1038 GTCAATATGCTTCAAGTCATGCAACTGGCAGCAGCTCCGGCTCCTGTCGAGTC 1097
Db 1 GTCAATATGCTTCAAGTCATGCAACTGGCAGCAGCTCCGGCTCCTGTCGAGTC 60

Qy 1098 CTCGCATCCCGATGGACACCGCAGCCACCCATTGAGGCTGTGATCCCGAAGTGAAG 1157
Db 61 CTCGCATCCCGATGGACACCGCAGCCACCCATTGAGGCTGTGATCCCGAAGTGAAG 120

Qy 1158 ACTGAGGCTTCGCTGACTCCTCCTTGTGTCAGCAGGCGATGAGACTGGGAGTCACT 1217
Db 121 ACTGAGGCTTCGCTGACTCCTCCTTGTGTCAGCAGGCGATGAGACTGGGAGTCACT 180

Qy 1218 CCATACAACTTGTCTTACAGGTGAGACACCTGTGCCACCTGTTTCCCTCGATACATAC 1277
Db 181 CCATACAACTTGTCTTAC----- 198

Qy 1278 TCTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTTTGAT 1337
Db 199 -----AGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGAT----- 239

Qy 1338 TTTCTACGAACAACTCGGCCCGCCGACTAATGTATTCTTAGGATCATTTACCAACCTGTGCAC 1397
Db 240 -----GATCATTTACCAACCTGTGCAC 260

Qy 1398 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTCAGCAAGGTTGATTT 1457
Db 261 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTCAGCAAG----- 311

Qy 1458 GCTCAGAAACCTTGTGTGTAATTAATCATTTGTTACTGACCCCTTTCAGATTTACCCACCTTT 1517
Db 312 -----GATTTACCCACCTTT 326

Qy 1518 GGGCCCTGCCACTCTCGTGGCTAGCATGGCATAGCCCTGGTCTCTACTTTCAATGTTCC 1577
Db 327 GGGCCCTGCCACTCTCGTGGCTAGCATGGCATAGCCCTGGTCTCTACTTTCAATGTTCC 386

Qy 1578 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 1637
Db 387 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 446

Qy 1638 TCTGCACGGCTCCCATCGCGTGGCCCTTTGATGGTGGCTGAAGATGTGACCTTCCC 1697
Db 447 TCTGCACGGCTCCCATCGCGTGGCCCTTTGATGGTGGCTGAAGATGTGACCTTCCC 506

Qy 1698 TGGCGAGTACAAGGATTAATACTTTCCCAACTACCAATCCGCGCCCTTCTGTGTGATCCA 1757
Db 507 TGGCGAGTACAAGGATTAATACTTTCCCAACTACCAATCCGCGCCCTTCTGTGTGATCCA 566

Qy 1758 TCACCACGCTTTCATGAAGGTATGCTACGAGCCTTTATCTTCTTGGCTACCTTTGGGCTA 1817
Db 567 TCACCACGCTTTCATGA----- 583

Qy 1818 ACCAACTTCTCTTCGTAGACTGCTGAGAACTGCTACTTTTGGTCAGGCTGGCGCTACATTT 1877
Db 584 -----AGACTGCTGAGAACTGCTACTTTTGGTCAGGCTGGCGCTACATTT 627

Qy 1878 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCTATGGCAGTTCGATATC 1937
Db 1937

Db 628 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGCGTATGCGGAGTTTCGATATC 687

Qy 1938 CCTCTGATCCTGACGGCCAACTACTATAACCCGATGATACCTTGGCTTCGACGAGGGT 1997

Db 688 CCTCTGATCCTGACGGCCAACTACTATAACCCGATGATACCTTGGCTTCGACGAGGGT 747

Qy 1998 GAGGACCAAGGACCTGTGGGAGATGTATCATCATGTCATCAACGACGACCCATGCGCTTTCCTT 2057

Db 748 GAGGACCAAGGACCTGTGGGAGATGTATCATCATGTCATCAACGACGACCCATGCGCTTTCCTT 807

Qy 2058 AACGTCCAGCCCGCCGAACTACCGTTTCGGATTCTCAACGCTGCGGTGCTCTCGTCTGG 2117

Db 808 AACGTCCAGCCCGCCGAACTACCGTTTCGGATTCTCAACGCTGCGGTGCTCTCGTCTGG 867

Qy 2118 CTCCTCTACCTTCGTCAGACCAAGCTCTCCCAACGTCAGAAATTCCTTTCCAAAGTCATTGCC 2177

Db 868 CTCCTCTACCTTCGTCAGACCAAGCTCTCCCAACGTCAGAAATTCCTTTCCAAAGTCATTGCC 927

Qy 2178 TCTGATGCTGGTCTCTTCAAGCCCGCGTTCAGACCTCTAACCTCTACCTTGTCTGTGCC 2237

Db 928 TCTGATGCTGGTCTCTTCAAGCCCGCGTTCAGACCTCTAACCTCTACCTTGTCTGTGCC 987

Qy 2238 GAGCGTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCAGCAATGAGTCAAGAATCTA 2297

Db 988 GAGCGTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCAGCAATGAGTCAAGAATCTA 1008

Qy 2298 AGACTTAACACTTGTAGACTTCACCAACTTTGCTGCCAGACTTGTGACCTCGCAACGTT 2357

Db 1009 -----GACTTCACCAACTTTGCTGCCAGACTTGTGACCTCGCAACGTT 1053

Qy 2358 GGTGAGCAACAGATGTGCGGACGAGGATGAGTACGCTCGCACTCTCGAGGTATGCGC 2417

Db 1054 GGTGAGCAACAGATGTGCGGACGAGGATGAGTACGCTCGCACTCTCGAGGTATGCGC 1113

Qy 2418 TTCGTGCTGAGCTTGGCACTGTGAGGACAAACAGCCAGGTCCCTCCACTCTCCGTGAC 2477

Db 1114 TTCGTGCTGAGCTTGGCACTGTGAGGACAAACAGCCAGGTCCCTCCACTCTCCGTGAC 1173

Qy 2478 GTTCCTTTCCCTCCCAAGGAAGCCCGCCGACAGCACTTCAAGTTTCAAGCGACG 2537

Db 1174 GTTCCTTTCCCTCCCAAGGAAGCCCGCCGACAGCACTTCAAGTTTGAACGACG 1233

Qy 2538 AACGGACACTACCTGATCAACGATTTGGCTTTGCCGATGTCATGAGCGTGTCTCGGCC 2597

Db 1234 AACGGACACTACCTGATCAACGATTTGGCTTTGCCGATGTCATGAGCGTGTCTCGGCC 1293

Qy 2598 AAGCCCGAGCTCGGACCGTTGAGTCTGGGAGCTCGAGACTCTCTGGAGCTGGAGC 2657

Db 1294 AAGCCCGAGCTCGGACCGTTGAGTCTGGGAGCTCGAGACTCTCTGGAGCTGGAGC 1353

Qy 2658 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCCTCAAGCGAACTGGTGGTCTGTGC 2717

Db 1354 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCCTCAAGCGAACTGGTGGTCTGTGC 1413

Qy 2718 CAGGTCATGCCCTACGAGTCTCTGGCTTTAAGGATGCTGTGGTGGGACGAGGTGAG 2777

Db 1414 CAGGTCATGCCCTACGAGTCTCTGGCTTTAAGGATGCTGTGGTGGGACGAGGTGAG 1473

Qy 2778 ACCCTGACATCGAGGCGCCACTACCAACCCCTGGAGTCTGAGGCTTACATGAGCACTGTAC 2837

Db 1474 ACCCTGACATCGAGGCGCCACTACCAACCCCTGGAGTCTGAGGCTTACATGAGCACTGTAC 1533

Qy 2838 AACCTCATTCACGAGGATACACATGATGGCTGTATTCAAGCTCACGCCCATGAGGAG 2897

Db 1534 AACCTCATTCACGAGGATACACATGATGGCTGTATTCAAGCTCACGCCCATGAGGAG 1593

Qy 2898 AAGGGATATCTTTCAGGAGACTTCGAGGACCCCATGAACCCCAAGTGGCGCCGCTTCCT 2957

Db 1594 AAGGGATATCTTTCAGGAGACTTCGAGGACCCCATGAACCCCAAGTGGCGCCGCTTCCT 1653

Qy 2958 TACACCGCAACGACTTTCATGCTCGCGTGGAAACTTCTCCGCGAGTCCATCACTGCC 3017

Db 1654 TACACCGCAACGACTTTCATGCTCGCGTGGAAACTTCTCCGCGAGTCCATCACTGCC 1713

Qy 3018 CGAGTGCAGGAGCTGGCCGACGAGGACCGTACAAACCCCTCGATGAGATCCTGGAGAT 3077

Db 1714 CGAGTGCAGGAGCTGGCCGACGAGGACCGTACAAACCCCTCGATGAGATCCTGGAGAT 1773

Qy 3078 CTTGGAATCGAGGAGTAA 3095

Db 1774 CTTGGAATCGAGGAGTAA 1791

RESULT 12

AAL47584

ID AAL47584 standard; cDNA; 1791 bp.

XX AAL47584;

XX AC AC

XX DT 13-SEP-2002 (first entry)

XX S chartarum phenol oxidising enzyme cDNA.

DE Phenol oxidising enzyme; enzyme; fungus; redox reaction; detergent;

XX paper industry; pulp industry; textile; food industry; gene; ss.

XX Stachybotrys chartarum.

OS

XX Key Location/Qualifiers

FT CDS 7..1791

FT /*tag= a

FT /product= "phenol oxidising enzyme"

XX US6399329-B1.

XX PD 04-JUN-2002.

XX PF 21-DEC-1999; 99US-0468578.

XX PR 12-DEC-1998; 98US-0220871.

XX PR 23-JUN-1999; 99US-0338723.

XX PA (GENV) GENENCOR INT INC.

XX PI Wang H, Bodie EA;

XX DR WPI; 2002-498835/53.

XX DR P-PSDB; AAO18210.

XX PT New polynucleotides encoding phenol oxidizing enzymes, useful for preventing the transfer of dyes in solution from one textile to another during detergent washing -

XX PS Disclosure; Fig 5; 37pp; English.

XX CC The present invention provides the protein and coding sequences of phenol oxidising enzymes from Stachybotrys chartarum, Bipolaris spicifera and Curvularia pallens. These enzymes are useful in the textiles, paper, pulp, detergent and food industries. In particular they are useful for preventing the transfer of dyes in solution from one textile to another during detergent washing (dye transfer inhibition). The present sequence is the S. chartarum phenol oxidising enzyme cDNA.

XX SQ Sequence 1791 bp; 380 A; 551 C; 451 G; 409 T; 0 other;

Query Match 40.1%; Score 1474; DB 24; Length 1791;

Best Local Similarity 87.0%; Pred. No. 0;

Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

Qy 1038 GTCATATGCTGTTCAAGTCAATGGCACTGGCAGAGCTCCGGGCTCTGTCTGGAGTC 1097

Db 1 GTCATATGCTGTTCAAGTCAATGGCACTGGCAGAGCTCCGGGCTCTGTCTGGAGTC 60

Qy 1098 CTCGGCATCCCGATGGACACCGGACGCCACCCATTGAGGCTGTTGATCCCGAAGTGAAG 1157

Db 61 CTCGGCATCCCGATGGACACCGGACGCCACCCATTGAGGCTGTTGATCCCGAAGTGAAG 120

QY 1158 ACTGAGGTCTTCGCTGACTCCCTCTGCTGCGACGAGCGGATGACGACTGGGAGTCACCT 1217
|||||
Db 121 ACTGAGGTCTTCGCTGACTCCCTCTGCTGCGACGAGCGGATGACGACTGGGAGTCACCT 180
QY 1218 CCATACAACTTGGCTTTACAGGTGAGACACCTGTGCCACCTGTTTCCCTCGATACAACTAC 1277
|||||
Db 181 CCATACAACTTGGCTTTAC 198
QY 1278 TCTTTATAGGAATGCCCTGCGCAATTCACACTGTCAAGCAGCCCAAGATGTATGCTTTTGAT 1337
|||||
Db 199 -----AGGAATGCCCTGCGCAATTCACACTGTCAAGCAGCCCAAGAT 239
QY 1338 TTTCTACGAAGCAACTGCGGCCCGGACTAATGTATCTAGGATCATPACCAACCTGTCTAC 1397
|||||
Db 240 -----GATCAITPACCAACCTGTCTAC 260
QY 1398 CGCAAGGACATTTGGTACTATGATGATCGAGATCAAGCCATTTCAAGCAAGGTTGATTT 1457
|||||
Db 261 CGCAAGGACATTTGGTACTATGATGATCGAGATCAAGCCATTTCAAGCAAG 311
QY 1458 GCTCAAAACCTTGTGGTAATTAAATCATTTGTTACTGACCCCTTTTCAGATTTACCCACCTT 1517
|||||
Db 312 -----GATTTACCCACCTT 326
QY 1518 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGTCTCTACTTTTCAATGTTCC 1577
|||||
Db 327 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGTCTCTACTTTTCAATGTTCC 386
QY 1578 CAGAGAACAGAGACTGTAGTTAGGTTTCATCAACATGCCACCGTGGAGAACTCGGTCCA 1637
Db 387 CAGAGAACAGAGACTGTAGTTAGGTTTCATCAACATGCCACCGTGGAGAACTCGGTCCA 446
QY 1638 TCTGCACGGCTCCCACTCGCGTCCCTTTTCGATGGTTGGGTGAAGATGTGACCTTTCC 1697
Db 447 TCTGCACGGCTCCCACTCGCGTCCCTTTTCGATGGTTGGGTGAAGATGTGACCTTTCC 506
QY 1698 TGGCGAGTACAGGATTTACTTTCCCAACTACCAATCCGCGCGCTTCTGTGGTACCA 1757
Db 507 TGGCGAGTACAGGATTTACTTTCCCAACTACCAATCCGCGCGCTTCTGTGGTACCA 566
QY 1758 TGACCACGCTTTTCATCAAGGTATGCTACGAGCCTTTATCTTTCTTGGCTACCTTTGGCTA 1817
Db 567 TGACCACGCTTTTCATCA 583
QY 1818 ACCAACTTCTCTTCTGTPAGACTGCTGAGATGCTCTACTTTGGTCAGGCTGGCGCTACATTT 1877
Db 584 -----AGACTGCTGAGATGCTCTACTTTGGTCAGGCTGGCGCTACATTT 627
QY 1878 ATCAAGCAGAGGCTGAGGATGCTTCGGTCTTCTCTAGTGGCTATGGCGAGTTTCGATATC 1937
Db 628 ATCAAGCAGAGGCTGAGGATGCTTCGGTCTTCTCTAGTGGCTATGGCGAGTTTCGATATC 687
QY 1938 CTTCTGATCCTGACGGCCAAAGTACTATAACGGCGATGTTACCTCGGTTTCGACCGAGGCT 1997
Db 688 CTTCTGATCCTGACGGCCAAAGTACTATAACGGCGATGTTACCTCGGTTTCGACCGAGGCT 747
QY 1998 GAGGACAGGACCTGTGGGAGATGTCATCCATGTCAACGGCAGACCATGGCTTTCCCTT 2057
Db 748 GAGGACAGGACCTGTGGGAGATGTCATCCATGTCAACGGCAGACCATGGCTTTCCCTT 807
QY 2058 AAGTCCAGCCCGCAAGTACCGTTTCGATTTCTCAACGCTGCCGTGCTCTCGTGGTTGG 2117
Db 808 AAGTCCAGCCCGCAAGTACCGTTTCGATTTCTCAACGCTGCCGTGCTCTCGTGGTTGG 867
QY 2118 CTCCTTACTCTGCTCAGGACCAAGCTCTCCCAAGCTCAGAAATTCCTTTCCAAGTCAATGCC 2177
Db 868 CTCCTTACTCTGCTCAGGACCAAGCTCTCCCAAGCTCAGAAATTCCTTTCCAAGTCAATGCC 927
QY 2178 TCTGATGCTGGTCTCTTCAAGCCCGCTTCAGACCTCTAACCTCTACCTTCTGCTGTGCC 2237
Db 928 TCTGATGCTGGTCTCTTCAAGCCCGCTTCAGACCTCTAACCTCTACCTTCTGCTGTGCC 987

QY 2238 GAGCGTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCACGAATCAGTCAAGAAGTCTTA 2297
|||||
Db 988 GAGCGTTACGAGATCATTTATTT 1008
QY 2298 AGACTAAACACTTTGTAGACTTTCACCAACTTTGCTGGCAGACTCTTGACCTGGCAACGTT 2357
|||||
Db 1009 -----GACTTCAACCAACTTTGCTGGCAGACTCTTGACCTGGCAACGTT 1053
QY 2358 GGTGAGACCAACGATGTTCGGCGACGAGGATGAGTAGCTCGCACTCTCGAGGTGATGCGC 2417
|||||
Db 1054 GCTGAGACCAACGATGTTCGGCGACGAGGATGAGTAGCTCGCACTCTCGAGGTGATGCGC 1113
QY 2418 TTCGTCGTGAGCTCTGCGCACTGTTCGAGGACACAGCCAGGTCCCTTCCACTCTCCGTGAC 2477
|||||
Db 1114 TTCGTCGTGAGCTCTGCGCACTGTTCGAGGACACAGCCAGGTCCCTTCCACTCTCCGTGAC 1173
QY 2478 GTTCTCTTCCCTCCCTCACAAAGGAAGCCCGCGACAAAGCACTTCAAGTTTGAACGACG 2537
|||||
Db 1174 GTTCTCTTCCCTCCCTCACAAAGGAAGCCCGCGACAAAGCACTTCAAGTTTGAACGACG 1233
QY 2538 AACGGACACTACCTGATCAACGATGTTCGCTTTTGGCGATGTCAATGAGCGTGTCTCTGGCC 2597
Db 1234 AACGGACACTACCTGATCAACGATGTTCGCTTTTGGCGATGTCAATGAGCGTGTCTCTGGCC 1293
QY 2598 AAGCCGGAGCTCGGCACCGCTTGAGGTCTGGAGCTCGAGAACTCTCTGGAGGCTGGAGC 2657
Db 1294 AAGCCGGAGCTCGGCACCGCTTGAGGTCTGGAGCTCGAGAACTCTCTGGAGGCTGGAGC 1353
QY 2658 CACCCGCTCCACATTCACCTTTGTTGACTTCAAGATCCTCAAGCGAACTGGTGTCTGTGCC 2717
Db 1354 CACCCGCTCCACATTCACCTTTGTTGACTTCAAGATCCTCAAGCGAACTGGTGTCTGTGCC 1413
QY 2718 CAGGTATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCTCTGGTGGCGAGGGGTGAG 2777
Db 1414 CAGGTATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCTCTGGTGGCGAGGGGTGAG 1473
QY 2778 ACCGTGACCATCGAGGCCCACTACCAACCTTGAGCTGGAGCTTTACATGTGGCACTGTCTAC 2837
Db 1474 ACCGTGACCATCGAGGCCCACTACCAACCTTGAGCTGGAGCTTTACATGTGGCACTGTCTAC 1533
QY 2838 AACCTCATTCACGAGGATAACGACATGATGGTGTATTCAAGCTCACCCCATGGAGGAG 2897
Db 1534 AACCTCATTCACGAGGATAACGACATGATGGTGTATTCAAGCTCACCCCATGGAGGAG 1593
QY 2898 AAGGATATCTTCAGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCGTTCCT 2957
Db 1594 AAGGATATCTTCAGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCGTTCCT 1653
QY 2958 TACACCGCAACGACTTCCATGCTCGCGTGGAAACTTCTCCGCCAGTCCATCACTGCC 3017
Db 1654 TACACCGCAACGACTTCCATGCTCGCGTGGAAACTTCTCCGCCAGTCCATCACTGCC 1713
QY 3018 CGAGTGCAGAGCTGGCCGAGGAGCGGTACAAACGCTCGATCAGATCAGATCCTGGAGGAT 3077
Db 1714 CGAGTGCAGAGCTGGCCGAGGAGCGGTACAAACGCTCGATCAGATCAGATCCTGGAGGAT 1773
QY 3078 CTTGGAATCGAGGAGTAA 3095
Db 1774 CTTGGAATCGAGGAGTAA 1791

RESULT 13
AAZ25727
ID AAZ25727 standard; cDNA; 1791 BP.
XX
AC AAZ25727;
XX
DT 05-JAN-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidising enzyme encoding cDNA.
XX Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
KW detergent; anti-dye transfer; stain removal; bleaching; ss.

```
XX Stachybotrys chartarum.
XX OS
XX PN
XX WO9949010-A2.
XX PD
XX 30-SEP-1999.
XX PF
XX 23-MAR-1999; 99WO-EP02042.
XX PR
XX 24-MAR-1998; 98US-0046969.
XX PR
XX 22-DEC-1998; 98US-0218702.
XX PA
XX (UNIL ) UNILEVER NV.
XX PA
XX (UNIL ) UNILEVER PLC.
XX
XX Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;
XX Wang C;
XX
XX WPI; 1999-601211/51.
XX DR
XX P-PSDB; AAY45222.
XX
XX PT
XX Detergent composition containing phenol oxidase from Stachybotrys, used
XX to bleach stains and prevent dye transfer -
XX
XX PS
XX Example 15; Fig 5; 56pp; English.
XX
XX The present invention describes a detergent composition containing a
XX purified phenol oxidising enzyme derived from Stachybotrys. The present
XX sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The
XX enzyme can be used to modify the colour of dyes and other coloured
XX compounds (e.g. for use in pulp and paper bleaching also for removing
XX stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
XX transfer during fabric washing.
XX
XX SQ
XX Sequence 1791 BP; 380 A; 554 C; 448 G; 409 T; 0 other;

Query Match 40.0%; Score 1469.2; DB 20; Length 1791;
Best Local Similarity 86.9%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 3; Indels 267; Gaps 5;

QY 1038 GTCATATGCTCTCAAGTCATGGAATGGCAGAGCTCGGGCTCCTGTCGTGAGTC 1097
DB 1 GTCATATGCTCTCAAGTCATGGAATGGCAGAGCTCGGGCTCCTGTCGTGAGTC 60
QY 1098 CTCGGCATCCCGATGGACACCGCGACGCCACCCATTGAGGCTGTTGATCCCGAAGTGAAG 1157
DB 61 CTCGGCATCCCGATGGACACCGCGACGCCACCCATTGAGGCTGTTGATCCCGAAGTGAAG 120
QY 1158 ACTGAGGCTTCGCTGACTCCCTCTTGGTGCGAGGGGATGAGACTGGGAGTCACT 1217
DB 121 ACTGAGGCTTCGCTGACTCCCTCTTGGTGCGAGGGGATGAGACTGGGAGTCACT 180
QY 1218 CCATACAACTTCTTACAGGTGAGACACCTGTCCACCTGTTTCCCTCGATACTAAC 1277
DB 181 CCATACAACTTCTTAC----- 198
QY 1278 TCTTTAGGAATGCCCTGCCAATTCACCTGTCAAGCAGGCCCAAGATGATGCTTTGAT 1337
DB 199 -----AGGAATGCCCTGCCAATTCACCTGTCAAGCAGGCCCAAGAT----- 239
QY 1338 TTTCTACGAAGCAACTCGGCCCCCGACTAATGATTTCTAGGATCATATACAAACCCGTGAC 1397
DB 240 -----GATCATTTACCAACCCGTGAC 260
QY 1398 CGGCAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAGGGTGATTT 1457
DB 261 CGGCAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAG----- 311
QY 1458 GCTCAGAAACCTTGTGGTAATTAATCATTTGACTGACCCCTTCAGATTTACCCCAACCTT 1517
DB 312 -----GATTTACCCCAACCTT 326
QY 1518 GCGCCCTGCCACTCTCGTCGGGTACGATGGCATGAGCCCTGGTCCTACTTTCAATGTTCC 1577
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DB 327 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGTCCTACTTTCAATGTTCC 386
QY 1578 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 1637
DB 387 CAGAGGAACAGAGACTGTAGTTAGTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 446
QY 1638 TCTGCAGGGCTCCCATCGCTGCCCTTTTCGATGGTTGGCTGAAGATGTGACTTCCC 1697
DB 447 TCTGCAGGGCTCCCATCGCTGCCCTTTTCGATGGTTGGCTGAAGATGTGACTTCCC 506
QY 1698 TGGCGAGTACAAGGATTACTACTTTCCAACTACCAATCCGCCGCCCTTCTGTGTATACA 1757
DB 507 TGGCGAGTACAAGGATTACTACTTTCCAACTACCAATCCGCCGCCCTTCTGTGTATACA 566
QY 1758 TGACCACGCTTTTCATGAAGGTATGCTACGAGCCTTTATCTTTCTTGGCTACCTTTGGCTA 1817
DB 567 TGACCACGCTTTTCATGA----- 583
QY 1818 ACCAACTTCTTTTCGTAGCTGCTGAGAAATGCCTACTTTGGTCAGGCTGGCGCCTACATT 1877
DB 584 -----AGACTGCTGAGAAATGCCTACTTTGGTCAGGCTGGCGCCTACATT 627
QY 1878 ATCAACGACGAGGCTGAGGATGCTCTCGTCTTCTCTAGTGGCTATGCGAGTTCGATATC 1937
DB 628 ATCAACGACGAGGCTGAGGATGCTCTCGTCTTCTCTAGTGGCTATGCGAGTTCGATATC 687
QY 1938 CCTCTGATCCTTGACGGCCAAAGTACTATTAACGCCGATGTACCTCGTTCGACCCAGGGT 1997
DB 688 CCTCTGATCCTTGACGGCCAAAGTACTATTAACGCCGATGTACCTCGTTCGACCCAGGGT 747
QY 1998 GAGGACGAGGACCTGTGGGAGATGTATCATGTATCAACGACGACGATGGCCTTTCCT 2057
DB 748 GAGGACGAGGACCTGTGGGAGATGTATCATGTATCAACGACGACGATGGCCTTTCCT 807
QY 2058 AACGTCAGGCCGCCCAAGTACCGTTTCGATTTCCATCAAGCTGCGCTCTCTCGTCTTGG 2117
DB 808 AACGTCAGGCCGCCCAAGTACCGTTTCGATTTCCATCAAGCTGCGCTCTCTCGTCTTGG 867
QY 2118 CTCCTCTACCTCGTCAGGACCAAGCTCTCCCAACGTCAGAAATTCCTTCCAAAGTCAATGCC 2177
DB 868 CTCCTCTACCTCGTCAGGACCAAGCTCTCCCAACGTCAGAAATTCCTTCCAAAGTCAATGCC 927
QY 2178 TCTGATGCTGGTCTCCTTCAAGCCCCCGTTGAGACCTCTAACCTCTACCTTGTCTTGGC 2237
DB 928 TCTGATGCTGGTCTCCTTCAAGCCCCCGTTGAGACCTCTAACCTCTACCTTGTCTTGGC 987
QY 2238 GAGCGTTACGAGATCATTTATGGTATGCCCTCCCTCTCACGAATGAGTCAAGAATCTTA 2297
DB 988 GAGCGTTACGAGATCATTTAT----- 1008
QY 2298 AGACTTAACACTTGTAGACTTTCACCAACTTTGCTGGCCAGACTCTTTGAGCTGCGCAACGTT 2357
DB 1009 -----GACTTCACCAACTTTGCTGGCCAGACTCTTTGAGCTGCGCAACGTT 1053
QY 2358 GCTGAGACCAAGATGTGCGGACGAGGATGATGAGTTCGCACTCTCGAGGTGATGGC 2417
DB 1054 GCTGAGACCAAGATGTGCGGACGAGGATGATGAGTTCGCACTCTCGAGGTGATGGC 1113
QY 2418 TTCGTCGTGAGTCTGCGACTGTTGAGGACACAGCCAGGTCCCTCCACTCTCGGTGAC 2477
DB 1114 TTCGTCGTGAGTCTGCGACTGTTGAGGACACAGCCAGGTCCCTCCACTCTCGGTGAC 1173
QY 2478 GTTCTCTTCCCTCCCTCACAAGGAAGCCCGCCGACAAAGCACTTCAAGTTTCAAGCGCAGC 2537
DB 1174 GTTCTCTTCCCTCCCTCACAAGGAAGCCCGCCGACAAAGCACTTCAAGTTTCAAGCGCAGC 1233
QY 2538 AACGACACTTACCTGATCAACGATGTGGCTTTGCCGATGTCAATGAGGCTGTCTGTGGCC 2597
DB 1234 AACGACACTTACCTGATCAACGATGTGGCTTTGCCGATGTCAATGAGGCTGTCTGTGGCC 1293
QY 2598 AAGCCCGAGCTCGGCACCGCTTGAGGTCTGGGAGCTCGAGAACTCTCTCGAGGCTGGAGC 2657
DB 1293 AAGCCCGAGCTCGGCACCGCTTGAGGTCTGGGAGCTCGAGAACTCTCTCGAGGCTGGAGC 2657
```

Db 1294 AAGCCGAGCTCGGCACCGTTGAGGTCCTGGGAGCTCGAGAACTCCTCTGGAGGCTGGACC 1353
QY 2658 CACCCGCTCCACATTCACCTTGTGACTTCAAGATCCCTCAAGCGAAGCTGGTGGTCTGGGC 2717
Db 1354 CACCCGCTCCACATTCACCTTGTGACTTCAAGATCCCTCAAGCGAAGCTGGTGGTCTGGGC 1413
QY 2718 CAGGTCATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCGTCTGGTGGGAGGGGTGAG 2777
Db 1414 CAGGTCATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCGTCTGGTGGGAGGGGTGAG 1473
QY 2778 ACCCTGACCATCGAGGCCACCTACCAACCCCTGGAGCTTACATGTGGCACTGTCTAC 2837
Db 1474 ACCCTGACCATCGAGGCCACCTACCAACCCCTGGAGCTTACATGTGGCACTGTCTAC 1533
QY 2838 AACCTATTACGAGGATAACGACATGATGGCTGTATTCAACGTCAACGCCCATGGAGGAG 2897
Db 1534 AACCTATTACGAGGATAACGACATGATGGCTGTATTCAACGTCAACGCCCATGGAGGAG 1593
QY 2898 AAGGATATCTTCAGGAGACTTCGAGGACCCATGAACCCCAAGTGGCGCCCTTCTT 2957
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QY 2958 TACAACCGCAACGACTTCCATGCTGGCGCTGGAAACTTCTCCGCCGAGTCCATCACTGCC 3017
Db 1654 TACAACCGCAACGACTTCCATGCTGGCGCTGGAAACTTCTCCGCCGAGTCCATCACTGCC 1713
QY 3018 CGAGTGCAGGAGCTGGCGGAGGAGCGGTACAAACCGCCTCGATGAGATCCTGGAGGAT 3077
Db 1714 CGAGTGCAGGAGCTGGCGGAGGAGCGGTACAAACCGCCTCGATGAGATCCTGGAGGAT 1773
QY 3078 CTTGGAATCGAGGAGTAA 3095
Db 1774 CTTGGAATCGAGGAGTAA 1791

RESULT 14
AAZ61243
ID AAZ61243 standard; DNA; 2110 BP.
XX
AC AAZ61243;
XX
DT 30-MAY-2000 (first entry)
XX
DE DNA encoding a phenol oxidising enzyme.
XX
KW Phenol oxidizing enzyme; fungus; redox reaction; detergent; bleaching;
KW fabric; pulp; paper; decolourisation; plant-derived food product;
KW coloured compound; porphyrin; tannin; polyphenol; carotenoid;
KW anthocyanin; Maillard reaction product; ss.
XX
OS Acremonium murorum.
XX
FH Key Location/Qualifiers
FT CDS 135..1943
FT /tag= a
FT /product= "phenol oxidising enzyme"
XX
PN WO200005349-A1.
XX
PD 03-FEB-2000.
XX
PF 13-JUL-1999; 99WO-EP04922.
XX
PR 21-JUL-1998; 98EP-0202454.
XX
PA (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
XX
PI (HIND-) HINDUSTAN LEVER LTD.
XX
DR Convents D, Gouka RJ, Van Der Heiden M, Swarthoff T, Verrips CT;
XX WPI; 2000-195101/17.
DR P-PSDB; AAY69204.

XX Phenol-oxidizing enzyme from Acremonium, used in detergent compositions
PT for bleaching stains on fabrics -
XX
PS Example 2; Page 37-40; 45pp; English.
XX
CC The present sequence encodes a phenol oxidizing enzyme from the
CC fungus Acremonium murorum. The enzyme has the CBS accession number
CC 157.72. The enzyme catalyses redox reactions and is specific for
CC molecular oxygen as the electron acceptor. The phenol oxidising enzyme
CC is specifically used in detergents for bleaching strains on fabrics,
CC but also for bleaching pulp and paper and for decolourisation of
CC plant-derived food products. The enzyme has a pH optimum in the
CC alkaline to neutral range and can bleach a wide variety of coloured
CC compounds, e.g. porphyrins, tannins, polyphenols, carotenoids,
CC anthocyanins and Maillard reaction products.
XX
SQ Sequence 2110 BP; 400 A; 732 C; 556 G; 422 T; 0 other;

Query Match 13.8%; Score 507.6; DB 21; Length 2110;
Best Local Similarity 61.3%; Pred. NO. 1.2e-139;
Matches 969; Conservative 0; Mismatches 479; Indels 134; Gaps 4;

QY 1501 CAGATTATCCCCACCTTGGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGT 1560
Db 459 CAGGTCCTTCCCTGACCTGGGGCTGCTGACCTCGTGGGCTACGAGCGCATCTCGCCCGGT 518
QY 1561 CCTACTTCAATGTTCCCGAGAGAACAGAGACTGTAGTTAGTTCATCAACAATGCCAC 1620
Db 519 CCTACTTCAATGTTCCCGAGAGAACAGAGACTGTAGTTAGTTCATCAACAATGCCAC 1620
QY 1621 GTGGAGAACTCGTCCATCTGCACGGCTCCCATCGCTGCCCTTTCGATGTTGGGCT 1680
Db 579 GTCGAGAGCTCCATCCATCTTCAAGGCTGTTGAGGCTGCGGCTTGTGAAAGGCCACT 578
QY 1681 GAAGATGTGACCTTCCCTGGCGAGTACAAGGATTACTACTTTCCTCCCACTACCAATCCGCC 1740
Db 639 GAGGATGTCAACACCCCGGCGAGTACAAGGACTACTACTATCCCAATGCGCAGCGGGG 698
QY 1741 CGCCTTCTGTGTACCATGACCAACGCTTTCATGAAGGTATGCTACGAGGCTTTATCTTTC 1800
Db 699 CGCTTCTGTGTACCATGACCAATGCT----- 725
QY 1801 TTGGCTACTTTTGGCTAACCAACTTCTTCTGTAGACTGCTGAGAATGCTACTTTTGGTTC 1860
Db 726 -----ATGCTATGAGACTGCGGAGAATGCTTACAACGGCC 759
QY 1861 AGGCTGGCGCTTACATTTATCAACGAGAGGCTGAGGATGCTCTCGTCTTCTTAGTGGCT 1920
Db 760 AGGCTGGTGGTGTACATCATCCACGACCTTCCGCGAGGATTCCTCTCGGTCTGCGCAGCGGAT 819
QY 1921 ATGGCGAGTTGCTGATATCCCTGCTGATCCTGACGGCCAAAGTACTATAACGCGGATGTACCC 1980
Db 820 ATGGAGAGTACGACATCCCTCTCATCTGACTTCAAGAGCAGTACAACCTCCGAGGTTACTTC 879
QY 1981 TCGGTTCCGACGAGGTTGAGGACGAGGCTGTGGGAGATGTATCCATGTCAACGGAC 2040
Db 880 TCTTCTCTACCAAGGTTGAGAGCGAGTCTCTGGGAGATGTATCCAGGTGAACGGAG 939
QY 2041 ACCCATGGCCCTTTCCTTAACGTTCCAGCCCGCCGAAGTACGGTTTCCGATTCCTCAACGGTG 2100
Db 940 TCCCGTGGCCCTTCTGACGCTTGAGCCCGAGGAAGTACCGCTTCCGCTTCTGCGCAGCGG 999
QY 2101 CCGTGTCTGCTGGTGGCTCTTACCTCGTCAAGCAGGCTCTCCCAACGTCAGAAATTC 2160
Db 1000 CCGTCTCTGCTGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1059
QY 2161 CTTTCCAAAGTCAATGCCCTCTGATGCTGGTCTCTTCAAGCCCGCCGTTTCAGACCTCTAACC 2220
Db 1060 CGTTCAGGTTCAATGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1119
QY 2221 TCTACCTTGTGTTGGCGGAGGTTACGAGATCATATTGTTGTTATGCGCTTCCCTCTCTCACA 2280
Db 1119 TCTACCTTGTGTTGGCGGAGGTTACGAGATCATATTGTTGTTATGCGCTTCCCTCTCTCACA

Db 1120 TCGTCTCTCCATTGCTGAGCGCTACGAGATCA----- 1152
Qy 2281 ATGAGTCAAGAACTCTAAGACTAATCTGTAGACTTCACCAACTTTGCTGGCGAGACTC 2340
Db 1153 -----TCCTCGACTTCTCCGACTTCGAGGGCAAGACCA 1185
Qy 2341 TTGACCTCGCAAGCTTGTCTGAGACCAACAGATGTCGGCGACGAGGATGAGTACGCTCGCA 2400
Db 1186 TCGAGCTCCGCAACAGAGCCCGGTCGGCGGCTCGGCATCGAGGTCAACTACGACGACA 1245
Qy 2401 CTCTCGAGGTGATGGGCTTCGTCGTGCTGACCTCTGGACTGTT-----GAGACACACGCC 2454
Db 1246 CCGACAGGTCTCGGCTTCAACGTCGCGAGGGCCCCCTCTCCTCGCCGACACCTCCG 1305
Qy 2455 AGGTCCCTCCACTCTCGTGCAGCTTCCTTTCCTCTCCTCAAGGAAGGCCCGCCGACCA 2514
Db 1306 TCGTCCCCCTCCACCTCCGTCGAGGTGCCCTTCCCCCTCCAGCACCTCGACCACCTCGACC 1365
Qy 2515 AGCACTTCAAGTTTGAACGCAAGCAACGACACACTACTCTGATCAACGATGTTGGCTTTTGCCG 2574
Db 1366 ACTCGTTCGGCTTCGCCCGCACCCGCCGCGAGTGAGGATCAACGGTGTCACTTCTCCG 1425
Qy 2575 ATGTCAATGAGCGTGTCTGCGCAAGCCCGAGCTCGCGCACCGTTGAGGTCTGGGAGCTCG 2634
Db 1426 ACGTCGAGAAGCGGCTGTGGCCAACTGTGCCCTTGGCACCGTCCAGCTGTGGCAGCTGA 1485
Qy 2635 AGAATCTCTCGGAGGCTGGAGCCAGCCCGTCCACATTCACCTTGTTCACCTCAAGATCC 2694
Db 1486 CGAAGCGGCGAGGCTGGAGCATCTATTCACATCCATCTTGTTCACCTCAAGATTC 1545
Qy 2695 TCAAGCGAAGTGGTGGTGGT-----GGCCAGGTGATGCCCTACGAGTCTG 2739
Db 1546 TGTCTCGCACGGTGTCTACGGGTGCTACGACCCGTGGTGTGCGAGCGTACGAGTCTG 1605
Qy 2740 CTGGTCTTAAGATGTCTGTGGTGGCGAGGGGTGAGACCCCTGACCATCGAGGCCCACT 2799
Db 1606 CTGGTCTGAAGGACGTCTGTACCTCGGCAAGGAGAGACGGTCTGCTCGAGGCTCACT 1665
Qy 2800 ACCAACCCTGGACTGGAGCTTACATGTGCACTGTCACAACTCATTCACGAGGATAACG 2859
Db 1666 AGCTTCCTTGGCCCGCGGTGTACATGTTCCACTGGCCACAACTCATCCACGAGGACAAG 1725
Qy 2860 ACATGATGGCTGTATTAACGCTACCCGATCGGAGGAGAGGATATCTTCAGGAGGACT 2919
Db 1726 ACATGATGGCGCCCTTCAAGCTCACCGTCTCCCGGACTACGGCTACAACTCGACGGCCC 1785
Qy 2920 TCGAGGACCCCATGAACCCCAAGTGGCGCGGTTCCTTACACCCGCAACGACTTCCATG 2979
Db 1786 TCGCTGACCCCATGACGACGAGTTCGCGCCCAAGCCGTACGTGGACAACGACGTCGAGG 1845
Qy 2980 CTCGCGCTGGAAACTTCTCCGCGAGTCCATCACTACGTCGCCGAGTGCAGGAGTGGCCGAGC 3039
Db 1846 TCGCGGAGAACCCCTTCAGCACCGAGAGATCGAGGCGAGGTCCAGCTGATGGCCAGCT 1905
Qy 3040 AGGAGCCGTACAAACCGCTCGA 3061
Db 1906 ACCTGCCCTACGACAACCCGGA 1927

RESULT 15
AAA50020
ID AAA50020 standard; DNA; 2905 BP.

AC AAA50020;

XX 10-OCT-2000 (first entry)

DE Bipolaris spicifera phenol oxidising enzyme gene.

KW Phenol oxidising enzyme; detergent; bleaching; ds.

XX Bipolaris spicifera.

OS

Key Location/Qualifiers
CDS 114..2179
FT /*tag= a
FT /note= "contains introns"
FT exon 114..361
FT /*tag= b
FT /number= 1
FT intron 362..417
FT /*tag= c
FT exon 418..698
FT /*tag= d
FT /number= 2
FT intron 699..763
FT /*tag= e
FT exon 764..828
FT /*tag= f
FT /number= 3
FT intron 829..889
FT /*tag= g
FT exon 890..2179
FT /*tag= h
FT /number= 4

WO200039306-A2.

06-JUL-2000.

20-DEC-1999; 99WO-EP10287.

23-DEC-1998; 98US-0220871.

23-JUN-1999; 99US-0338723.

(UNIL) UNILEVER NV.

(UNIL) UNILEVER PLC.

(HIND-) HINDUSTAN LEVER LTD.

Bodie EA, Van Der Velden S, De Vries CH, Wang H;

WPI: 2000-514528/46.

P-PSDB; AAY95538.

Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition -

Example 5; Fig 2; 45pp; English.

XX The present sequence is that of the Bipolaris spicifera phenol oxidising enzyme gene. The gene was isolated from genomic DNA using primers (see AAA50025-26) based on the phenol oxidising enzyme of Stachybotrys chartarum (see AAY95537) and the bilirubin oxidase of Myrothecium verruaria. The invention relates to detergent compositions comprising novel phenol oxidising enzymes that have at least 60% identity with the phenol oxidising enzymes of Stachybotrys chartarum, and which are obtained from a bacterium, yeast or non-Stachybotrys fungus, especially B. spicifera, Curvularia pallescens (see AAY95539) and Amerosporium atrum (see AAY95540). The phenol oxidising enzyme is capable of modifying the colour associated with dyes or coloured compounds, and can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. It may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidising enzyme, methods for producing the phenol oxidising enzyme, and methods for constructing expression hosts are provided.

SQ Sequence 2905 BP; 714 A; 792 C; 664 G; 734 T; 1 other;

Query Match 12.5%; Score 460.8; DB 21; Length 2905;

Best Local Similarity 59.3%; Pred. No. 1.2e-125;

Matches 976; Conservative 0; Mismatches 537; Indels 133; Gaps 6;

QY 1491 CTGACCCCTTTCAGATTACCCACCTTGGCCCTGCCACTCTCGTCGGCTACGATGGCAT 1550
Db 478 CTCACCCAGCAGGCTATATCAAGCTCGGCCCTCTCGTTTAGTAGGCTATGACGGCAT 537
QY 1551 GAGCCCTGTCTACTTCAATGTTCAGAGAAACAGAGACTGTAGTTAGGTTTCATCAA 1610
Db 538 CTCGCCAGGTCTACGATCATAGTCCGAGAGAACAGAGCTGTGTACGGTTTATAAA 597
QY 1611 CAATGCCACCGTGGAGAACTCGGTCCATCTGCACGGCTCCCGATCGCGTCCCTTCGA 1670
Db 598 CCAGGGTATCGCGAAGCTCCATCATCTCCACGGCTCCCGCTCCCGTGGCCCTTTTGA 657
QY 1671 TGGTTGGCTGAAGATGTGACCTTCCCTGGCGAGTACAA----- 1709
Db 658 CGGATGGCTGATGATATGATCATGAAGGGGAATACAAAGGTACGATAGCGTGTGATTC 717
QY 1710 -----GGATTACTACTTTCCC 1725
Db 718 TACGCATCAGGAAGCTCTATCATACTAACAGGACTTTCTCTCAGACTACTACTACCG 777
QY 1726 AACTACCAATCGCCCGCTCTGTGTGATACCATGACCGCTTTCATGAAGGTA--TGCT 1783
Db 778 AACAAACCAAGCTGCCAGATTTTGTGGTACCACGATCATGCTATGCATGTTGTAAGTCTT 837
QY 1784 AGGACCTTTATCTTTCTTGGCTACTTTGGCTAACCAACTTCTTTCGTAGACTGCTGA 1843
Db 838 TACCCAGCTTTCATGGTAGTGAAGGAAGGATTAAGCTAATCATCTGTGCAGACCGCAGA 897
QY 1844 GAATGCCTACTTTGGTCAGGCTGGCCCTACATATCAACAGCAGGCTGAGGATGCTCT 1903
Db 898 AAATGCCATTTTCGGGCAAGCGGCCCTACTCTGATCACAGCCGGCTGAGGATGCTCT 957
QY 1904 CGGTCTTCTAGTGCTATGGCGAGTTCGATATCCCTCTGATCGAGGCCAAGTACTA 1963
Db 958 CGGCCCTCTCAGGTTACGGGAAATACGACATTCGCTGCTCCTCAGTTCCTCAAGTACTA 1017
QY 1964 TAACCCGATGTAACCTGCGTTCGACCGAGGGTGCAGACAGGACCTGTGGGAGATGT 2023
Db 1018 CAACCCGATGGAACCTTTAAGACCAAGTGTGGGGAAGAACAGAGTGTGTGGGCGACAT 1077
QY 2024 CATCATGTCAACGACAGCCATGCTTCTTAACCTCCAGCCCGCCCAAGTACCGTTT 2083
Db 1078 CATCATGTCAACGCTGAGCCTGCGCATTTCTTAATGTTGAGCCTCGAAAGTATCGCT 1137
QY 2084 CGATTCCTCAACGCTGCGGTGTCTGCTGCTTGGCTCTCTACCTCTCAGGACCAAGCTC 2143
Db 1138 TCGATTCTCAACGGGCTGTTTCTAGGAACCTTGGCCCTTACTTCGTCAAGCAAGACAA 1197
QY 2144 TCCCAACGTCAGAACTCTCTTCCAAAGTCAATTCCTCTCATGCTGGTCTCAAGCCCT 2203
Db 1198 CACTGCCACTAGGCTTCTCTTCCAGGTCATTTGCCCTCTGATCGAGGGCTACTCACACACC 1257
QY 2204 GGTTCAGACCTCTAACCTCTACCTTGTGTTGCGAGGTTACGAGATCATTTTGGTAT 2263
Db 1258 GGTTCAAACCTCAGATATGTATGTTGAGCGCGCAGAGCGCTACGAGAT----- 1305
QY 2264 GCCCTCCCTCTCAGGAATGAGTCAAGAACTCTAAGACTAACACTTGTAGACTTCACCAA 2323
Db 1306 -----TGTGTTTCGATTTCCGCC 1323
QY 2324 CTTTCTCGCCAGACTCTTGACCTGCGCAAGTGTCTGAGACCAACGATGTGGCGGAGA 2383
Db 1324 CTATCGCGGCAAGGTTGGATCTCGGCAACTTCGCAAGGCAATGGTATCGGTATCCGA 1383
QY 2384 GGATGAGTACGCTCGCACTCTCGAGGTGATGGCTTCGCTCAGCTGCGCACTGTGTA 2443
Db 1384 CGAGACTTACCGCAAACTGACAAAGGTATGCGTTTCCAGCTCAGCAGCCAAACAGTCGT 1443
QY 2444 GGACAACAGCAGGTCCCTCCACTCTCCGTGAGGTTCTTTCCTCTCCTCAAGGAAG 2503
Db 1444 CGATAACTCCGTGATCCGAGCAGCTATCTCAGATCCAGTTCGCCGGGACA---AAAC 1500
QY 2504 CCCCGCGACAAGCACTTCAAGTTTGAACGCAAGCAAGCACTACCTGTATCAACGATGT 2563

Db 1501 CGACATAGACCATCACTTCCGTTTCCATCGTACCACCGGAGTGGCGCATCAACGGCAT 1560
QY 2564 TGGCTTTTCCGATGTCAATGAGCGTGTCTTGCCCAAGCCGAGCTCGGCACCGTTGAGGT 2623
Db 1561 CGGGTTTCAGACGCTCGAGAACCGTGTCTTGCCCAAGGTACCGCGGCTACTGTGAGCT 1620
QY 2624 CTGGAGCTCGAGAACTCTCTGGAGGCTGGAGCCACCCGTCACATTCACCTTTGTTGA 2683
Db 1621 TTGGGAACCTTGAGAACAGCTCGCGGCTGTGTACACCCCATCCACCTCCACCTAGTAGA 1680
QY 2684 CTTCAAGATCTCAAGCAACTGG-----TGGTCTGGCCAGGTTCATGCCCTACGAGTC 2737
Db 1681 CTTCCGAGTCTGTCCGACGCTACGGCGAGAAAGGCACTCGCGCGTTCATGCCCTATGAGGC 1740
QY 2738 TGCTGCTCTTAAGGATGTCTGTGGTGGCAGGCGGTGAGAGCCCTGACCATCGAGGCCCA 2797
Db 1741 CGCCGCTCTCAAGGACGCTGTGTGCTCGGCCGTACGAGAGGGTCTCTCGTCAAGACACA 1800
QY 2798 CTACCAACCCCTGGAGCTGGAGCTTACATGTGGACTGTTCACAACCTCATTCACGAGGATAA 2857
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QY 2858 CGACATGATGGCTGTATTCAACGTCACCGCATCCCGCATGGAGGAGGATATCTTCAGGAG-- 2915
Db 1861 AGACATGATGGCGGCTTTCGACGTGACTTAACTTCCAGAACTTTGGGTACAACGAGACGAC 1920
QY 2916 -GACTTTCGAGGACCCCATGAACCCCAAGTGGCGCGCGCTTCTTACAAACCGCAACGACTT 2974
Db 1921 TGATTTCCACGATCCTGAGGATCCTCGCTGGTCAACAAGACCTTTACCGCGGGTGATCT 1980
QY 2975 CCATGCTCGCGCTGAAACTTCTCGCGCAGTTCCTACTGCCCCAGTGCAGGAGCTGGC 3034
Db 1981 CACGCGCGATCGGGTATCTTTTCAAGAAATCCATCAGGGCTAGAGTAAATGAGTTGGC 2040
QY 3035 CGAGCAGGAGCGGTACAACCCGCTCG 3060
Db 2041 GCTCGAGCAGCCTTACAGCGAACTCG 2066

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SUMMARIES

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3	2054	55.9	2067	4	US-09-218-702-5
4	1474	40.1	1791	4	US-09-468-578-5
5	1474	40.1	1791	4	US-09-218-702-1
6	460.8	12.5	2905	4	US-09-468-578-3
7	455.6	12.4	2063	4	US-09-468-578-6
8	300.4	8.2	1958	4	US-09-401-476-1
9	300.4	8.2	2095	4	US-09-401-476-3
10	150	4.1	858	4	US-09-468-578-8
11	58	1.6	7218	1	US-08-232-463-14
12	43.2	1.2	5468	4	US-09-535-008-66
13	43.2	1.2	5477	4	US-09-535-008-74
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c 23	39.6	1.1	5118	4	US-08-669-785-3
c 24	39	1.1	289	4	US-09-007-005-17
c 25	39	1.1	289	4	US-09-244-796-17
c 26	38.8	1.1	4108	4	US-08-981-729-8
27	38.8	1.1	4108	4	US-08-981-446B-1

28	38.6	1.0	686	4	US-08-998-416-715	Sequence 715, App
c 29	38	1.0	4649	6	5183745-1	Patent No. 5183745
c 30	38	1.0	6441	4	US-08-669-785-1	Sequence 1, Appl
c 31	38	1.0	6443	6	5183745-5	Patent No. 5183745
c 32	37.8	1.0	1872	2	US-08-743-637B-17	Sequence 17, Appl
c 33	37.8	1.0	1872	3	US-08-526-840B-17	Sequence 17, Appl
c 34	37.2	1.0	969	4	US-09-134-001C-109	Sequence 109, App
c 35	36.4	1.0	2923	1	US-08-243-542-6	Sequence 6, Appl
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c 37	36.4	1.0	2923	1	US-08-484-355-6	Sequence 6, Appl
c 38	36.4	1.0	4377	2	US-08-804-227C-7	Sequence 7, Appl
c 39	36.4	1.0	4377	2	US-08-804-198-1	Sequence 7, Appl
c 40	36.2	1.0	1292	4	US-09-198-603C-7	Sequence 7, Appl
c 41	35.6	1.0	49272	1	US-08-614-770A-1	Sequence 1, Appl
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ALIGNMENTS

RESULT 1

US-09-468-578-1
; Sequence 1, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-468-578-1

Query Match	100.0%	Score	3676.6;	DB	4;	Length	3677;
Best Local Similarity	100.0%	Pred. No.	0;				
Matches	3677;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	CTGGCTAGCCTCAGTGGTGTAGACAGCCCTGACAGCTCACTGGCTGGGGTGGAAAGGCC	60				
Db	1	CTGGCTAGCCTCAGTGGTGTAGACAGCCCTGACAGCTCACTGGCTGGGGTGGAAAGGCC	60				
QY	61	AGTCAATATCTTTGGTCACTGCTTAATAGTTCTTGTACCGCAAAAGCTCTTGGCGAA	120				
Db	61	AGTCAATATCTTTGGTCACTGCTTAATAGTTCTTGTACCGCAAAAGCTCTTGGCGAA	120				
QY	121	GGGGCAGACATCAAGTGTAGACATATAGGATGATGTCTTTTCATAGCCACAGTTAGGG	180				
Db	121	GGGGCAGACATCAAGTGTAGACATATAGGATGATGTCTTTTCATAGCCACAGTTAGGG	180				
QY	181	TGGTGACCTACTCGAAGAGGCCCGCCACTTGCATGACATGACATGCGCTTCATGCAAC	240				
Db	181	TGGTGACCTACTCGAAGAGGCCCGCCACTTGCATGACATGACATGCGCTTCATGCAAC	240				
QY	241	ATGTATGCGACATCGGGATCAGGACCCCTCTGATGACAGATAGAACCCCTCGGTTT	300				
Db	241	ATGTATGCGACATCGGGATCAGGACCCCTCTGATGACAGATAGAACCCCTCGGTTT	300				
QY	301	CCTTTTGTTCCTTTCTTCTCAAGGCGGTGAGCGTGTAACTTGAGCAAGGCCGA	360				
Db	301	CCTTTTGTTCCTTTCTTCTCAAGGCGGTGAGCGTGTAACTTGAGCAAGGCCGA	360				

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DB 361 GTGGTCTGTTACGAGGTTACCATGAACTCTCTCTTTTCCCAATCATGACCTGCCCCC 420
QY 421 GAGTTAGCCCCCATCAGCGCTGTGAAATCCACTTCGATTAATCTTAGCTAGCTACTC 480
DB 421 GAGTTAGCCCCCATCAGCGCTGTGAAATCCACTTCGATTAATCTTAGCTAGCTACTC 480
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DB 481 TTCAATAGTTGCTCTGATGGGGCACTTTGGTTCACATTCGCTTGGTTTCTCTACTCTGT 540
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DB 541 TCTCTTCGCAATCAAGCCTCTATGCCCGAGCAACACCTCATTTGGCCGGACCACTTTTG 600
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DB 661 GGAGTTTGGTCTATTTGTATGATCACCTCACATTCAGTATACAGGATCCTGGAAGA 720
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RESULT 2
US-09-218-702-3
; Sequence 3, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-218-702-3

Query Match 100.0%; Score 3676.6; DB 4; Length 3677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	661	GGAGTTTTGGTGTCTATTTGTCTATGATCACTCACTCACTAGATCAAGGATCTCTGGAAGA	720
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	Qy	721	GGGTGTGGAGGCCAGACAGCTGTCCCTGTCTCTTGAGACTCAGCTCAGCTCCTAGCGG
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	Qy	841	TGCTTAATTTGGCTATCTCTATGCCGTAGACGGCTTTTGGCTACAACTGGCTGCCATG
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	Qy	901	GCTGAAGCATCGTGAGATCTATAAAGGTCTCCGAATCCTCGGTCAAATCAGATCTCGTCTC
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	Qy	1021	ACTCTTCCCTCTTTTCGTCATATGCTGTTCAGTCAATGCAACTGGCAGCAGCTCCG
Db	1021	ACTCTTCCCTCTTTTCGTCATATGCTGTTCAGTCAATGCAACTGGCAGCAGCTCCG	1080
	Qy	1081	GGCTCTGTCTGGAGTCCCTCGGCATCCCGATGGACACCGGCAGCCACCCCATTTGAGCGTG
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	Qy	1141	TTGATCCGAAGTGAAGACTGAGGCTTTCGCTGTACTCCTCTCTTGTCTGCAGCAGCGCATG
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	Qy	1201	ACGACTGGGAGTCAACTCCATCAAACTTTCGTTTACAGTGTGAGACACCTGTCCCACTGTT
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	Qy	1261	TTCCCTCGATTAACCTACTCTTATAGGAATGCCCTGCCAAATTCACACTGTCAAGCAGCCCA
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	Qy	1321	AGATGTATGTCTTTTGATTTTCTACGAAGCAACTCGGCCCGGACTTAATGTATTTCTAGGATC
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	Qy	1381	ATTACCAACCTGTCAACGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTT
Db	1381	ATTACCAACCTGTCAACGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTT	1440
	Qy	1441	CAGCAAGGCTGAGTTTGCTCAGAAACCTTTGGGTAAATTAATCATTTGTTACTGACCCCTTT
Db	1441	CAGCAAGGCTGAGTTTGCTCAGAAACCTTTGGGTAAATTAATCATTTGTTACTGACCCCTTT	1500
	Qy	1501	CAGATTTACCCCACTTTGGCCCTGCCACTCTCTGCTGGCTACGATGGCATGAGCCCTGGT
Db	1501	CAGATTTACCCCACTTTGGCCCTGCCACTCTCTGCTGGCTACGATGGCATGAGCCCTGGT	1560
	Qy	1561	CCTACTTTCAATGTTCCCAAGAAACAGAGACTGTAGTTAGGTTTCAACAATGCCACC
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	Qy	1621	GTGAGAACTCTGGTTCATCTGCACGGCTCCCATCGGTGGCCCTTTTCGATGGTTGGCT
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	Qy	1681	GAAGATGTACCTTCCCTGGCGAGTACAGGATTAATACTTTTCCCACTACCAATCCGCC
Db	1681	GAAGATGTACCTTCCCTGGCGAGTACAGGATTAATACTTTTCCCACTACCAATCCGCC	1740
	Qy	1741	CGCCTCTGTGGTACCATGACCACGCTTTCATGAAGGATGCTAGGAGCCTTATCTTTC

Db	1741	CGCCTTCGTGGTACCATGACCAGCCTTTCATGAAGGTATGCTACGAGCCCTTATCATCTTC	1800
Qy	1801	TTGGCTACCTTTGGCTAACCAACTTCCTTTCGTAGACTGCTGAGAAATGCCTACTCTTGGTC	1860
Db	1801	TTGGCTACCTTTGGCTAACCAACTTCCTTTCGTAGACTGCTGAGAAATGCCTACTCTTGGTC	1860
Qy	1861	AGGCTGGCGCCTACATATATCAACAGCAGAGGCTGAGGATGCTCTCGGTCTTTCCTAGTGGCT	1920
Db	1861	AGGCTGGCGCCTACATATATCAACAGCAGAGGCTGAGGATGCTCTCGGTCTTTCCTAGTGGCT	1920
Qy	1921	ATGGCGAGTTTCGATATCCCTCTGATCCTACGGCCCAAGTACTATTAACGCCGATGGTACCC	1980
Db	1921	ATGGCGAGTTTCGATATCCCTCTGATCCTACGGCCCAAGTACTATTAACGCCGATGGTACCC	1980
Qy	1981	TGCGTTCCACCGAGGCTGAGGACAGGACCTCTGGGGAGATGTCATCCATGCTCAACGGAC	2040
Db	1981	TGCGTTCCACCGAGGCTGAGGACAGGACCTCTGGGGAGATGTCATCCATGCTCAACGGAC	2040
Qy	2041	AGCCATGGCCTTTCTTAAAGTCCAGCCCGCCGAAGTACCGTTTCCGATTCCTCAACGCTG	2100
Db	2041	AGCCATGGCCTTTCTTAAAGTCCAGCCCGCCGAAGTACCGTTTCCGATTCCTCAACGCTG	2100
Qy	2101	CCGTGTCCTGTGGCTTGGCTCCTCTACCTCGTCAGAACAGCTCTCCCAACGCTCAGAATTC	2160
Db	2101	CCGTGTCCTGTGGCTTGGCTCCTCTACCTCGTCAGAACAGCTCTCCCAACGCTCAGAATTC	2160
Qy	2161	CTTTTCCAAGTCATTGGCTCTGATGTGGTCTCCTCTCAAGCCCCCGTTTCAGACCTCTAACC	2220
Db	2161	CTTTTCCAAGTCATTGGCTCTGATGTGGTCTCCTCTCAAGCCCCCGTTTCAGACCTCTAACC	2220
Qy	2221	TCTACCTTGTGTGGCGAGCTTACGAGATCATTTATGGTATGCCCTCCCTCTCAACG	2280
Db	2221	TCTACCTTGTGTGGCGAGCTTACGAGATCATTTATGGTATGCCCTCCCTCTCAACG	2280
Qy	2281	ATGAGTCAAGAAGCTTAAGACTTAACACTTTGATAGACTTCACCAACTTTGCTGGCCAGACTC	2340
Db	2281	ATGAGTCAAGAAGCTTAAGACTTAACACTTTGATAGACTTCACCAACTTTGCTGGCCAGACTC	2340
Qy	2341	TTGACCTTCGCAAGTGTCTGAGACCAACGATGTCTGGCGACGAGATGAGTACGCTCGCA	2400
Db	2341	TTGACCTTCGCGAACGTTGCTGAGACCAACGATGTCTGGCGACGAGATGAGTACGCTCGCA	2400
Qy	2401	CTCTCGAGGTGATCGCCTTCGTCTGATGATCAACGATGTGGCTTTGGCGGATGCA	2460
Db	2401	CTCTCGAGGTGATCGCCTTCGTCTGATGATCAACGATGTGGCTTTGGCGGATGCA	2460
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Qy	2521	TCAAGTTTGAACGAGCAACGGACACTACTGATCAACGATGTGGCTTTGGCGGATGCA	2580
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Qy	2581	ATGAGCTGTCTGGCCAAAGCCCGAGCTCGGACCCCTTGAGTCTGGGAGCTCGAGAAT	2640
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Qy	2641	CCTCTGAGGCTGGAGCCACCCGTCACATTCACCTTGTGACTTCAAGATCTCTCAAGC	2700
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Qy	2701	GAACCTGTGTGGTGGCCAGGTCATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCTGCT	2760
Db	2701	GAACCTGTGTGGTGGCCAGGTCATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCTGCT	2760
Qy	2761	GTTTGGGCGAGGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTT	2820
Db	2761	GTTTGGGCGAGGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTT	2820
Qy	2821	ACATGTGGCACTGTCAACACCTCATTTCAAGAGGATTAACGACATGATGGCTGTATTCAACG	2880

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Qy 2941 AGTGGCGGCGTTCCTTACAAACCCCAAGACTTCCATGCTCGCGCTGGAACTTCTCCG 3000
Db 2941 AGTGGCGGCGTTCCTTACAAACCCCAAGACTTCCATGCTCGCGCTGGAACTTCTCCG 3000
Qy 3001 CCGAGTCCATCACTCCCGAGTGCAGGAGCTGGCGGACGAGGCGTACAAACCCCTCG 3060
Db 3001 CCGAGTCCATCACTCCCGAGTGCAGGAGCTGGCGGACGAGGCGTACAAACCCCTCG 3060
Qy 3061 ATGAGATCCTGAGAGATCTTGAATCGAGGAGTAACACCCCGAGCCACAGCTCTACAATC 3120
Db 3061 ATGAGATCCTGAGAGATCTTGAATCGAGGAGTAACACCCCGAGCCACAGCTCTACAATC 3120
Qy 3121 GTTTTGTAGTCTTAAGACAGGCTCTTGGTGGGTATTTCTTTTCCCTACGGGGAACTCC 3180
Db 3121 GTTTTGTAGTCTTAAGACAGGCTCTTGGTGGGTATTTCTTTTCCCTACGGGGAACTCC 3180
Qy 3181 GCTGTCCACTGGATGTGAAGGACCATCACAAAGCAACGTATATTTGGACTCACCACTG 3240
Db 3181 GCTGTCCACTGGATGTGAAGGACCATCACAAAGCAACGTATATTTGGACTCACCACTG 3240
Qy 3241 TCATTACGCCCCACTGTACCTATTTCGATTTCTGTGTTCTTCTTAACTTTTCTAGTGGAGAGTGT 3300
Db 3241 TCATTACGCCCCACTGTACCTATTTCGATTTCTGTGTTCTTCTTAACTTTTCTAGTGGAGAGTGT 3300
Qy 3301 CCATAGTCAAGAAACGCCCATAGGCTATCGTCTTAACTGAACATATTTGGTGGTCTGTGA 3360
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Qy 3361 CGTGAGTAGATGTCAATTTGTATGAGACACAGTAACGTATATCTTTTCCCTAGGAC 3420
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Qy 3421 TACAGGATCAGTTTCTCATGAGATTACATCGCTCTTAATTTTGTCCATGAGAGTCTAGCT 3480
Db 3421 TACAGGATCAGTTTCTCATGAGATTACATCGCTCTTAATTTTGTCCATGAGAGTCTAGCT 3480
Qy 3481 AAGTTGAGATGCATCAGACGGAATCATTTGATGCTCTCAGCTCGTATATACCGATGTA 3540
Db 3481 AAGTTGAGATGCATCAGACGGAATCATTTGATGCTCTCAGCTCGTATATACCGATGTA 3540
Qy 3541 GACAAAGTTAGTTAGTTCCTTGGTATCCGAAATGACTCAGGCTCCCTCATTTAGGTTGCA 3600
Db 3541 GACAAAGTTAGTTAGTTCCTTGGTATCCGAAATGACTCAGGCTCCCTCATTTAGGTTGCA 3600
Qy 3601 TGTGAAAACCTTCAGCAACTCATGCTGTTGGGACCAATCATCCATACCTGATTTTGTAT 3660
Db 3601 TGTGAAAACCTTCAGCAACTCATGCTGTTGGGACCAATCATCCATACCTGATTTTGTAT 3660
Qy 3661 AACTGACCTGGGTCAAT 3677
Db 3661 AACTGACCTGGGTCAAT 3677
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RESULT 3

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US-09-218-702-5
; Sequence 5, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huang
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218.702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2067
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid
US-09-218-702-5
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Query Match 55.9%; Score 2054; DB 4; Length 2067;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1101 GGCATCCCGATGGACACCGGCGAGCCACCCATTGAGGCTGTTGATCCCGAACTGAAGACT 1160
Db 67 GGCATCCCGATGGACACCGGCGAGCCACCCATTGAGGCTGTTGATCCCGAACTGAAGACT 126
Qy 1161 GAGGTCTTCGGTGAAGTCCCTGCTGCTGAGCAGCGGATGAGACTGGGAGTCACCTCCA 1220
Db 127 GAGGTCTTCGGTGAAGTCCCTGCTGCTGAGCAGCGGATGAGACTGGGAGTCACCTCCA 186
Qy 1221 TACAACTTGTCTTACAGCTGAGACACCTGTCCACCTGTCTTTCCTCGATAAATCTCT 1280
Db 187 TACAACTTGTCTTACAGCTGAGACACCTGTCCACCTGTCTTTCCTCGATAAATCTCT 246
Qy 1281 TATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTCTTTGATTTT 1340
Db 247 TATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTCTTTGATTTT 306
Qy 1341 CTACGAACAACTCGGCCCCGACTAATGTATCTTAGGATCATTTACCAACCCCTGTCCCGG 1400
Db 307 CTACGAACAACTCGGCCCCGACTAATGTATCTTAGGATCATTTACCAACCCCTGTCCCGG 366
Qy 1401 CAAGGACATTTGGTACTATGAGATCAGATCAAGCCATTTAGCAAGAGGTCAGTTGCT 1460
Db 367 CAAGGACATTTGGTACTATGAGATCAGATCAAGCCATTTAGCAAGAGGTCAGTTGCT 426
Qy 1461 CAGAAACCTTGTGTAATTAATCATTTGTTACTGACCCCTTTCAGATTTACCCCACTTGGG 1520
Db 427 CAGAAACCTTGTGTAATTAATCATTTGTTACTGACCCCTTTCAGATTTACCCCACTTGGG 486
Qy 1521 CCCTGCCACTCTCGTGGCTAGGATGGCATGAGCCCTGGTCTCTACTTTCAATGTTCCCGAG 1580
Db 487 CCCTGCCACTCTCGTGGCTAGGATGGCATGAGCCCTGGTCTCTACTTTCAATGTTCCCGAG 546
Qy 1581 AGGAACAGAGACTGTAGTTAGGTTTCATCAACATCCACCGTGGAGAACTCGGTCATCT 1640
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Qy 1641 GCACGGCTCCCATCGCTGCCCCCTTTCGATGGTGGCTGAAGATGTGACCTTCCCTGG 1700
Db 607 GCACGGCTCCCATCGCTGCCCCCTTTCGATGGTGGCTGAAGATGTGACCTTCCCTGG 666
Qy 1701 CGAGTACAAGGATTAATCTACTTTCCAACTACCAATCCGCGCCCTTCTGTGTGATACATGA 1760
Db 667 CGAGTACAAGGATTAATCTACTTTCCAACTACCAATCCGCGCCCTTCTGTGTGATACATGA 726
Qy 1761 CCACGCTTTCATGAAGGATGCTACGAGCCCTTATCTTTCCTGGCTACCTTTGGCTAAC 1820
Db 727 CCACGCTTTCATGAAGGATGCTACGAGCCCTTATCTTTCCTGGCTACCTTTGGCTAAC 786
Qy 1821 AACTTCCCTTTCGTAGACTGCTGAGAAATGCTACTTTTGGTGGCTGGCCCTACATATTATC 1880
Db 787 AACTTCCCTTTCGTAGACTGCTGAGAAATGCTACTTTTGGTGGCTGGCCCTACATATTATC 846
Qy 1881 AACGACGAGGTCAGGATGCTCTCGGCTTCTCTAGTGGCTATGGCCAGTTCGATATCCCT 1940
Db 847 AACGACGAGGTCAGGATGCTCTCGGCTTCTCTAGTGGCTATGGCCAGTTCGATATCCCT 906
Qy 1941 CTGATCCTTGACGGCCAAAGTACTATAACCCGATGTTACCTCGCTTCGACCCAGGCTGAG 2000
Db 907 CTGATCCTTGACGGCCAAAGTACTATAACCCGATGTTACCTCGCTTCGACCCAGGCTGAG 966
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QY	2001	GACCAGGACCTGTGGGAGATGTCATCCATGTCAACGACAGCCATGGCCTTTCCCTTTAAC	2060
Db	967		
		GACCGAGACTGTGGGAGATGTCATCCATGTCAACGACAGCCATGGCCTTTCCCTTTAAC	1026
QY	2061	GTCCAGCCCGCAAGTACGGTTTCCGATTTCTCAACGCTCCGCTGTCTCGTGGCTTGCGCTC	2120
Db	1027		
		GTCCAGCCCGCAAGTACCGTTTCCGATTTCTCAACGCTCCGCTGTCTCGTGGCTTGCGCTC	1086
QY	2121	CTCTACTCGTCAAGACAGCTCTCCCAACGTCAGAATTCTTTTCCAAGTCAATTGGCCTCT	2180
Db	1087		
		CTCTACTCGTCAAGACAGCTCTCCCAAGTCAAGAATTCCTTTCAAGTCAATTGGCCTCT	1146
QY	2181	GATGTGGTCTCTTCAAGCCCGCGTTCAAGCTCTTAACCTCTAACCTTGTGTGGTGGCGAG	2240
Db	1147		
		GATGTGGTCTCTTCAAGCCCGCGTTCAAGCTCTTAACCTCTAACCTTGTGTGGTGGCGAG	1206
QY	2241	CGTTACGAGATCATTTAGTATGCCCTCCCTCTCAAGATGAGTCAAGAACCTCTAAGA	2300
Db	1207		
		CGTTACGAGATCATTTAGTATGCCCTCCCTCTCAAGATGAGTCAAGAACCTCTAAGA	1266
QY	2301	CTAACACTTGTAGACTTCAACAACTTGTGCGCCAGACTCTTGACCTGCGCAAGCTTGCT	2360
Db	1267		
		CTAACACTTGTAGACTTCAACAACTTGTGCGCCAGACTCTTGACCTGCGCAAGCTTGCT	1326
QY	2361	GAGACAACGATGTGCGCGACGAGGATGAGTACGCTCCGACTCTCGAGGTGATGCGGCTTC	2420
Db	1327		
		GAGACAACGATGTGCGCGACGAGGATGAGTACGCTCCGACTCTCGAGGTGATGCGGCTTC	1386
QY	2421	GTGCTCAGCTCTGGCACTGTTGAGGACAACAGCCAGGTCCCTCCACTCTCCGTTGAGCTT	2480
Db	1387		
		GTGCTCAGCTCTGGCACTGTTGAGGACAACAGCCAGGTCCCTCCACTCTCCGTTGAGCTT	1446
QY	2481	CCTTTCCCTCTCACAAAGGAAGCCCGCGACAAGCACTTCAAGTTTGAACGACGACAAC	2540
Db	1447		
		CCTTTCCCTCTCACAAAGGAAGCCCGCGACAAGCACTTCAAGTTTGAACGACGACAAC	1506
QY	2541	GGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCAATGAGCGTGTCTGGGCCAAG	2600
Db	1507		
		GGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCAATGAGCGTGTCTGGGCCAAG	1566
QY	2601	CCGAGCTCGGCACCGTTGAGGCTCTGGAGCTCGAGAACTCCTCTGGAGGCTTGAGGCCAC	2660
Db	1567		
		CCGAGCTCGGCACCGTTGAGGCTCTGGAGCTCGAGAACTCCTCTGGAGGCTTGAGGCCAC	1626
QY	2661	CCCGTCCACATTCACCTGTTGACTTCAAGATCTCAAGCGAACTGGTGTGTGGGCCAG	2720
Db	1627		
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QY	2721	GTATGCCCTACAGTCTCGTGTCTTAAGGATGTCTGTGGTGGCAGGGGTGAGACC	2780
Db	1687		
		GTATGCCCTACAGTCTCGTGTCTTAAGGATGTCTGTGGTGGCAGGGGTGAGACC	1746
QY	2781	CTGACCATGAGGCCCACTACCAACCTGGACTGGAGCTTACATGTGGCACTGTCAACAAC	2840
Db	1747		
		CTGACCATGAGGCCCACTACCAACCTGGACTGGAGCTTACATGTGGCACTGTCAACAAC	1806
QY	2841	CTCATTTACGAGGATAACGACATGATGGCTGTATTTCACGTCAACGCCCATGGAGGAGAAG	2900
Db	1807		
		CTCATTTACGAGGATAACGACATGATGGCTGTATTTCACGTCAACGCCCATGGAGGAGAAG	1866
QY	2901	GGATATCTTCAGGAGCACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCTTCCTTAC	2960
Db	1867		
		GGATATCTTCAGGAGCACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCTTCCTTAC	1926
QY	2961	AACCGAACGACTTCCATGCTCGCGGTGGAACTTCTCCGCCGAGTCCCATCACTGCCCGA	3020
Db	1927		
		AACCGAACGACTTCCATGCTCGCGGTGGAACTTCTCCGCCGAGTCCCATCACTGCCCGA	1986
QY	3021	GTGACGAGCTGGCCGACGAGGCGGTACAAACCCCTCTGATGAGATCCTGGAGGATCTT	3080
Db	1987		
		GTGACGAGCTGGCCGACGAGGCGGTACAAACCCCTCTGATGAGATCCTGGAGGATCTT	2046

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Qy 3081 GGAATCGAGGAGTA 3094
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Db 2047 GGAATCGAGGAGTA 2060

RESULT 4
US-09-468-578-5
; Sequence 5, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA
US-09-468-578-5

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Query Match 40.1%; Score 1474; DB 4; Length 1791;
Best Local Similarity 87.0%; Pred. NO. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267

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QY	1098	CTCGGATCCGGATGGACACCGCGACCCACCTATTGAGGCTGTGATCCGGAAGTCGAAG	1157
DB	61	CTCGGATCCGGATGGACACCGCGACCCACCTATTGAGGCTGTGATCCGGAAGTCGAAG	120
QY	1158	ACTGAGGTCTTCGCTGACTCCCTTCCTTGCTGCGACGAGCGATGACGACTGGGAGTCACT	1217
DB	121	ACTGAGGTCTTCGCTGACTCCCTTCCTTGCTGCGACGAGCGATGACGACTGGGAGTCACT	180
QY	1218	CCATACAACTTGCCTTTACAGGTGAGACACTGTGCCACTGTTTTCCTCGATACCTAAC	1277
DB	181	CCATACAACTTGCCTTTAC	198
QY	1278	TCATTATAGGAATGCCCTGCCAATTCACACTGCAAGCAGCCCAAGATGATGCTTTGAT	1337
DB	199	-----AGGAATGCCCTGCCAATTCACACTGCAAGCAGCCCAAGAT-----	239
QY	1338	TTTCTAGGAAGCAACTCGGCCCGGACTAATGTATTCTAGGATCATTTACCAACCTGTGCAC	1397
DB	240	-----GATCATTTACCAACCTGTGCAC	260
QY	1398	CGGAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAGGGTGAGTTT	1457
DB	261	CGGAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAG-----	311
QY	1458	GCTCAGAAACCTTGGGTAAATTAATGTTACTCACCTTTTCAGATTATACCCACCTT	1517
DB	312	-----GATTTACCCACCTT	326
QY	1518	CGGCCCTGCCACTCTCGCTCGGCTACGATGGCATGAGCCCTGCTCCTACTTTCAATGTTCC	1577
DB	327	CGGCCCTGCCACTCTCGCTCGGCTACGATGGCATGAGCCCTGCTCCTACTTTCAATGTTCC	386
QY	1578	CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA	1637
DB	387	CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA	446

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Db 447 TCTGCACGGCTCCCATCGCGTGGCCCTTTTCGATGGTTGGGCTGAAGATGTGACCTTCCC 506
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QY 1698 TGGCGAGTACAGGATTTACTATTTCCCAACTACCAATCCGCCGCCCTTCTGTGGTACCA 1757
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Db 507 TGGCGAGTACAGGATTTACTATTTCCCAACTACCAATCCGCCGCCCTTCTGTGGTACCA 566
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Db 567 TGACCACGGTTTCATGA ----- 583
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QY 1818 ACCAACTTCTTTCGTAGACTGCTGAGATGCCTACTTTTGTGAGGCTGGCCCTACATTT 1877
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Db 584 -----AGACTGCTGAGAATGCTACTTTGGTCAGGCTGGCGCCTACATTT 627
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Db 628 ATCAACGAGGAGGCTGAGGATGCTCTCGGTCTTCCTAGTGGCTATGGCGAGTTCATATC 687
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QY 1938 CCTCTGATCCTGACGGCCAAAGTACTATACGCGGATGTACCTCGGTTTCGACCGAGGT 1997
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Db 688 CCTCTGATCCTGACGGCCAAAGTACTATACGCGGATGTACCTCGGTTTCGACCGAGGT 747
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QY 1998 GAGGACCGAGGACCTGTGGGGAGATGTATTCATGTCAACGGGACAGCCATGGCCTTTTCCTT 2057
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Db 928 TCTGATGCTGTGTCCTTTCAAGCCCCGGTTTCAGACCTCTAACCTCTACCTTGTCTTGGC 987
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QY 2418 TTCGTGTCAGCTTGGCACTTTGAGGACACACGCCAGGTCCCTCCACTCTCCGTGAC 2477
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Db 1174 GTTCTTTCCCTCTCAAGAAGCGCCCGCCGACAGCACTTCAAGTTTGAACCGACG 1233
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QY 2538 AACGGACACTACCTGATCAACGATGTTGGCTTTGGCCGATGTCAATGAGCGTGTCTGGCC 2597
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QY 2658 CACCCCGTCCACATTCACCTTGTACATTCAGATTCCTCAAGCGAACTTGGTGGTGGTGGC 2717
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Db 1354 CACCCCGTCCACATTCACCTTGTGACTTCAAGATTCCTCAAGCGAACTTGGTGGTGGTGGC 1413
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QY 2718 CAGGTCATGCCCTACGAGTCTGCTGTCTTAAAGGATGTGCTGTGGTGAGGGGTGAG 2777
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QY 2778 ACCCTGACCATCGAGGCCCACTACCAACCTGGACTGGAGCTTACATGTGGCACTGTCTAC 2837
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Db 1474 ACCCTGACCATCGAGGCCCACTACCAACCTGGACTGGAGCTTACATGTGGCACTGTCTAC 1533
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QY 2838 AACCTCATTCAGGAGTAACGACATGATGGCTGTATTCAACGTCACCCCATGGAGGAG 2897
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QY 2898 AAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCAAAGTGGCGGCCCTTCT 2957
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Db 1594 AAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCAAAGTGGCGGCCCTTCT 1653
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QY 2958 TACAACCGCAAGACTTCCATGCTCGCGTGGAACTTCTCCGCCGAGTCCATCACTGCC 3017
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QY 3018 CGAGTGCAGGAGCTGGCCGAGCAGGAGCGGTACAAACCGCTCGATGAGATCCTGGAGGAT 3077
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Db 1714 CGAGTGCAGGAGCTGGCCGAGCAGGAGCGGTACAAACCGCTCGATGAGATCCTGGAGGAT 1773
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QY 3078 CTTGGAATCGAGGAGTAA 3095
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Db 1774 CTTGGAATCGAGGAGTAA 1791
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RESULT 5
US-09-218-702-1
; Sequence 1, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Stachybotrys sp.
US-09-218-702-1

Query Match 40.1%; Score 1474; DB 4; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

QY 1038 CTCATATGCTGTTCAAGTCAATGGCACTGGCAGCAGCTCCGGGCTCCTGTCTGGAGTC 1097
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QY 1098 CTCGGCATCCCCGATGGACACCGCAGCCACCCATTGAGGCTGTTGATCCCGAAGTGAAG 1157
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Db 61 CTCGGCATCCCCGATGGACACCGCAGCCACCCATTGAGGCTGTTGATCCCGAAGTGAAG 120
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QY 1158 ACTGAGGCTTTCGTGACTTCCCTCTGCTGCAGCAGGCGATGAGCACTGGGAGTCACT 1217
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Db 121 ACTGAGGCTTTCGTGACTTCCCTCTGCTGCAGCAGGCGATGAGCACTGGGAGTCACT 180
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QY 1218 CCATACACTTGTCTTACAGGTGAGACACTGTCACCTGTTTCCCTCGATAACTAAC 1277
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Db 181 CCATACAACTTGTCTTAC ----- 198
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QY 1278 TCTTTAGTAGATGCCCTGCCAATTCACCTGTCAGCAGCCCAAGATGTATGCTTTGAT 1337
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QY 1338 TTTCTACGAAGCAACTCGGCCCGCCGACTAATGTATTCTAGGATCATTTAGCAACCCCTGTCTAC 1397
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Db 240 -----GATCATTACCAACCCCTGTCCAC 260
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Db 261 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGAAAG----- 311
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Db 312 -----GATTTACCCACCTT 326
Qy 1518 GCGCCCTGCCACTCTGTCGGCTAGATGGCATGAGCCCTGGTCTACTTTCAATGTATTC 1577
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Qy 2298 AGACTAACACTTTGTAGACTTCAACCACTTTGCTGCCAGACTTTTGACCTGGCGAACGTT 2357
Db 1009 -----GACTTCAACCACTTTGCTGCCAGACTCTTGACCTGGCGAACGTT 1053
Qy 2358 GCTGAGACCAACGATGTCTGGCGACGAGGATGATGAGTACGCTCGCACTCTCGAGGTGATGGCC 2417
Db 1054 GCTGAGACCAACGATGTCTGGCGACGAGGATGATGAGTACGCTCGCACTCTCGAGGTGATGGCC 1113
Qy 2418 TTCGTCTGACGCTCTGGCACTCTTGGAGACACGCCAGGTCCCTCCACTCTCCGTGAC 2477
Db 1114 TTCGTCTGACGCTCTGGCACTCTTGGAGACACGCCAGGTCCCTCCACTCTCCGTGAC 1173

Query Match 12.5%; Score 460.8; DB 4; Length 2905;
Best Local Similarity 59.3%; Pred. No. 6,3e-129;
Matches 976; Conservative 0; Mismatches 537; Indels 133; Gaps 6;

Qy 2478 GTTCCTTTCCCTCCTCACAAAGAGGCCCGCCGACAAAGCACTTCAAGTTTGAACGCAGC 2537
Db 1174 GTTCCTTTCCCTCCTCACAAAGAGGCCCGCCGACAAAGCACTTCAAGTTTGAACGCAGC 1233
Qy 2538 AACGGACACTACCTGATCAACGATGTTTGGCTTTCGCCGATGTCAATGAGCGTGTCTTGGCC 2597
Db 1234 AACGGACACTACCTGATCAACGATGTTTGGCTTTCGCCGATGTCAATGAGCGTGTCTTGGCC 1293
Qy 2598 AAGCCCGAGCTCGCACCGTTGAGGCTGCGAGCTCGAGAACTCCTCTGAGAGGTGAGC 2657
Db 1294 AAGCCCGAGCTCGCACCGTTGAGGCTGCGAGCTCGAGAACTCCTCTGAGAGGTGAGC 1353
Qy 2658 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCTCAAGCGAACTGGTGGTCTGGC 2717
Db 1354 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCTCAAGCGAACTGGTGGTCTGGC 1413
Qy 2718 CAGGTCAATGCCCTACGAGTCTGCTGCTTAAAGGATGTCGCTGTTGGGCGAGGGTGGAG 2777
Db 1414 CAGGTCAATGCCCTACGAGTCTGCTGCTTAAAGGATGTCGCTGTTGGGCGAGGGTGGAG 1473
Qy 2778 ACCCTGACCATCGAGGGCCACTACCAACCCCTGGAGCTTACATGTGGCACTGTGCAC 2837
Db 1474 ACCCTGACCATCGAGGGCCACTACCAACCCCTGGAGCTTACATGTGGCACTGTGCAC 1533
Qy 2838 AACCTCATTCAGAGGATAACGACATGATGGCTGTATTTCACGCTCACGCCCATGGAGGAG 2897
Db 1534 AACCTCATTCAGAGGATAACGACATGATGGCTGTATTTCACGCTCACGCCCATGGAGGAG 1593
Qy 2898 AAGGATATCTTCAGGAGGACTTCGAGGACCCCTGAACCCCAAGTGGCGCGCTTCCCT 2957
Db 1594 AAGGATATCTTCAGGAGGACTTCGAGGACCCCTGAACCCCAAGTGGCGCGCTTCCCT 1653
Qy 2958 TACAACCCCAACGACTTCCATCTCGCGCTGGAACCTTCTCCGCCGAGTCCATCACTGCC 3017
Db 1654 TACAACCCCAACGACTTCCATCTCGCGCTGGAACCTTCTCCGCCGAGTCCATCACTGCC 1713
Qy 3018 CGAGTGCAGGAGCTGGCGGACGAGGCCGTAACACCCCTCGATGAGATCCTGGAGGAT 3077
Db 1714 CGAGTGCAGGAGCTGGCGGACGAGGCCGTAACACCCCTCGATGAGATCCTGGAGGAT 1773
Qy 3078 CTTGGAATCGAGGAGTAA 3095
Db 1774 CTTGGAATCGAGGAGTAA 1791

RESULT 6
US-09-468-578-3
; Sequence 3, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Bipolaris spicifera
US-09-468-578-3

Qy 1491 CTGACCCCTTTCAGATTTTACCCGACCTTCGGCCCTGCGCACTCTCGTGGCTACGATGGCAT 1550
Db 478 CTTCAACCCAGCAGGCTCTATCCAAAGCTTCGGCCCTGCGCTGTTTATAGGCTATGACGGCAT 537
Qy 1551 GAGCCCTGCTCTACTTTCAATGTTCCAGAGGAACAGAGACTGTAGTTAGTTTCATCAA 1610
Db 538 CTCCCAAGGTCTACGATCATAGTGGCCGAGAGAACAGACTGTGTACCGTTTATAAA 597
Qy 1611 CAATGCCACCTGGGAGAACTCGGTCCATCTGACGGCTCCCATCGCTGCGCCCTTCGA 1670
Db 598 CCAGSGTGATCGGGAAGCTCCATCCATCTCCACGGCTCCCGCTCCCGCTTTTGA 657
Qy 1671 TGGTTGGCTGAAGATGTGACCTTCCCTGGCGAGTACAA----- 1709
Db 658 CGGATGGCTGATGATATGATGATGAAGGGGGAATACAAAGGTACGATAGGCTGTGATTC 717
Qy 1710 -----GGATTACTACTTTCCC 1725
Db 718 TACGATCAGGAAGCCTCTATCATACTAACAGGACTTTCCTTCAGACTACTACTACCGG 777
Qy 1726 AACTACCAATCCGCCGCTTCTGTGTGTTACCATGACCAAGCTTTCATGAAGGTA--TGCT 1783
Db 778 AACAAACCAAGCTGCCAGATTTTGTGGTACCAGGATCATGCTATGCTATGTGTAAAGTCTT 837
Qy 1784 AGGAGCCTTTATCTTCTTGGCTACCTTTGGCTAACCAATTCCTTTCGTAGAGTGTGA 1843
Db 838 TACCGACTTTTCATGGTAGTGAAGGAAAGGATTAAGCTAACATCTGTGCAGAGCGCAGA 897
Qy 1844 GAATGCCCTACTTGTGAGGCTGGCGCTACATATATCAACAGGAGGCTGAGGATGCTCT 1903
Db 898 AAATGCCCTATTTCGGGCAAGCGCGGCTACTCTGATCACAGCCGCGCTGAGGATGCTCT 957
Qy 1904 CGGTCTCCTTAGTGGCTATGCGAGTTGCGATATCCCTCTGATCCTGACGGCCAAAGTACTA 1963
Db 958 CGGCCTTCTCAGGTTACGGAAATACGACATTCGGCTGCTCAGTTCCAAAGTACTA 1017
Qy 1964 TAACGCCGATGGTACCCCTGCGTTCGACCGAGGGTGAGAACAGGACCTGTGGGAGATGT 2023
Db 1018 CAACCCGATGGAATCTTAAGAACGAGTGTGGGAGAACGAAGAGTGTGTGGGCGACAT 1077
Qy 2024 CATCATGCTCAACGAGACAGCATGCTTCTTAACTGTCAGCGCCGCAAGTACCGTTT 2083
Db 1078 CATCATGCTCAACGCTGAGCCCTGCGCAATCTTAATGTTGAGCCTCGAAAGTATCGTCT 1137
Qy 2084 CCGATTCTCAACGCTGCGCTGTCTGCTGCTTGGCTCCTCTACCTGCTCAGGACGAGTCT 2143
Db 1138 TCGATTCTCAACGCGGCTGTTTCTAGGAATTTGCCCTTTACTTCGTCAAGCAAGACAA 1197
Qy 2144 TCCCAACGTCAGATTCCTTTCCAAAGTCAATTCGCTCTGATGCTGCTTCCTTCAAGCCCC 2203
Db 1198 CACTGCCACTAGGCTTCCTTTCCAGGTCATTTGCCCTCTGATGCGGGCTACTCACACACCC 1257
Qy 2204 CGTTCAGACCTCTAACCTCTACCTTGTGTTGCGGAGGTTACGAGATCAITATTGGTAT 2263
Db 1258 GGTTCAAACCTTCAGATATGATGTGTGACCGCGAGACGCTTACGAGAT----- 1305
Qy 2264 GCCCTCCCTCTCACGAATAGTCAAGAATCTTAAGACTAACACTTGPAGACTTGCACCAA 2323
Db 1306 -----TGTTTCGATTCGCGCC 1323
Qy 2324 CTTTGTGCGCCAGACTCTTGTAGCTTCGCGCAAGTGTGCTGAGACCAACAGATGTGCGCGAGA 2383
Db 1324 CTATGCGCGCAAGGTTGGATCTGCGCAACTTCGCAAGGCAATGTTATCGGTATACCGA 1383
Qy 2384 GGATGAGTACCTCGCACTCTCGAGGTGATGGCTTCGCTGCTGAGCTTGGCACTGTGTA 2443
Db 1384 CGAGACTTACCGAAACACTGACAAAGGTATGCGTTTCACCTGACGACGCAACAGTCTGT 1443
Qy 2444 GGACAACAGCCAGCTCCCTCCACTCTCCGTGAGCTTCTTTCCTCTCTCACAAGGAAGG 2503
Db 1444 CGATTAACCTCCGTGTACCCGAGCAGCTATCTCAGATCCAGTTCCCGCGGACA---AAAC 1500
Qy 2504 CCCGCGGACAAAGCACTTCAAGTTTGAACGCAAGCAAGCACACTTACCTGATCAACGATGT 2563

Db 1501 CGACATAGACCATCACCTTCCGTTTCCATFCGTACCAACGCGAGTGGCGCATCAACGGCAT 1560
Qy 2564 TGGTTTTCCCATGTCATAGAGCTGTCTGCGCAAGCCGAGCTCGGCACCGCTTGAAGGT 2623
Db 1561 CGGTTTGCAGACGCTCGAGAACCCTGTTCTTGGCCAAGGTACCGCGCGTACTGTGCGAGCT 1620
Qy 2624 CTGGAGCTCGAGAACTCCTCTGGAGGCTGGAGCCACCCGCTCCACATTCACCTTGTGTA 2683
Db 1621 TTGGAACTTGAGAACAGCTCCGGCGGCTGTGTCAACCCCATCCACGTTCCACCTTAGTAGA 1680
Qy 2684 CTTCAAGATCTCAAGCGAACTGG-----TGGTCTGGCCAGGTCATGCCCTACGAGTC 2737
Db 1681 CTTCCGAGTCTGTCGACACTACGCGGACGAAGGCACTCGCGCGCTCATGCCCTATGAGGC 1740
Qy 2738 TGCTGGTCTTAAGGATGCTGCTGTTGGCAGGAGGCTGAGACCTTGACATCGAGGCCCA 2797
Db 1741 CGCGGCTCAAGGACGCTGCTGTGCTGCGCGCTCACAGACGCTCTCTGTCGAAGCACA 1800
Qy 2798 CTACCAACCCCTGGACTGGAGCTTACATGTGCACTGTTCACAACCTCATTCACGAGGATAA 2857
Db 1801 TTACGCCCCATGGGACGAGTCTACATGTTCCACTGCCACAACCTCATCCACGAAGACCA 1860
Qy 2858 CGACATGATGCTGTATTCAAGCTCACGCCCATGGAGGAGAGGATATCTTTCAGGAG-- 2915
Db 1861 AGACATGATGGCCGCTTCGACGCTGACTTAACTCCAGAACTTTGGGTACAACGAGACGAC 1920
Qy 2916 -GACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCTTCTTACAAACCGCAACGACTT 2974
Db 1921 TGATTTCCACGATCCTGAGGATCTCTGCTGCTGCTGTCAGCAAGACCTTTTACCGGGGTGATCT 1980
Qy 2975 CCATGCTCGCGCTGGAACCTTCTCGCGGAGTCCATCACTGCGCGAGTGCAGGAGCTGGC 3034
Db 1981 CACGGCGGATCGGATATCTTTTTCAGAAAGATCCATCAGGCTAGAGTAAATGAGTTGGC 2040
Qy 3035 CGAGCAGGAGCGGTACAAACCCCTCG 3060
Db 2041 GCTCGAGCAGCTTACAGCGAACTCG 2066

RESULT 7
US-09-468-578-6
; Sequence 6, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Curvularia pallescens
US-09-468-578-6

Query Match 12.4%; Score 455.6; DB 4; Length 2063;
Best Local Similarity 59.1%; Pred. No. 1.9e-127;
Matches 971; Conservative 0; Mismatches 544; Indels 129; Gaps 6;
Qy 1501 CAGATTTACCACCACTTCGCGCCCTGCCACTCTCGTGGCTACGATGGCATGAGCCCTGGT 1560
Db 376 CAGGCTCATCCAACTACGTCCTGCTGCTTGGTAGGCTATGATGGCATTTCCACGAGC 435
Qy 1561 CCTACTTTTCAATGTTCCAGAGGAACAGAGACTGTAGTTAGTTTCAATCAACAATGCCACC 1620

Db 436 CCTACGATCATCGTGCCGAGAGGAACAGAACCGCTTGACGATTCGTAACACCGGATGAT 495
Qy 1621 GTGGAGAACTCGGTCCATCTGACACGGCTCCCATCGCTGCCCTTTTCGATGGTGGGCT 1680
Db 496 CCGAGAGATTGATTCATCTCATGTTCTCCCTCCCGTGCCTTTGACGGATGGGCT 555
Qy 1681 GAAGATGTGACCTTCCCTGGGAGTACAAAGT----- 1713
Db 556 GAAGATTTGATATGAAGGCGCAATTCAAAGGTACAAAGGTACAAAGCAACAACTCTATGCATCAGG 615
Qy 1714 ----- 1714
Db 616 TGCCCTCTTTTACTAAACAGACTCGTTCTTAGAGTACTACTACCCGAACAAACAGGCTG 675
Qy 1739 CCCGCTTCTGTGGTACCATGACACGCT-TTCATGAAGGTATGCTACGAGCCTTTAATCT 1797
Db 676 CCAGATTCCTGTGGTACCACGATCATGCTATGCATGTTGTAACTTTCGACGACTAATCAT 735
Qy 1798 TTCTTTGGCTACTTTTGGCTAACCAACTTCTTTCGTAGACTGCTGAGAAATGCTACTTTG 1857
Db 736 GGGAGCGAAACGGAAAGATCGGCTGACACTTATGCAGACTCGGAAATGCTATTTTG 795
Qy 1858 GTCAGGCTGGGCGCTACATTTATCAAGAGAGGCTGAGGATGCTCTCGGTCTTCCTAGTG 1917
Db 796 GACAGGCTGGGCGCTTACCTGATCAGAGACCCAGGCTGAGAGCGCCCTCGGCGCTTCCTCGG 855
Qy 1918 GCTATGGCGAGTTGATATCCCTCTGATCCTGACGGCCAAAGTACTATAACGCCGATGTA 1977
Db 856 GTTACGGAAATACGACATCCCACTGTGGTCTCAGTTCCAAAGTTCTACAAACAGTGATGAA 915
Qy 1978 CCTCGGTTTCGACCGAGGTTGAGGACCGAGGCTGTGGGAGATGTCATCCATGTCACG 2037
Db 916 CTCCTCAGACCACTGTGGGAGAAAGACACAGTCTCTGGGCGAGCTCATCCATGTCAACG 975
Qy 2038 GACAGCCATGGCCTTTCCTTAACGTCAGAGCCCGCAAGTACGGTTTCCGATTCCTCAACG 2097
Db 976 GTCAGCCCTGGCCATTTCTCAACGCTGAGCCTCGAAAGATATCGCCTTCGATTCCTCAATG 1035
Qy 2098 CTGCGCTGCTCGTGTGGCTTCTCTACCTCGTCAGACCAAGCTCTCCCAACGTCAGAA 2157
Db 1036 CGGCTGTTTCTCGGNACTTTGCCCTCTATTTCGTCAACACACAGCCCACTGCTACTAGAC 1095
Qy 2158 TTCCTTTCCAAAGTCAATGCCCTCTGATGCTGTCTCTTCAAGCCCGCTTCAGACCTCTA 2217
Db 1096 TTCCCTTCCAGTCAATGCCCTCTGATGACGGCTACTCACGACCCGCTTCCAAACCTCAG 1155
Qy 2218 ACCTCTACCTTGTCTGCCAGCGTTACGAGATCAATTTAGTATGCCCTCCCTCTCA 2277
Db 1156 ATATTACGTTGGCAGCAGCAGCGCTACGAGAT----- 1189
Qy 2278 CGAATGAGTCAAGAACTCTAAGACTTAACACTTGTAGACTTCACCAACTTTGCTGCCCAGA 2337
Db 1190 -----TGATTTCGACTTTGGCGCTTATGAGGCCAGA 1221
Qy 2338 CTCATTGACCTGGCAACGCTTGTGAGACCAACGATGTGCGGACGAGGATGAGTACGCTC 2397
Db 1222 CGATAGATTTCGTAACCTTTGCAAAAGGCAATGGGGTCGGCAGCGATGACGATTATGCAA 1281
Qy 2398 GCACCTCTCGAGGTGATGGCTTCTGCTGCATGCTGCGACCTGTTGAGGACAAACGCCAGG 2457
Db 1282 ACATGCAAGGTATGTCGGCTTCCATTTGTCAGCAGCAAGCAGTCTGATTAACCTCGGTGG 1341
Qy 2458 TCCCTCTCACCTCTCGTACGCTTCTCTTCCCTCTCTCAAGGAAGGCCCGCCGACAAAGC 2517
Db 1342 TACCGGCACAGCTATCTCAGATTCAGTTCCCGCGGACA---AAACCGGATTCGACCACC 1398
Qy 2518 ACTTCAAGTTTGAAGCGCAGCAACGGACACTACCTGATCAACGATGTTTGGCTTTGCGCATG 2577
Db 1399 ACTTCCCGCTTCCATCGCACCAACAGCGAGTGGCGATCAACGGCATCGGGTTTCGAGACG 1458
Qy 2578 TCAATGACGCTGTCTGCGCAAGCCCGAGCTCGGACCGCTTGAGGTCGTGGAGCTCGAGA 2637
Db 1459 TCCAGAACCGTATCCTGGCCCAAGGTACCGCGCGGCACTGTCTGAGCTATGCGAACTCGAGA 1518

Qy 2638 ACTCCTCTGGAGGCTGGAGCCACCCCGTCCACATTTCACTTGTGTTGACTTCAAGATCCTCA 2697
Db 1519 ACAGCTCGCGGGCTGTGTCGACCCCATCAGTCCACCTGGTCGACTTCGAGTCTGTCG 1578
Qy 2698 AGCGAACTGGTG-----GTGCTGGCCAGGTATGCCCCCTACGAGTCTGCTGCTTAAAG 2751
Db 1579 CACGCTACGGTGACGAAAGCACTCGCGGCGTCATGCCCTACGAGTCCGCGCTCTCAAGG 1638
Qy 2752 ATGTCGCTGTGGTGGGAGGGTGAGACCTGAGACCTGACCATCGAGGCCACCTACCAACCTCGA 2811
Db 1639 ACGTGTGTGCTGCGCGCGCACGAGAGCGTCTGCTGGAAGCACACTACGCCCCCTGGG 1698
Qy 2812 CTGAGGCTTACATGTGACACTGTCTACAACTCATTCACGAGGATACACATGATGGCTG 2871
Db 1699 ACGGAGTCTACATGTTCCACTGCCACAACCTGATCCAGAGAACAAAGACATGATGGCGG 1758
Qy 2872 TATTCAAGCTCACGCCCATGAGGAGAGGATATCTTCA---GGAGGACTTCGAGGACC 2928
Db 1759 CGTTTGACGTGACTAAGCTCCAGAACTTTGGCTACAACGAGACGAGATTTCCACGACC 1818
Qy 2929 CCATGAACCCCAAGTGGCGCGCTTCTTACAAACCGCAACGACTTCCATGCTCGCGTG 2988
Db 1819 CGGAAGATTCTCGTGTGCTGCAAGACCTTTCACCGCGCTGACTTGACGGCGCATCGG 1878
Qy 2989 GAACTTCTCGCGGAGTCCATCTACTCGCGCTGAGTGCAGAGTGGCGGAGGAGCCGT 3048
Db 1879 GTATCTCTCAGAGCATCCATCAGGCTAGAGTGAACGAGTTGGCGCTGGAACAGCCGT 1938
Qy 3049 ACAACCGCTTCGATGAGATCTCTGG 3072
Db 1939 ACAGCGAACTGGCACAGGTCAACGG 1962

RESULT 8
US-09-401-476-1
; Sequence 1, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401.476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ. ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1958
; TYPE: DNA
; ORGANISM: Stachybotrys chararum
US-09-401-476-1

Query Match 8.2%; Score 300.4; DB 4; Length 1958;
Best Local Similarity 55.2%; Pred. No. 1.7e-80;
Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;

Qy 1491 CTGACCCCTTTTCAGATTTACCCACCTTGGCGCCTGCCACTCTCGTCGCTACGATGGCAT 1550
Db 316 CTTCTCCACCAAGTCTTACCTGATCTGGAGCGGCCCAACATGGTTGGATACGATGGCAT 375
Qy 1551 GAGCCCTGGTCTACTTTCAATGTTTCCAGAGAAACAGAGACTGTAGTTAGTTTCATCAA 1610
Db 376 GTCCCCAGGACCTACCATCATCGTTCTCTCGTGGCACTGAGAGTGTGTCCGCTTCGTGA 435
Qy 1611 CA-----ATGCCACTGGAGAACTCGGTCCATCTGCACGGCTCCCATCCGCTGCC 1664
Db 436 CAGCGGAGAGAACACCTCTCCCAACAGCGTGCATTTGCACGGCTCTTCTCTCGAGCTCC 495
Qy 1665 TTTGATGTTGGCTGAAGATGTGACCTTCCCTGGCGAGTACAGGATTACTACTTTC 1724
Db 496 CTTTGTGTTGGCTGAGGACACTACCCAGCCTGGCGAGTACAGGATTACTACTACC 555
Qy 1725 CAACTACCAATCCGCGCCCTTCTGTGTGTTACCATGACCACGCTTTCATGAAGGATGCTA 1784

[illegible]

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Db 1523 CCACTGCCCGTGG---AGTCGAGCCCTTATGAGGCTGCTGGTCTCAAGGATGTTGTCGTGGC 1579
Qy 2764 TGGCGAGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCCCTGGAC-----2812
Db 1580 TGGCTCGTGTGAGTGTGCTATGTTGAGGCCCACTACGCTCCTTTCCCGTAAGTTCGTG 1639
Qy 2813 -----TGGAGCTTACATGTCGCA 2830
Db 1640 CTTTTFACCTAACCTGGTTTCTACTCATGCTAACTCTACAAGTGGTGCTTACATGTTGCA 1699
Qy 2831 CTGTCACAACTCATTTACGAGGATAACACACATGATGGCTGTATTCAACGTCACGCGCAT 2890
Db 1700 CTGCCAACCTCATCCACGAGGACCACACATGATGCTGCTTTCAATGTCACGTGTTCT 1759
Qy 2891 GGAGGAGAAGGGATATCTTCAGGAGGACTTCAGGAGCCCATGACCCCAAGTGGCGGCG 2950
Db 1760 CGGTGACTATGGCTACAATACACCGAGTTCAATGACCCCATGGAGCCTCTCTGGAGGCC 1819
Qy 2951 CGTTCCTTTACAACCGCAAGGACTTCCATGCTCGCGCTGGAACTTCTCCGCGCGAGTCCAT 3010
Db 1820 CCGCCCTTCTCTCTCGAGAGTTCCGAGAATGCTCGGGTGACTTCACGAGCTTGCCAT 1879
Qy 3011 CACTGCCCGAGTCAGGAGCTGGCCGAGCAGGCGGTACAAACGCCCTCGATGA 3064
Db 1880 CACTGACCGCATTCAGGAGATGCTAGCTTCAACCCCTACGCCCAAGGCTGATGA 1933

RESULT 9
US-09-401-476-3
; Sequence 3, Application US/09401476
; Patent No. 6186936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6186936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Stachybotrys chararum
; US-09-401-476-3

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Query Match	8.2%	Score 300.4;	DB 4;	Length 2095;
Best Local Similarity	55.2%	Pred. No. 1.8e-80;		
Matches 957; Conservative	0;	Mismatches 501;	Indels 276;	Gaps

[illegible]


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Db 296 GATGCAAGTATCAAC-----TTCTCTGTCATCGGTGCCGATACCTGGTCTCTTG 346
Qy 2196 CAAGCCCGGTTACAGACCTCTAACCTCTACCTGTTGGCGAGCGTTACGAGATCAATT 2255
Db 347 ACCAAGCCGTTTACAGCAAGCAACCTTGAGATCTCTATGCGCGAGCGCTGGGAGTGTGT 406
Qy 2256 ATTG 2259
Db 407 TTTG 410

RESULT 11
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match 1.6%; Score 58; DB 1; Length 7218;
Best Local Similarity 6.1%; Pred. No. 9.le-07;
Matches 26; Conservative 228; Mismatches 174; Indels 0; Gaps 0;

Qy 286 GAACCCCGCTGGTTCCCTTTGTTCTTTCTTCTCAACGACGCGTGACGGTGTAA 345
Db 1064 GATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1123
Qy 346 CTTGACGAAGCCGAGTGGTCTGTTACGAGGTTACCACTCTCTCTTCCCAAT 405
Db 1124 VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV 1183
Qy 406 CATGACCTGCCCGCGAGTTAGTACCCCATCAGCGCTGTGAATCCACTTCGATAATCCT 465
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Db 1184 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1243
Qy 466 AGCCTAGTGTACTCTTCAATAGTTGCTCCTCATGGGCGACACTTTGCTCACATTCGCTTGG 525
Db 1244 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1303
Qy 526 TTYCTCTACCTCGTTCTCTCCGCATCAAGCCTCTATGCCGAGACAAACACCTCATTTG 585
Db 1304 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1363
Qy 586 GCCCGGACCACTTTGAGCGCGCACACCTTCGCCGCCGAGAGTTGATAACACCTTCA 645
Db 1364 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1423
Qy 646 CCCTTGCCCAATGATGAGTGTGTTGCTATTGTCATGATCACCTCACATTCACCTAGATC 705
Db 1424 YYYYYYYYYYGTACCAATCTCTCTATCTCTTTAACTACTTGTCATAGTAGTAATTAC 1483
Qy 706 ACGGATCC 713
Db 1484 AGTGATGC 1491

RESULT 12
US-09-535-008-66
; Sequence 66, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535.008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 66
; LENGTH: 5468
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(5012)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1780)
; OTHER INFORMATION: GenBank Accession No. 6465629 U29175 shows a C at this
; OTHER INFORMATION: position (position 1784 in GenBank) rather than
; OTHER INFORMATION: the G shown here.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)
; OTHER INFORMATION: Polymorphism of either T or C in this noncoding
; OTHER INFORMATION: region.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1583)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1598)
; OTHER INFORMATION: Polymorphism of T or C resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1892)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
```

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; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (4498)..(4499)
; OTHER INFORMATION: A CAG is missing between these bases as compared
; OTHER INFORMATION: to SEQ ID NO:1.
US-09-535-008-66

Query Match      1.2%; Score 43.2; DB 4; Length 5468;
Best Local Similarity 45.5%; Pred. No. 0.023;
Matches 153; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Qy 2765 GGGGAGGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTTACAT 2824
Db 4493 GGACAGAGTGGAGCTCAGCTCAGGAGGTCTTCATCAGCTGCCCTCGCGAAGGAGCT 4552
Qy 2825 GTGGCACTGTGCACACCTTCATTCACGAGGATAACGACATGATGGCTGTATTCAACGTCAC 2884
Db 4553 GCCCGAGTACTACGAGCTCATCCGCAAGCCGTGGACTTCAAGAAGATAAAAGGAGCGCAT 4612
Qy 2885 CGCATGGAGGAGGAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTG 2944
Db 4613 TCGCAACCAACAGTACCGACGCTCAACGACCTAGAGAAGGAGCTCATGCTCTGTGCCA 4672
Qy 2945 GCGGCGCCGTTCCTTACAAACCCGCAACGACTTCATGCTCGCGCTGGAACCTTCTCGCCGA 3004
Db 4673 GAACGCACAGACCTTCACCTGGAGGGCTCCCTGATCTATGAAGACTCCATCGTCTTCCA 4732
Qy 3005 GTCCATCACTGCCGAGTGCAGGAGCTGGCGGAGCAGGAGCGGTACAAACCGCTCGATGA 3064
Db 4733 GTCGGTCTTCAACCGCTGCGCGCAGAAAATCGAAGGAGGATGACAGTGAAGGCGAGGA 4792
Qy 3065 GATCCTCGAGGATCTTGAATCGAGGAGTAACCCC 3100
Db 4793 GAGTGAGGAGGAGGAAGAGGCGGAGGAGGAGGCTC 4828

RESULT 13
US-09-535-008-74
; Sequence 74, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRL1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 5477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(5021)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1780)
; OTHER INFORMATION: GenBank Accession No. 6465629 U29175 shows a C at this
; OTHER INFORMATION: position (position 1784 in GenBank) rather than
; OTHER INFORMATION: the G shown here.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)
; OTHER INFORMATION: Polymorphism of either T or C in this noncoding
; OTHER INFORMATION: region.
; FEATURE:

; NAME/KEY: allele
; LOCATION: (1583)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1598)
; OTHER INFORMATION: Polymorphism of T or C resulting in a silent
; OTHER INFORMATION: mutation.
; NAME/KEY: allele
; LOCATION: (1892)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; NAME/KEY: misc-feature
; LOCATION: (1445)..(1453)
; OTHER INFORMATION: Insertion of 9 basepairs as compared to SEQ ID
; OTHER INFORMATION: NO:1.
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (4507)..(4508)
; OTHER INFORMATION: Deletion of CAG between these basepairs as
; OTHER INFORMATION: compared to SEQ ID NO:1 (basepairs 4499-4501 of
; OTHER INFORMATION: SEQ ID NO:1).
US-09-535-008-74

Query Match      1.2%; Score 43.2; DB 4; Length 5477;
Best Local Similarity 45.5%; Pred. No. 0.023;
Matches 153; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Qy 2765 GGGGAGGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTTACAT 2824
Db 4502 GGACAGAGTGGAGCTCAGCTCAGCGAGGTCTTCATCAGCTGCCCTCGCGAAGGAGCT 4561
Qy 2825 GTGGCACTGTGCACACCTTCATTCACGAGGATAACGACATGATGGCTGTATTCAACGTCAC 2884
Db 4562 GCCCGAGTACTACGAGCTCATCCGCAAGCCGTGGACTTCAAGAAGATAAAAGGAGCGCAT 4621
Qy 2885 CGCATGGAGGAGGAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTG 2944
Db 4622 TCGCAACCAACAGTACCGACGCTCAACGACCTAGAGAAGGAGCTCATGCTCTGTGCCA 4681
Qy 2945 GCGGCGCCGTTCCTTACAAACCCGCAACGACTTCATGCTCGCGCTGGAACCTTCTCGCCGA 3004
Db 4682 GAACGCACAGACCTTCACCTGGAGGGCTCCCTGATCTATGAAGACTCCATCGTCTTCCA 4741
Qy 3005 GTCCATCACTGCCGAGTGCAGGAGCTGGCGGAGCAGGAGCGGTACAAACCGCTCGATGA 3064
Db 4742 GTCGGTCTTCAACCGCTGCGCGCAGAAAATCGAAGGAGGATGACAGTGAAGGCGAGGA 4801
Qy 3065 GATCCTCGAGGATCTTGAATCGAGGAGTAACCCC 3100
Db 4802 GAGTGAGGAGGAGGAAGAGGCGGAGGAGGAGGCTC 4837

RESULT 14
US-09-535-008-68
; Sequence 68, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRL1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 68
; LENGTH: 5564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(5108)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1780)
; OTHER INFORMATION: GenBank Accession No. 6465629 U29175 shows a C at this
; OTHER INFORMATION: position (position 1784 in GenBank) rather than
; OTHER INFORMATION: the G shown here.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)
; OTHER INFORMATION: Polymorphism of either T or C in this noncoding
; OTHER INFORMATION: region.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1598)
; OTHER INFORMATION: Polymorphism of T or C resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1892)
; OTHER INFORMATION: Polymorphism of T or C resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4245)..(4340)
; OTHER INFORMATION: This is a 96 base insertion compared to SEQ ID
; OTHER INFORMATION: NO:1.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4594)..(4595)
; OTHER INFORMATION: A deletion of CAG occurs between these bases as
; OTHER INFORMATION: compared to SEQ ID NO:1 (bases 4499-4501 of SEQ ID
; OTHER INFORMATION: NO:1).
US-09-535-008-68

Query Match      1.2%; Score 43.2; DB 4; Length 5564;
Best Local Similarity 45.5%; Pred. No. 0.023;
Matches 153; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Qy 2765 GGGCAGGGGTGAGACCTGACCATCGAGGCCCACTACCAACCCCTGGAGCTTGAGCTTACAT 2824
Db 4589 GGACAGCAGTGGACGTCAGCTCAGCGAGGTCTTCATCAGCTGCCCTCGCGAAGAGGCT 4648
Qy 2825 GTGGCAGCTGTACACACCTATTCAGAGATTAACGACATGATGGCTGTATTCAACGTCAC 2884
Db 4649 GCGCGAGTACTACGAGCTCATCCGCAAGCCCGTGGACTTCAGAAGATAAAGGAGCGCAT 4708
Qy 2885 CCGCATGGAGGAGAGGGATATCTTCAGAGGACTTCGAGGACCCCATGAACCCCAAGTG 2944
Db 4709 TCGCAACCAACAGTACCGAGCTCAACGACCTAGAGAAGGAGCTGCTCTCTGTGCA 4768
Qy 2945 GCGCGCGGTTCCTTACAACCGCAAGACTTCATCTCGCGCTGGAAACTTCTCGCGCGA 3004
Db 4769 GAACGCACAGACTTCAACCTGGAGGCTCCCTGATCTATGAAGACTCATCTGCTTGA 4828
Qy 3005 GTCCATCACTGCCGAGTGTCAGAGCTGGCGGAGCAGGACCGGTACAAACCGCTTCGATGA 3064
Db 4829 GTCTGCTTTCACCGCTGTCGCGCAGAAAATCGAAGGAGGATGACAGTGAAGGCGAGGA 4888
Qy 3065 GATCTCGAGGATCTTGAATCGAGGATTAACCC 3100
Db 4889 GAGTGAAGGAGGAAGAGGCGGAGGAGGAGGCTC 4924

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RESULT 15
US-09-535-008-76
; Sequence 76, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; TITLE OF INVENTION: AND OTHER CANCER TYPES
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 5573
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(5117)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1780)
; OTHER INFORMATION: GenBank Accession No. 6465629 U29175 shows a C at this
; OTHER INFORMATION: position (position 1784 in GenBank) rather than
; OTHER INFORMATION: the G shown here.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)
; OTHER INFORMATION: Polymorphism of either T or C in this noncoding
; OTHER INFORMATION: region.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1583)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1598)
; OTHER INFORMATION: Polymorphism of T or C resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1892)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; NAME/KEY: misc_feature
; LOCATION: (4245)..(4349)
; OTHER INFORMATION: Addition of 105 basepairs compared to SEQ ID NO:1.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4603)..(4604)
; OTHER INFORMATION: Deletion of CAG between these two basepairs as
; OTHER INFORMATION: compared to SEQ ID NO:1 (deletion of basepairs
; OTHER INFORMATION: 4499-4501 of SEQ ID NO:1).
US-09-535-008-76

Query Match      1.2%; Score 43.2; DB 4; Length 5573;
Best Local Similarity 45.5%; Pred. No. 0.023;
Matches 153; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Qy 2765 GGGCAGGGGTGAGACCTGACCATCGAGGCCCACTACCAACCCCTGGAGCTTGAGCTTACAT 2824
Db 4598 GGACAGCAGTGGACGTCAGCTCAGCGAGGTCTTCATCCAGCTGCCCTCGCGAAGAGGCT 4657
Qy 2825 GTGGCAGCTGTACACACCTATTCAGAGATTAACGACATGATGGCTGTATTCAACGTCAC 2884

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Db	4658	GCCCCGAGTACTACGAGCTCATCCGCAAGCCCGTGGACTTCAAGAAGATAAAAGGAGCGCAT	4717
Qy	2885	CGCCATGGAGGAGAGGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTG	2944
Db	4718	TGGCAACCACAAAGTACCGCAGCCTCAAGCAGCTAGAGAAGGACGTCATGCTCCTGTGCCA	4777
Qy	2945	GCGCGCCGTTCTTTACAACCCGCAAGGACTTCCATGCTCGCGCTGGAAACTTCTCCGCCGA	3004
Db	4778	GAACGCACAGACCTTCAACCTGGAGGGCTCCCTGATCTATGAAGACTCCATCGTCTTGCA	4837
Qy	3005	GTCCATCACTGCCCGAGTGCAGGAGCTGGCCGAGCAGGCGCGTACAAACCGCCTCGATGA	3064
Db	4838	GTGCGTCTTCAACCGCTGCGGCGAGAAAATCGAGAAGGAGGATGACAGTGAAGGCGAGGA	4897
Qy	3065	GATCCTGGAGGATCTTGAATCGAGGAGTAACCCC	3100
Db	4898	GAGTAGGAGGAGGAAGAGGGCGAGGGAAGGCTC	4933

Search completed: February 13, 2003, 05:12:08
Job time : 193.68 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 20:54:16 ; Search time 166.097 Seconds
(without alignments)
11275.230 Million cell updates/sec

Title: US-09-218-702-3

Perfect score: 3677

Sequence: 1 ctggctgacctacttgta.....gataactgacctgggtcaat 3677

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published.Applications_NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3676.6	100.0	3677	12	US-10-080-210-1
2	3676.6	100.0	3677	12	US-10-080-233-3
3	3675.8	100.0	3677	12	US-09-338-723A-1
4	2054	55.9	2067	12	US-10-080-233-5
5	1474	40.1	1791	10	US-09-338-723A-5
6	1474	40.1	1791	12	US-10-080-210-5
7	1474	40.1	1791	12	US-10-080-233-1
8	460.8	12.5	2905	10	US-09-338-723A-3
9	460.8	12.5	2905	12	US-10-080-210-3
10	455.6	12.4	2063	12	US-10-080-210-6
11	300.4	8.2	1958	9	US-09-942-185-1
12	300.4	8.2	2095	9	US-09-942-185-3
13	150	4.1	1858	12	US-10-080-210-8
14	60	1.6	1533	9	US-09-738-626-1053
15	44.6	1.2	1470	10	US-09-974-300-2204
c 16	42.8	1.2	1082	10	US-09-822-830A-368
17	41.4	1.1	390	10	US-09-750-399-7
18	39.2	1.1	1467	10	US-09-981-900B-6
c 19	38	1.0	6442	9	US-09-950-335A-11

20	37.8	1.0	1872	10	US-09-452-599-17	Sequence 17, Appl
21	37.6	1.0	1512	9	US-10-124-800-31	Sequence 31, Appl
22	37.6	1.0	4509	9	US-10-124-800-5	Sequence 5, Appl
23	37.6	1.0	4512	9	US-10-124-800-27	Sequence 27, Appl
c 24	37.4	1.0	615	9	US-10-125-815-4	Sequence 4, Appl
25	37	1.0	2223	9	US-09-984-245-120	Sequence 120, App
26	36.6	1.0	1707	9	US-09-936-842A-186	Sequence 186, App
27	36.2	1.0	2187	9	US-09-984-245-93	Sequence 93, Appl
28	35.8	1.0	500	9	US-10-047-542-33	Sequence 33, Appl
29	35.8	1.0	1642	10	US-09-765-231A-25	Sequence 25, Appl
30	35.6	1.0	651	9	US-09-738-626-2385	Sequence 2385, Ap
c 31	35.6	1.0	2148	9	US-09-738-626-2384	Sequence 2384, Ap
c 32	35.4	1.0	698	9	US-09-764-868-156	Sequence 156, App
33	35.2	1.0	1002	9	US-09-738-626-1755	Sequence 1755, Ap
34	35.2	1.0	2748	9	US-09-738-626-2853	Sequence 2853, Ap
35	35	1.0	951	9	US-09-975-719-432	Sequence 432, App
c 36	35	1.0	1050	9	US-09-975-719-428	Sequence 428, App
37	35	1.0	1104	10	US-09-815-242-7676	Sequence 7676, Ap
38	35	1.0	42235	9	US-09-975-719-1	Sequence 1, Appl
39	34.8	0.9	1185	10	US-09-887-576-784	Sequence 784, App
40	34.8	0.9	6442	9	US-09-950-335A-11	Sequence 11, Appl
41	34.6	0.9	2787	10	US-09-815-242-6320	Sequence 6320, Ap
c 42	34.4	0.9	417	10	US-09-960-352-14176	Sequence 14176, A
43	34.4	0.9	927	9	US-10-029-180-97	Sequence 97, Appl
c 44	34.2	0.9	522	10	US-09-860-107-1314	Sequence 1314, Ap
45	34.2	0.9	1764	9	US-09-920-923-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-10-080-210-1
; Sequence 1, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-10-080-210-1

Query Match	100.0%	Score	3676.6;	DB 12;	Length	3677;
Best Local Similarity	100.0%;	Pred. No.	0;			
Matches 3677;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;					
Qy	1	CTGGCTAGCCTC	CACCTTGGT	TAGACAGCCCT	GACAGCCT	CACCTGGCTGGGGT
Db	1	CTGGCTAGCCTC	CACCTTGGT	TAGACAGCCCT	GACAGCCT	CACCTGGCTGGGGT
Qy	61	AGTCAATATCT	TGGTCACT	GTGCTAAT	AGTATAGT	TGCTAGCGCAAAAGCT
Db	61	AGTCAATATCT	TGGTCACT	GTGCTAAT	AGTATAGT	TGCTAGCGCAAAAGCT
Qy	121	GGGCACAGACT	ATCAAGT	GAGACATAT	AGGATG	ATGCTTTTCATAGCCAGT
Db	121	GGGCACAGACT	ATCAAGT	GAGACATAT	AGGATG	ATGCTTTTCATAGCCAGT
Qy	181	TGGTGACCT	ACTCGAAG	AGGCCCC	ACCTG	CATGATGACATGCT
Db	181	TGGTGACCT	ACTCGAAG	AGGCCCC	ACCTG	CATGATGACATGCT


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Db 2401 CTCCTGAGGTGATGGCTTCGTCGACGCTCGGCACATGTTGAGGACAAACGCCAGGTCC 2460
QY 2461 COTCCACTCTCGTGACGTTCTCTTCCCTCTCTCAACAAGGAAGCCCGCCGACAAAGCACT 2520
Db 2461 COTCCACTCTCGTGACGTTCTCTTCCCTCTCTCAACAAGGAAGCCCGCCGACAAAGCACT 2520
QY 2521 TCAAGTTTGAACGACGACAAAGCACTACCTGATCAACGATGTTGGCTTGGCCGATGCA 2580
Db 2521 TCAAGTTTGAACGACGACAAAGCACTACCTGATCAACGATGTTGGCTTGGCCGATGCA 2580
QY 2581 ATGAGCGTGTCTGCGCAAGCCCGAGCTCGGCACACGTTGAGGCTCGGAGCTCGGAGAACT 2640
Db 2581 ATGAGCGTGTCTGCGCAAGCCCGAGCTCGGCACACGTTGAGGCTCGGAGCTCGGAGAACT 2640
QY 2641 COTCTGGAGGCTGGAGCCACCCCGTCCACATTCACATCTGTTGACTTCAAGATCTCTCAAGC 2700
Db 2641 COTCTGGAGGCTGGAGCCACCCCGTCCACATTCACATCTGTTGACTTCAAGATCTCTCAAGC 2700
QY 2701 GAACCTGGTGGTGGCGCAGGTCATGCCCTAGGAGTCTGCTGGTCTTAAAGGATGCTGCT 2760
Db 2701 GAACCTGGTGGTGGCGCAGGTCATGCCCTAGGAGTCTGCTGGTCTTAAAGGATGCTGCT 2760
QY 2761 GGTGGGAGGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCCCTGGAGCTGAGCTT 2820
Db 2761 GGTGGGAGGGGTGAGACCCCTGACCATCGAGGCCCACTACCAACCCCTGGAGCTGAGCTT 2820
QY 2821 ACATGTGGCACTGTCCACAACTCATTCAGGAGTAAGCACATGATGGCTGTATTCAACG 2880
Db 2821 ACATGTGGCACTGTCCACAACTCATTCAGGAGTAAGCACATGATGGCTGTATTCAACG 2880
QY 2881 TCACGCCCATGAGGAGAGGATATCTTTCAGGAGGACTTCGAGGACCCCATGAACCCCA 2940
Db 2881 TCACGCCCATGAGGAGAGGATATCTTTCAGGAGGACTTCGAGGACCCCATGAACCCCA 2940
QY 2941 AGTGGCGGCGCTTCTTACAAACCCGACGACTTCCATGCTCGCGCTGGAACCTTCTCGG 3000
Db 2941 AGTGGCGGCGCTTCTTACAAACCCGACGACTTCCATGCTCGCGCTGGAACCTTCTCGG 3000
QY 3001 CCGAGTCCATCACTGCCGAGTGCAGGAGCTGGCCGAGCAGGAGCCGTACAAACCCCTCG 3060
Db 3001 CCGAGTCCATCACTGCCGAGTGCAGGAGCTGGCCGAGCAGGAGCCGTACAAACCCCTCG 3060
QY 3061 ATGAGATCCTGGAGATCTTGAATCGAGGAGTAACCCCGAGCCACAACTCTACAATC 3120
Db 3061 ATGAGATCCTGGAGATCTTGAATCGAGGAGTAACCCCGAGCCACAACTCTACAATC 3120
QY 3121 GTTTTGAAGTCTTAAGCAGGCTCTTGTGCGTATTTCTTCTTCCCTACGGGAACCTCC 3180
Db 3121 GTTTTGAAGTCTTAAGCAGGCTCTTGTGCGTATTTCTTCTTCCCTACGGGAACCTCC 3180
QY 3181 GCTGTCCACTGCGATGTGAAGGACCATCACAAAGCAAGTATATATTGGACTTCACCACTG 3240
Db 3181 GCTGTCCACTGCGATGTGAAGGACCATCACAAAGCAAGTATATATTGGACTTCACCACTG 3240
QY 3241 TCATTACGCCCCCACTGTGACCTATTTCGATCTTGTTCGATTTTCTAGTCGAGAGTGT 3300
Db 3241 TCATTACGCCCCCACTGTGACCTATTTCGATCTTGTTCGATTTTCTAGTCGAGAGTGT 3300
QY 3301 CCATAGTCAAGAAACGCCCATAGGCTATCTGCTAAACTGAACCTATTGTGGTCTGTGA 3360
Db 3301 CCATAGTCAAGAAACGCCCATAGGCTATCTGCTAAACTGAACCTATTGTGGTCTGTGA 3360
QY 3361 COTGGAGTAGATGTCAATTGTGATGAGACACAGTAAGTACGGTATATCTTTTCCCTAGGAC 3420
Db 3361 COTGGAGTAGATGTCAATTGTGATGAGACACAGTAAGTACGGTATATCTTTTCCCTAGGAC 3420
QY 3421 TACAGGATCAGTTTCTCATGAGATTACATCCGCTCTAAATGTTTGTCCATCAGAGTCTAGCT 3480
Db 3421 TACAGGATCAGTTTCTCATGAGATTACATCCGCTCTAAATGTTTGTCCATCAGAGTCTAGCT 3480
QY 3481 AAGGTTGAGATGCATCAGACCGGAATCATTTGATGCTCTCAGCTCGTATACCGGATGTAA 3540
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Db 3481 AAGGTTGAGATGCATCAGACGGGAATCATTTGATGCTCTCAGCTCGTATTACCGGATGTAA 3540
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RESULT 2
US-10-080-233-3
; Sequence 3, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/10/080.233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-10-080-233-3
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Query Match 100.0%; Score 3676.6; DB 12; Length 3677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-09-338-723A-1
; Sequence 1, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huaming, Wang

; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338.723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-338-723A-1

Query Match 100.0%; Score 3675.8; DB 10; Length 3677;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3675; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 2821 ACATGTGGCACTGTCCACAACTTCATTCAGGAGGATTAACGACATGATGGCTGTTTCAAGC 2880
QY 2881 TCACCGCATGAGGAGAGGGATATCTTCAGGAGACTTCGAGGACCCCATGAACCCCA 2940
DB 2881 TCACCGCATGAGGAGAGGGATATCTTCAGGAGACTTCGAGGACCCCATGAACCCCA 2940
QY 2941 AGTGGCGGCCGCTTCTTACAACCCGCAAGCTTCCATGCTCGCGTGGAACTTCTCCG 3000
DB 2941 AGTGGCGGCCGCTTCTTACAACCCGCAAGCTTCCATGCTCGCGTGGAACTTCTCCG 3000
QY 3001 CCGAGTCCATCACTGCCCGAGTGCAGGAGCTGGCCGAGCAGGAGCGGTACAACCCGCTCG 3060

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Db 3001 CCGAGTCCATCTACTGCCGAGTGCAGGAGCTGGCCGAGCAGGCGGTACAAACCGCCTCG 3060
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Db 3061 ATGAGATCTGGAGGATCTTGGAAATCGAGGAGTAAACCCCGAGCCACAAGCTCTACAATC 3120
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Db 3121 GTTTTGAGTCTTAAAGCAGAGGCTCTTGGTGCATATCTTTTCTCCCTACGGGGAACTCC 3180
Qy 3181 GCTGTCCACTCGCATGTGAAGCACCATCAAGAAGCAACGTATATATGGACTCACCACCTG 3240
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RESULT 4
US-10-080-233-5
; Sequence 5, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC367
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid
US-10-080-233-5
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Query Match 55.9%; Score 2054; DB 12; Length 2067;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3021 GTGCGAGGAGCTGGCGAGCAGGAGCGGTACACCGCCTCGATGAGATCTGAGGAGATCT 3080
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QY 3081 GGAATCGAGGAGTA 3094
Db 2047 GGAATCGAGGAGTA 2060

RESULT 5

US-09-338-723A-5
; Sequence 5, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huaming, Wang

; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-338-723A-5

Query Match 40.1%; Score 1474; DB 10; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

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Db 584 -----AGACTGCTGAGAAATGCTACTTTGGTCAGGCTGGCGCCTACATT 627

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Db 628 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGCGAGTTTCGATATC 687
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RESULT 6

US-10-080-210-5
; Sequence 5, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA
US-10-080-210-5

Query Match 40.1%; Score 1474; DB 12; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

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Db 1414 CAGTCTATGCCCTACGAGTCTGCTGGTCTTAAAGATGTCGTTGGGCGAGGGTGAG 1473
Qy 2778 ACCCTGACATTCGAGGGCCACTACCAACCTCGAGCTTACATGTGCACTGTGCAC 2837
Db 1474 ACCCTGACATTCGAGGGCCACTACCAACCTCGAGCTTACATGTGCACTGTGCAC 1533
Qy 2838 AACCTCATTCAGAGGATAACGACATGATGGCTGTATTTCAACGTCACGCCCATGGAG 2897
Db 1534 AACCTCATTCAGAGGATAACGACATGATGGCTGTATTTCAACGTCACGCCCATGGAG 1593
Qy 2898 AAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCTTCCT 2957
Db 1594 AAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCTTCCT 1653
Qy 2958 TACAACCGCAACGACTTCCATCTCGCGCTGGAACCTTCTCCGCCGAGTCCATCACTGCC 3017
Db 1654 TACAACCGCAACGACTTCCATCTCGCGCTGGAACCTTCTCCGCCGAGTCCATCACTGCC 1713
Qy 3018 CGAGTGCAGGAGCTGGCGGACGAGGCGGTACAACCCCTCGATGAGATCCTGGAGAT 3077
Db 1714 CGAGTGCAGGAGCTGGCGGACGAGGCGGTACAACCCCTCGATGAGATCCTGGAGAT 1773
Qy 3078 CTTGGAATCGAGGAGTAA 3095
Db 1774 CTTGGAATCGAGGAGTAA 1791
RESULT 7
US-10-080-233-1
; Sequence 1, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/10/080.233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Stachybotrys sp.
US-10-080-233-1
Query Match 40.1%; Score 1474; DB 12; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
Qy 1038 GTCAATATGCTTTCAAATCATGCAACTGGCACTGGCAGCAGCCTCGGGGCTCCTGTCTGGAGTC 1097
Db 1 GTCAATATGCTTTCAAATCATGCAACTGGCACTGGCAGCAGCCTCGGGGCTCCTGTCTGGAGTC 60
Qy 1098 CTCGGCATCCCGATGGACACCGGACGCCACCCATTGAGGCTGTGATCCCGAAGTGAAG 1157
Db 61 CTCGGCATCCCGATGGACACCGGACGCCACCCATTGAGGCTGTGATCCCGAAGTGAAG 120
Qy 1158 ACTGAGGCTTTCGCTGACTTCCCTTCTGCTGAGCAGCGCATGACGACTGGGAGTCACT 1217
Db 121 ACTGAGGCTTTCGCTGACTTCCCTTCTGCTGAGCAGCGGATGACGACTGGGAGTCACT 180
Qy 1218 CCAATACAATCTGCTTTACAGGTGAGACACCTGTCCCACTGTTTTCCCTCGAATAACTAAC 1277
Db 1 CCAATACAATCTGCTTTACAGGTGAGACACCTGTCCCACTGTTTTCCCTCGAATAACTAAC 1277

Db 181 CCATACAACCTTGCCTTAC----- 198

Qy 1278 TCTTATAGGAATGCCCTGCCAATTCACACTGTCAAGCAGCCCCAAGATGATGTCTTTTGAT 1337

Db 199 -----AGGAATGCCCTGCCAATTCACACTGTCAAGCAGCCCCAAGAT----- 239

Qy 1338 TTTCTACGAAGCAACTCGGCCCGACCTAATGTATCTAGGATCATTTACCAACCCCTGTAC 1397

Db 240 -----GATCATTTACCAACCCCTGTAC 260

Qy 1398 CGGCAAGGACATTTGGTACTATAGATCGAGATCAAGCATTTTCAGCAAAAGGGTGAGTTT 1457

Db 261 CGGCAAGGACATTTGGTACTATAGATCGAGATCAAGCATTTTCAGCAAG----- 311

Qy 1458 GUTCAGAAACCTTGTGGTAATTAATCATTTGTACTGACCCCTTTTCAGATTTTACCCACACTT 1517

Db 312 -----GATTTACCCACACTT 326

Qy 1518 GCGCCCTGCCACTCTCGTCGSGCTAGGATGGCATGAGCCCTGGTCTCTACTTTTCAATGTTCC 1577

Db 327 GCGCCCTGCCACTCTCGTCGSGCTAGGATGGCATGAGCCCTGGTCTCTACTTTTCAATGTTCC 386

Qy 1578 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 1637

Db 387 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 446

Qy 1638 TCTGCACGGCTCCCCATCGCGTGCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCC 1697

Db 447 TCTGCACGGCTCCCCATCGCGTGCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCC 506

Qy 1698 TGGCAGTACAAAGGATTTACTACTTTCCCACTACCAATCCGCGCGCTTCTGTGTACCA 1757

Db 507 TGGCAGTACAAAGGATTTACTACTTTCCCACTACCAATCCGCGCGCTTCTGTGTACCA 566

Qy 1758 TGACCACGCTTTTCATGAAGGTATGCTACGAGCCTTTATCTTTCTTGGCTACTCTTTGGCTA 1817

Db 567 TGACCACGCTTTATGA----- 583

Qy 1818 ACCAACTTCTTTTCGTAGACTGCTGAGAAATGCCTACTTTTGGTCAGGCTGGCGCCTACATT 1877

Db 584 -----AGACTGCTGAGAAATGCCTACTTTTGGTCAGGCTGGCGCCTACATT 627

Qy 1878 ATCAACGACGAGGCTGAGGATGCTCGGTTCTCGTAGTGCTATGGCGAGTTGATATC 1937

Db 628 ATCAACGACGAGGCTGAGGATGCTCGGTTCTCGTAGTGCTATGGCGAGTTGATATC 687

Qy 1938 CCTCTGATCTTGACGGCCAAAGTACTATAACCGCGATGTACCCCTGCGPTTCGACCGAGGGT 1997

Db 688 CCTCTGATCTTGACGGCCAAAGTACTATAACCGCGATGTACCCCTGCGPTTCGACCGAGGGT 747

Qy 1998 GAGGACCAAGACCTGTGGGAGATGTCATCCATGTCAACGACAGCCATGGCCTTTCCTT 2057

Db 748 GAGGACCAAGACCTGTGGGAGATGTCATCCATGTCAACGACAGCCATGGCCTTTCCTT 807

Qy 2058 AACGTCCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCGGTCTCGTGTGG 2117

Db 808 AACGTCCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCGGTCTCGTGTGG 867

Qy 2118 CTCCTCTACCTCTGTCAGACCAAGTCTCCCAAGCTCAGAATTCCTTCCAAAGTCAATTGCC 2177

Db 868 CTCCTCTACCTCTGTCAGACCAAGTCTCCCAAGCTCAGAATTCCTTCCAAAGTCAATTGCC 927

Qy 2178 TCTGATGCTGGTCTCTTTCAAGCCCCCTTTCAGACCTCTAACCTCTACTTGTCTTGGC 2237

Db 928 TCTGATGCTGGTCTCTTTCAAGCCCCCTTTCAGACCTCTAACCTCTACTTGTCTTGGC 987

Qy 2238 GAGCCTTACGAGATCATTTATTTGGTATGCCCCCTCTCAAGAATAGTCAAGAACTCTA 2297

Db 988 GAGCCTTACGAGATCATTTAT----- 1008

Qy 2298 AGACTTAACACTTTGTAGACTTCAACCAACTTTTGTGGCCAGACTCTTGACCTGGCAACGTT 2357

Db 1009 -----GACTTCAACCAACTTTTGTGGCCAGACTCTTGACCTGGCAACGTT 1053

RESULT 8

US-09-338-723A-3

; Sequence 3, Application US/09338723A

; Patent No. US20020019038A1

; GENERAL INFORMATION:

; APPLICANT: Huaming, Wang

; TITLE OF INVENTION: Phenol Oxidizing Enzymes

; FILE REFERENCE: GC561-2

; CURRENT APPLICATION NUMBER: US/09/338,723A

; CURRENT FILING DATE: 1999-06-23

; PRIOR APPLICATION NUMBER: 09/220,871

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 2905

; TYPE: DNA

; ORGANISM: Bipolaris spicifera

US-09-338-723A-3

Query Match		12.5%	Score 460.8;	DB 10;	Length 2905;
Best Local Similarity		59.3%;	Pred. No. 3.1e-131;		
Matches 976;		Conservative 0;	Mismatches 537;	Indels 133;	Gaps 6;
Qy	1491	CTGACCCCTTTCAGATTTACCCCACTTGGCGCCCTGCCACTCTCGCGGCTACGATGGCAT	1550		
Db	478	CTTACCCAGCAGCTCTATCCAGGCTCGGCCCTGCTCGTTAGTAGGCTATGACGGCAT	537		
Qy	1551	GAGCCCTGGTCTACTTTCAATGTTCCAGAGACACAGAGACTGTAGTTAGTTTCATCAA	1610		
Db	538	CTCCCCAGGTCTACGATACATAGTGGCGAGAGAACAGAGCTGTGTACGGTTTATAAA	597		
Qy	1611	CAATGCCACCGTGGAGAACTCGGTCCTATCTGCAGGGCTCCCATCTCGGCTTTTCGA	1670		
Db	598	CCAGGGTATCGCGAAGACTCCATCCATCTCCAGGGTCCCGCTCCCGTGCCCTTTTGA	657		
Qy	1671	TGGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAA	1709		
Db	658	CGGATGGGCTGATGATGATGATGATGAAGGGGAATACAAAGGTACGATAGCGTGTGATTC	717		
Qy	1710	-----GGATTACTACTTTCC	1725		
Db	718	TACGCATCAGGAAGCCTATATATACTAACAGGACTTTCTTCAGACTACTACTACCCG	777		
Qy	1726	AACTACCAATCCGCCCGCTTCTGTGGTACCATGACCACGCTTTTCATGAAGTA--TGCT	1783		
Db	778	AACAACCAAGCTGCCAGATTTTGTGGTACCACGATCATGTATGCATGTGTGAAGTCTT	837		
Qy	1784	ACGAGCCCTTATCTTCTTGGCTACCTTTGGCTAACCAACTTCCCTTCGTAGACTGTGA	1843		
Db	838	TACCGACTTTTCATGGTAGTGAACGGAAGGATTAAGCTAATCATCTGTGCAGACGCCAGA	897		
Qy	1844	GAATGCCCTACTTTGGTCAGGCTGGGCCCTACATTTATCAACACGAGGCTGAGGATGCTCT	1903		
Db	898	AAATGCCCTATTTCCGGCAAGCGCGCTACTCTGATCACAGCCCGCTGAGGATGCTCT	957		
Qy	1904	CGGTCTTCTCTAGTGGCTATGGGAGTTCCGATATCCCTCTGATCTGACGGCCAACTACTA	1963		
Db	958	CGGCCTTCTCTCAGTTACGGNAATACGACATTCGGCTGGTCTCAGTTCCAACTACTA	1017		
Qy	1964	TAAACCGGATGGTACCCCTGGCTTCGACCGAGGGTGAGACAGGACCTGTGGGGAGATGT	2023		
Db	1018	CAACCCGATGGAACCTTTAAGACCAGTGTGGGAGAAAGAGTGTGTGGGGCGACAT	1077		
Qy	2024	CATCCATGTCACGACAGCATGCGCTTCTTAACTCCAGCCCGCAAGTACCGCTT	2083		
Db	1078	CATCCATGTCACGCTCAGCCCTGGCCATTTCTTAAATGTTGAGCCTCGAAAGTATCGTCT	1137		
Qy	2084	CGGATTCCTCAACGCTGCGGTGCTCTCGTGGCTCTACCTCTCGTCAGGACCAAGCTC	2143		
Db	1138	TCGATTCCTCAACGCGGCTGTTCTAGGAACCTTTTGCCCTTTACTTCGTCAAGCAGACAA	1197		
Qy	2144	TCCCAACGTCAAGATTCCTTCCAAAGTCATTCGCTCTGATGCTGTCTCTTCAAGCCCC	2203		
Db	1198	CACTGCCACTAGGCTCTCTTCCAGGCTATTCGCTCTGATGCGGGCTACTCACACACC	1257		
Qy	2204	CGTTCAGCCCTCACTACCTTACCTTGTGTTGCCAGGCTTACGAGATCATTTATGGTAT	2263		
Db	1258	GGTTCAACCTCAGATATGTATGTTGCGCGCCGACGAACGCTACGAGAT	1305		
Qy	2264	GCCCTCCCTCTCAGGAATGAGTCAAGAACCTAAGACTATGATGATGATGATGATGATGAT	2323		
Db	1306	-----TGTTTCGATTTCCGCC	1323		
Qy	2324	CTTTCCTGGCCAGACTTTGACCTCGCAACGTTGCTGAGACCAACGATGTGGCGGACGA	2383		
Db	1324	CTATCGCGCCAAACGTTGGATCTCGCAACTTCGCAAAAGGCCAATGGTATCGGTACCGA	1383		
Qy	2384	GGATGAGTACGCTCCGACTCTCGAGGTTCGGCTTCGTCGCTCAGCTCTGGGACATGTTGA	2443		
Db	1384	CGACGACTACGCAAAACACTGTACAAGGTCATGCGTTTCCACGCTCAGCAGCAAAACAGTCGT	1443		

Qy	2444	GGACAACGACGAGTCCCTCCACTCTCCGTGACGTTCTTCTTCCCTCCTCACAAGGAAGG	2503		
Db	1444	CGATAACTCCGTGCTACCCGAGCAGCTATCTCAGATCCAGTTCCCGCGGACA---AAAC	1500		
Qy	2504	CCCCCGCAGACAGCACTTCAAGTTTGAACGACGACGACGACACTACCTGATCAACGATGT	2563		
Db	1501	CGACATAGACCATCACTTCCGTTTCCATCTGTAACGCGGAGTGGCGCATCAACGGCAT	1560		
Qy	2564	TGGCTTTGGCCATGCTCAATGAGCTGCTTGGCCAAAGCCGAGCTCGGCACCGTTGAGGT	2623		
Db	1561	CGGTTTGCAGACGCTCGAGAACCGTGTCTTTCGCAAGGTACCGCGGCTACTGTCTGAGCT	1620		
Qy	2624	CTGGAGCTCGAGAACTCTCTGGAGGCTGGAGCCACCCCTCCACATTCACCTTGTGTGA	2683		
Db	1621	TTGGAACTTCGAGAACAGCTCCGCGGCTGTCTACACCCCATCCACGCTCCACCTAGTGA	1680		
Qy	2684	CTTCAAGATCTCTCAAGCGAACTGG-----TGGTGTGGCCAGGTCATGCCCTTACGAGTC	2737		
Db	1681	CTTCCGAGTCTCTGCACGCTACGCGGAGAGGACACTCGCGGCGTCAATGCCCTATGAGGC	1740		
Qy	2738	TGCTGGTCTTAAGGATGCTGCTGTTGGCAGGGGTGAGACCTTGACCATCGAGGCCCA	2797		
Db	1741	CGCCGGTCTCAAGGACGCTGCTGTGGCTCGCCGTCACAGAGCGTCTCTCTCGAAGCACA	1800		
Qy	2798	CTACCAACCCCTGGACTGGAGCTTACATGTGCACCTGTCCAAACCTCATTCACGAGGATAA	2857		
Db	1801	TTACGCCCATGGGAGGAGTCTACATGTTCCACTTGCACCAACCTCATCCACGAAGACCA	1860		
Qy	2858	CGACATGATGGCTGTATTCACGCTCACGCCATCGCCCATGGAGAGAAGGATATCTTCAGGAG--	2915		
Db	1861	AGACATGATGGCGGCTTCGACGTGACTTAACTCCAGAACTTTGGGTACAAACGAGACAC	1920		
Qy	2916	-GACTTCCGAGCACCCATGAACCCCAAGTGGCGGCGCTTCTTCAACCCCAACGACTT	2974		
Db	1921	TGATTTCCACATCTCTGAGGATCTCGCTGTGTCAGCAAGACCTTTACCCCGGGGTGATCT	1980		
Qy	2975	CCATGCTCGCCTGGAACCTTCTCCGCGAGTCCCATCACTACCTGCCGAGTGCAGGAGCTGGC	3034		
Db	1981	CACGCGCGATCGGGTATCTTTTCAGAAAGATCCATCAGGCTAGAGTAAATGAGTTGGC	2040		
Qy	3035	CGACGAGGAGCGGTACACCCGCTCG	3060		
Db	2041	GCTCGAGCAGCTTACAGCGAACTCG	2066		

RESULT 9
US-10-080-210-3
; Sequence 3, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Bipolaris spicifera
US-10-080-210-3

Query Match		12.5%	Score 460.8;	DB 12;	Length 2905;
Best Local Similarity		59.3%;	Pred. No. 3.1e-131;		
Matches 976;		Conservative 0;	Mismatches 537;	Indels 133;	Gaps 6;
Qy	1491	CTGACCCCTTTCAGATTTACCCCACTTGGCGCCCTGCCACTCTCTCGTGGCTACGATGGCAT	1550		

Qy 1665 TTTCGATGTTGGGCTGAAGATGTGACCTTCCTCGGAGTACAAGATTACTTTCC 1724
Dy 496 CTTTGTGTTGGGCTGAGGACACTACCCAGCCTGGCGAGTACAAGATTACTACTACC 555
Qy 1725 CAACCTACCAATCCGCCCTCTCTGTGTACCATGACACGCTTTCATGAAGATTGCTA 1784
Dy 556 CAACAGGAGGCTGCCCGATGCTTTGTGTACCATGACCATGC----- 597
Qy 1785 CGAGCCTTTATCTTTCTTTGGCTACCTTTGGGCTAACCACTTTCCTTCGTAGACTGCTGAG 1844
Dy 598 -----CATGCTCCATCACCGCCGAG 616
Qy 1845 AATGCTACTTTGGTGCAGGCTGGCGCCTACATTTATCAACGAGGAGGTGAGATGCTCTC 1904
Dy 617 AACGCCTACATGGGTGAGGCTGGTGTCTATACATGATCCAGGACCCGGCTGAGGATGCCCTG 676
Qy 1905 GGTCTTCTAGTGGGTATGGGAGTTTCATATCCCTCTGTATCTCTGACGCGCAAGTACTAT 1964
Dy 677 AACCTCCCGAGGCTACGGGAGTTTATATCCCTTTGGTCTGACTGCGCAAGCGATAC 736
Qy 1965 AACGCGGATGTTACCTCGCTTCGACCCGAGGCTGAGGACCAAGGACCTGTGGGAGATGTC 2024
Dy 737 AACGAGAGGCACTCTCTCTCCACCAATGGAGAGTTTCCAGCTTCTGGGTTGACGTT 796
Qy 2025 ATCCATGT----- 2032
Dy 797 ATTCAAGTGGTAAGTTGAGCCCATTTGAGATGCTTCAGATCCTAGAAGTATGATGTATGA 856
Qy 2033 -----CAACGGACAGCCATGGCTTTCCTTAAGC 2061
Dy 857 AATTGTGATGCTTAACCAAGTGCTATCACAGAAGGGTCAGCCCTTGGGCTATGTCAACG 916
Qy 2062 TCCAGCCCCGGAAGTACCGTTTCCGATTTCCTCAACGCTGCCGTGTCTGCTGGCTGCC 2121
Dy 917 TGCAGCCGCGAAGTACCGCTTCGCTTCCTCAACGCTGCCGTCTCAGGCTCTTCGGCTC 976
Qy 2122 TCTACTCGTCAAGGACCAAGCTCTCCCAAGTCAAGTAATTCCTTTTCCAAAGTCAATGCTCTG 2181
Dy 977 TGTATCTTGTACCTCTCAGGATTCAGAGACCAAGTTCCTCCCTCCAGGTCATTCGCGCTG 1036
Qy 2182 ATGCTGTCTCTTCAACGCCCTTCAGACCTCTAACCTCTACCTTCTGCTGTGCCGAGC 2241
Dy 1037 ACGGTGGTCTGCTGAGGCCCTGTGTACACTGACACTCTGTATCTCTATGCGCCGAGC 1096
Qy 2242 GTTACGAGATCATTTATGTTGATGCTCCCTCCCTCTCACGAATGAGTCAAGAACTCTAAGAC 2301
Dy 1097 GCTGGAGGTTGTTATC----- 1113
Qy 2302 TAACACTTGTAGCTTACCAACTTTGCTGGCCAGACTCTTTGACCTGGCGCAACGTTGCTG 2361
Dy 1114 -----GACTTCTCCACCTTCGCTGGCCAGTCCATCGATTCGCAACCTTCCCTG 1162
Qy 2362 AGACCAAGATGTGGGACAGGATGAGTACGCTCGACACTCTCGAGGTGATGGCTTCG 2421
Dy 1163 GTGCTGAGGCTTCGGTGTGAGCTTGTGATTAACACTGACAAAGGTGATGCGATTTCG 1222
Qy 2422 TCGTCAAGTCTGGCACTGTTGAG---GACAACAGCAGGTCCTCCCTCTCGCTGAGC 2478
Dy 1223 TCGTTGATGAAGTCTTGAAGTGGCCGACACTCTGAGGTGCTTCCCAACCTCCGAGATG 1282
Qy 2479 TTCTCTCCCTCTCTACAAAGGAAGCCCGCCGACAAGCAC-----TTTCA 2523
Dy 1283 TTCTTTCCCGAGGGCGCAACTGGGACCCCGCAACCCCACTGATGACGAGACTTTCA 1342
Qy 2524 AGTTTGAACGAGCAGCAGCACTACCTGATCAACGATGTTGGCTTTCGCCATGTCAATG 2583
Dy 1343 CTTTGGCGGCTGAATGGAGAGTGGACAATCAACGGAGTTTACCTTCTCGGATTCGAGA 1402
Qy 2584 AGCGTGTCTGGCAAGCCGAGCTCGCAGCTGTGAGGTCTGGGAGCTTCGAGAACTCT 2643
Dy 1403 ACCGTCTCGGCAATGTGCCCCGCGACACTGTTGAGATCTGGGACTTGGAGAACACT 1462

Qy 2644 CTGAGAGGTGAGGACCCCGCTCCACATTTCACTACCTTTGTTGACTTCAAGATCTCTCAAGCGAA 2703
Dy 1463 CCAACGGTTGAGCTCACCTCTGTTCACATTTCACTTCACTTCCGAGTCTCTTCCTGTT 1522
Qy 2704 CTGGTGGTGTGGCAGGTCATGCCCTACGATCTGCTGTTTAAAGATGTCTGCTCTGGT 2763
Dy 1523 CCAGTGGCCGGTGG---AGTCGAGGCTTATGAGGCTGCTGGTCTCAAGGATGTTGCTCGC 1579
Qy 2764 TGGGAGGCGGTGAGACCTTCAGCATTCGAGGCGCCACTACCAACCCCTGGAC----- 2812
Dy 1580 TGGCTCGTGTGAGTGTCTATGTTGAGGCCCACTACGCTCTTTCCCGTAAGTTCTCG 1639
Qy 2813 -----TGGAGCTTACATGTGGCA 2830
Dy 1640 CTTTTTACCTAACTGGTTTTTCACTCATGCTAACATCTACAAGTGGTGTCTACATGTTGCA 1699
Qy 2831 CTGTCAACAACCTATTCACGAGGATAACGATGATGCTGTATTCACGCTCACCGCCAT 2890
Dy 1700 CTGCCAACAACCTGATCCACGAGGACCAAGCATGATGCTGCTTCAATGTCACTGTTCT 1759
Qy 2891 GGAGGAGAAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGC 2950
Dy 1760 CGGTGACTATGCTACAACTACACCGAGTTCTATGACCCCATGGAGCCTCTCTGAGGCC 1819
Qy 2951 CGTTCTTTACACCGCAACGAGCTTCCATGCTCGGCTCGAAACTTCTCGCGGAGTCCAT 3010
Dy 1820 CCGCCCTTCTCTCGGAGAGTTCGAGAATGCGTTCGGGTGACTTTCAGCGAGCTTGGCAT 1879
Qy 3011 CACTGCCGAGTGGAGGAGCTGGCGGAGCAGGAGCCGTACAACCCCTCGATGA 3064
Dy 1880 CACTGACCGCATTCAGGAGATGGGTAGCTTCAACCCCTACGCCAGGCTGATGA 1933

RESULT 12
US-09-942-185-3
; Sequence 3, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, wolfgang
; APPLICANT: Convents, Daniel
; APPLICANT: Doornink, Monique
; APPLICANT: van Gastel, Frans
; APPLICANT: Rodrigues, Amr
; APPLICANT: Topozada, Amr
; APPLICANT: De Vries, Cornelis Hendrikus
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1e1 Phenol
; FILE REFERENCE: C7567
; CURRENT APPLICATION NUMBER: US/09/942,185
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-942-185-3

Query Match 8.2%; Score 300.4; DB 9; Length 2095;
Best Local Similarity 55.2%; Pred. No. 8e-82;
Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;
Qy 1491 CTGACCCCTTTTCAGATTTACCCCACTTCGCGCCCTGCCACTCTCGTGGCTACGATGGCAT 1550
Dy 380 CTTCTCCACCAAGTCTACCTGTATCTGGAGCCGCCCAACATGGTTGGATACGATGGCAT 439
Qy 1551 GAGCCCTGGTCTACTTTCAATGTTCCAGAGAACAGAGACTGTAGTTAGTTAGTCAAA 1610
Dy 440 GTCCCCAGGACCTACCATCATCTCTTCCTCGTGGCACTGAGAGTGTGTGCCCTTCGTGAA 499
Qy 1611 CA-----ATCCCACTGGAGAACTCGGTCCATCTGCAACGGCTCCCGATCGCGTCC 1664
Dy 500 CAGCGGAGAGAACACCTCTCCCAACAGCGCTCCACTTGCACGGCTCTTTCTCTCGAGTCC 559

Oy 1665 TTTCGATGGTTGGGCTGAAGATGTGACCTTCCTGGCGAGTACAGGATTTACTACTTCC 1724
Db 560 CTTTGATGGTTGGGCTGAGGACACTACCAGCTGGCGAGTACAGGATTTACTACTACC 619
Oy 1725 CAACCTACCAATCCGCCCTTCTGTGTAGTACATGACACACGCTTTTCATGAAGTATGTA 1784
Db 620 CAACAGGAGGCTGCCCGCATGCTTTGTGTACATGACCATGC----- 661
Oy 1785 CGAGCCTTTATCTTCTTGGCTACCTTTGGCTTAACCAACTTCCTTTCTAGACTGCTGAG 1844
Db 662 -----CATGTCCATCACGCCCGAG 680
Oy 1845 AATGCTACTTTTGGTCAAGCTGGCCCTACATTTATCAACGAGGCTGAGGATGCTCTC 1904
Db 681 AACGCTACATGGGTCAAGCTGGTGTCTACATGATCCAGGACCCGGCTGAGGATGCCCTG 740
Oy 1905 GGTCTTCTAGTGGCTATGGCGAGTTCGATATCCCTCTGATCCCTGACGCCCAAGTACTAT 1964
Db 741 AACCTCCCACGGCTACGGCGAGTTGATATCCCTTTGGTTCTGACTGCCAAGCGATAC 800
Oy 1965 AACGCCGATGTACCTCGCTTCGACCGAGGTGAGGACGAGGCTGTGGGAGATGTC 2024
Db 801 AACGACAGCGCATCTCTTCTCCACCAATGGAGAGGTTTCCAGCTTCTGGGGTGACGTT 860
Oy 2025 ATCCATGT----- 2032
Db 861 ATTCAAGTGGTAAGTTGAGCCCATTTGAGATGCTTCAGATCTCAGATATCATGATATGA 920
Oy 2033 -----CAACGGACAGCCATGGCCTTTTCCTTAACG 2061
Db 921 AATTGTGATGCTCTAACCAAGTGCTATCACAGAAGGTCAGCCTTGGCCTATGCTCAACG 980
Oy 2062 TCCAGCCCGGAGTACGTTTCCGATTTCCATCAAGCTGCGGTGCTCTCGTGGTGGCTCC 2121
Db 981 TGCAGCCCGCAAGTACGCTTCCGCTTCCCTCAACGCTGCGGTCTCACGCTCTTTCGCTC 1040
Oy 2122 TCTACTCTGTCAAGACAGCTCTCCCAAGTCAGAAATTTCTTCCAACTCATTTGGCTCTG 2181
Db 1041 TGTATCTGTACCTCTGAGGATTCAGACAGAGTATCCCTTCCAGGTCATGCGCGTG 1100
Oy 2182 ATGCTGGTCTCCTCAAGCCCGCTTCAGACCTCTAACCTCTACCTTCTGTGTGCCGAGC 2241
Db 1101 ACGGTGGTCTGCTTCAAGGCCCTGTGTGACACTGACACTCTGTACATCTCTATGGCCGAGC 1160
Oy 2242 GTTACGAGATCATATTATTTGGTATGCCCTCCCTCTCACGAATGAGTCAAGAACTTAAGAC 2301
Db 1161 GCTGGGAGGTTGTTATC----- 1177
Oy 2302 TAACACTTGTAGACTTCAACAACTTTTGTGGCGAGACTCTTGACCTGCGCAACGTTGCTG 2361
Db 1178 -----GACTTCTCCACTTTCGCTGGCCAGTCCATCATGATATCCGCAACCTTCTCTG 1226
Oy 2362 AGACCAACGATGTCGGGACGAGGATGAGTAGCTCGCACTCTCGAGGTGATGCGCTTCG 2421
Db 1227 GTGCTGACGGTCTCGGTGTTGAGCCTGAGTTGATTAACACTGACAAGGTTCATGCGATTCTG 1286
Oy 2422 TCGTCACTCTGGCACTGTTGAG---GACAACAGCCAGGTCCCTCCACTCTCCGCTGAGC 2478
Db 1287 TCGTTGATGAAGTCTCTGAGTGGCCGACACTTCTGAGGTGCGCTCCCAACCTCCGAGATG 1346
Oy 2479 TTCCCTTTCCCTCTCACAAAGGAAGGCCCGCGCAAGAC-----TTTCA 2523
Db 1347 TTCCCTTTCCCGAGGGCGCACTGGGACCCCGCAACCCCACTCATGACGAGACTTTCA 1406
Oy 2524 AGTTTGAACGACGACGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCATG 2583
Db 1407 CTTTGGCGGCTGCTAATGGACAGTGGACAAATCAACGGAGTTACCTTCTCGGATGTCGAGA 1466
Oy 2584 ACGGTGCTGCGCAAGCCCGAGCTGGGACCGTGTGAGGTCTGGGAGCTCGAGAACTCCT 2643
Db 1467 ACCGTCTGCTCGCAATGTGCCCGCGACACTGTTGAGATCTGGCGACTTTGAGAACT 1526

Oy 2644 CTGGAGGTGGAGCCACCCCGTCCACATTCACCTTGTGTACTTCAAGATCCTCAAGCGAA 2703
Db 1527 CCAAGGTTGGACTCACCTGTTTACATTCACCTCGTTGACTTCGAGTCTCTTCGCTGTT 1586
Oy 2704 CTGGTGTGCTGGCAGGCTCATGCCCCTACGAGTCTGCTGGTCTTAAGGATGCTGCTCGT 2763
Db 1587 CCACCTGCCCGTGG---AGTCGAGCCTTATGAGGCTGCTGGTCTCAAGGATGTTGCTGGC 1643
Oy 2764 TGGCAGGGTTCAGACCTTGACCATCGAGGCCCACTACCAACCCCTGGAC----- 2812
Db 1644 TGGCTGCTGAGGTTGCTATGTTGAGGCCCACTACGCTCTTCCCGTAAGTTCG 1703
Oy 2813 -----TGGAGCTTACATGTGCA 2830
Db 1704 CCTTTTACCTAACTGGTTTTCACATCATGCTAACATCTACAAGTGGTGTCTACATGTGCA 1763
Oy 2831 CTGTCACAACCTCATTTACGAGGATAACGATGATGCTGTATTTCAACGTCACGCCCAT 2890
Db 1764 CTGCCACAACCTGATCCACGAGGACGACATGATGCTGCTTTCAATGTCACTGTTCT 1823
Oy 2891 GGAGGAGAAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGC 2950
Db 1824 CGGTGACTATGGCTACAACTACACGAGTTTCAATTGACCCCATGGAGCTCTCTGGAGGCC 1883
Oy 2951 CGTTCCTTACAAACGCAACGACTTCCATCTCGCTCGCTGAAACTTCTCCGCGAGTCCAT 3010
Db 1884 CGCCCTCTCTCTCGGAGAGTTTCGAGATGGCTCGGTCGACTTCAGGAGCTTGCCAT 1943
Oy 3011 CACTGCCGAGTGCAGGAGCTGGCGGACGAGCCGTACAAACCCCTCGATGA 3064
Db 1944 CACTGACCGCATTCAGGAGATGGCTAGCTTCAACCCCTACGCCAGGCTGATGA 1997

RESULT 13

US-10-080-210-8
; Sequence 8, Application US/10080210
; Patent No. US2020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 858
; TYPE: DNA
; ORGANISM: *Amerosporium atrum*
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(858)
; OTHER INFORMATION: n = A,T,C or G
US-10-080-210-8

Query Match 4.1%; Score 150; DB 12; Length 858;
Best Local Similarity 63.4%; Pred. No. 1.1e-35;
Matches 269; Conservative 0; Mismatches 140; Indels 15; Gaps 2;

Oy 1836 ACTGCTGAGATGCTACTTGTGGTCAAGTGGCGCTTACATATCAACGACGAGGCTGAG 1895
Db 2 ACCGCCGAGAGCGCTTACTTTGGTCAAGTGGCTTTTACATTTCTGCAGACCCCGCTGAA 61
Oy 1896 GATGCTCTCGGTCTTCTAGTGGCTATGCGAGTTCGATATCCCTCTGATCCTGACGGCC 1955
Db 62 GATGATTTGGGTCTGCCT-----TCTGGCAAGTATGATGTACCTCTTGCATCTGCTCC 115
Oy 1956 AAGTACTATAACGCGATGTTACCTTGGTTCGACCGAGGTTGAGGACGAGCCTGTGG 2015


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Db 116 AGCAGTACAACAGCGACGGTACCTCTTCGACCCAAAGGAGGACGACCGATTCACTGTTC 175
Qy 2016 GGAGATGTCATCCATGTCTAACGAGACGACCATGGCCTTTCTTAAAGCTCCAGCCCGCAAG 2075
Db 176 GCGGATGTCATCCAGCTCAACGAGACGACCATGGCCTACTTTAAGTCCGAGCTCGCAAG 235
Qy 2076 TACCGTTTCGGATTGCTCAACGCTGCGGTGCTCGTGTGGCTCCTCTACCTCCTCAGG 2135
Db 236 TACCGTCTCGGTTCTCTCAATGCTCTATCAGCCGCTGCTTCAAGCTCACTTTTCAGGGCT 295
Qy 2136 ACCAGCTCTCCCAACGTCAGAAATTCCTTTCCAAAGTCATTCGCCTCTGATGCTGCTCTCTT 2195
Db 296 GATGGCAAGTGATCAAC-----TTTCTGTATCGGTGGCGGATCTGCTCTTG 346
Qy 2196 CAAGCCCGCGTTTCAGACCTCTAACCTCTACCTTGCTTTCGCGAGCGGTACGAGATCAIT 2255
Db 347 ACCAAGCCTGTTTCAGACAAACCACTTGAGATCTCTATGTCGCGAGCGCTGGGAGGTGTT 406
Qy 2256 ATTG 2259
Db 407 TTTG 410

RESULT 14
US-09-738-626-1053
; Sequence 1053, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1053
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1053

Query Match 1.6%; Score 60; DB 9; Length 1533;
Best Local Similarity 51.5%; Pred. No. 1e-07;
Matches 138; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

Qy 1835 GACTGCTGAGAAATGCTACTTTGGTCAGGCTGGCGCCTACATATTACAACGACGAGGCTGA 1894
Db 483 GACAGGTTTGATGCTACCGTGGTTGGCGGGGATGATCATTTGGAAGATGAAGCAAC 542
Qy 1895 GGATGCTCTCGTCTCTCTAGTGGGTATGGCGAGTTCGATATCCCTCTGATCCTCACGGC 1954
Db 543 AGACAAGCTGGATGCTGCCACCGGAGTAGCGGTGTGACCATATTCCGCTGGTTTTAATGA 602
Qy 1955 CAAGTACTATAACGCGCGATGGTACCTGCGTTCGACCGAGGGGTGAGGACCGACCGACTGTG 2014
Db 603 TCACCGCTTCTTAGAAGAGGGTTCCCTTGATGAGGAAGACCTCCCGGATCTTGGGCTGTT 662
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Qy 2015 GGGAGATGTCATCCATGTCAACGGACAGCCATGGCCTTTCTTAAAGTCCACGCCCGGCA 2074
Db 663 GGGCGATACCCCACTGGCAATGGCAATACCAATCGCACTTTGATGCCACCAACGCGCG 722
Qy 2075 GPACCGTTTCCGATTCCCTCAACGCTGCC 2102
Db 723 GGTTCGGTTCCGCTGCTCAACGGCTCC 750

RESULT 15
US-09-974-300-2204
; Sequence 2204, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2204
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2204

Query Match 1.2%; Score 44.6; DB 10; Length 1470;
Best Local Similarity 65.7%; Pred. No. 0.0058;
Matches 65; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 2004 CAGGACCTGTGGGAGATGTCTATCCATGTCAACGACGACCCATGGCCTTTCTTAAAGTC 2063
Db 598 CCGGCTTTTTCGGTGATACCATTTTAGTCAACGGCAAGGTATGGCCTTTCGCTGAACGTG 657
Qy 2064 CAGCCCCCGCAAGTACCGTTTCCGATTCTCTCAACGCTGCC 2102
Db 658 GAACCCCGAAAAATACCGTTTTCGGGATCTGAACGCTCC 696

Search completed: February 13, 2003, 05:15:42
Job time : 207.097 secs
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(oiden) uspto

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 18:21:11 ; Search time 4958.71 Seconds
(without alignments)
12009.347 Million cell updates/sec

Title: US-09-218-702-3

Perfect score: 3677

Sequence: 1 ctgctagcctcacttgta.....gataactgaactgggtcaat 3677

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vrt:*
 - 22: em_gss_fun:*
 - 23: em_gss_mam:*
 - 24: em_gss_mus:*
 - 25: em_gss_Other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112.4	3.1	600	10	BE188240
2	112.4	3.1	700	10	BE187716
3	60.4	1.6	664	10	BE188099
4	51.8	1.4	580	13	BJ159802
5	50.2	1.4	557	10	AW339201
6	48.6	1.3	599	12	BF258534

c	7	48.4	1.3	465	12	BG053739
	8	47.8	1.3	461	9	AI623533
	9	47	1.3	848	10	BE216983
	10	46.2	1.3	475	12	BF115462
	11	44.8	1.2	463	12	BF059036
	12	44.8	1.2	481	9	AI394530
	13	44.4	1.2	541	9	AI432408
	14	44	1.2	416	9	AI933417
	15	43.4	1.2	467	14	W15474
	16	43.2	1.2	409	9	AA731500
	17	43.2	1.2	426	9	AA807669
	18	43.2	1.2	442	9	AA687287
	19	43.2	1.2	451	9	AI189014
	20	43.2	1.2	463	10	AW576243
	21	43.2	1.2	500	9	AI126707
	22	43.2	1.2	507	9	AA977691
	23	43.2	1.2	538	10	BE379236
	24	43.2	1.2	571	10	AW007209
	25	43.2	1.2	646	14	BM794003
	26	43.2	1.2	777	12	BG744974
c	27	43	1.2	337	9	AA788842
	28	42.8	1.2	435	10	AW575077
	29	42.8	1.2	463	12	BF446871
	30	42.8	1.2	480	9	AA481991
	31	42.8	1.2	486	9	AA825413
	32	42.8	1.2	496	9	AI860612
	33	42.8	1.2	497	9	AI187025
	34	42.8	1.2	505	9	AA411507
	35	42.8	1.2	508	9	AI200611
	36	42.8	1.2	511	9	AA829600
	37	42.8	1.2	511	9	AI223314
	38	42.8	1.2	511	9	AA262448
	39	42.8	1.2	511	9	AA478433
	40	42.8	1.2	515	9	AA854735
	41	42.8	1.2	526	9	AI077527
	42	42.8	1.2	530	12	BF445939
	43	42.8	1.2	535	9	AI159881
	44	42.8	1.2	592	9	AI279006
	45	42.8	1.2	610	9	AI336193

ALIGNMENTS

RESULT 1

BE188240

LOCUS

DEFINITION

W7ATIG In vitro expressed cDNAs Cladosporium fulvum

Accession

BE188240

VERSION

EST

KEYWORDS

SOURCE

ORGANISM

Cladosporium fulvum.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

600 bp mRNA linear EST 25-SEP-2000
W7ATIG In vitro expressed cDNAs Cladosporium fulvum CDNA similar to
Bilirubin oxidase precursor, mRNA sequence.

Accession BE188240.1 GI:8667479

Version EST

Keywords Cladosporium fulvum.

Source Cladosporium fulvum

Reference 1 (bases 1 to 600)

Authors Clark A.J., Rasmussen, S.W. and Oliver, R.P.

Title In vitro expressed genes of Cladosporium fulvum

Journal Unpublished (2000)

Comment Contact: R.P. Oliver

Necrotrophic Phytopathology Research Centre

Murdoch University

SABC, Perth 6150, Western Australia

Tel: +61-8-9360-7404

Fax: +61-8-9360-6303

High quality sequence stop: 600

POLYA-No.

Location/Qualifiers

1..600

/organism="Cladosporium fulvum"

FEATURES

source

1..600

/organism="Cladosporium fulvum"

Query Match		3.1%	Score 112.4	DB 10	Length 600
Best Local Similarity		55.9%	Pred. No. 1.7e-19	Indels 9	Gaps 5
Matches 313		Conservative 0	Mismatches 238		
QY	2366	CAACGATGTCGGCAGCAGGATGATGACGTCGCGACTCTCGAGGTGATGCGCTTCGTCGT	2425		
DB	42	CAACAGGGGGCCAAACACACGNGTNCATAACACGACAGGTCATGAGGTCGTCGT	101		
QY	2426	CAG---CTCTGGCACTGTTGAGGACACAGCCAGGTCCTCCACTCTCCGTGACGTTCC	2482		
DB	102	TGGAGACAGCGTCACCGACGAGTCCAAACAACAGTACCATCAACTCTGAACGGTGCCAT	161		
QY	2483	TTTCCTCTCACAAGGAGGCCCCGGCGGACACGACTTCAAGTTTGAACCCGACGACGG	2542		
DB	162	CGACTGGCCAGCGCAGCGAGACACTATTGACAGACCTTCAACTTCCAGATGGCGCGGC	221		
QY	2543	ACACTACCTGA---TCAACGATGTTGGCTTTGCCGAGTGCTCAATCAGCGGTGCTCTGGCCAA	2599		
DB	222	GGAGTGTGGACCGTCAATGCGGTGGATTTACGACCCGAACTCGCGTGTCTGGGTAG	281		
QY	2600	CGCCGAGCTCGGCACCGCTTGAGGCTCTGGAGCTCAGAACTCCTCTGGAGGCTGGAGCCA	2659		
DB	282	GCGCCACAAGGCACTGTCGAGCGCTTGGCGCTCGTGACACTCGCGGTCCGGCTGTCCA	341		
QY	2660	CCCGCTCACATTCACCTGTTGACTTCAAGATCCTCAAGCGAAGTGTGTCTGGTGCGCA	2719		
DB	342	CCCAGTACATATCCATCTGTCAACATCGACGTCCTCTCGCGTACTGGTGGTCCCGTGG	401		
QY	2720	GGTCATGCCCTACGAGTCTGCTGGTCTTAAAGATGTCGTCTGGTGGCGAGGTGAGAC	2779		
DB	402	CCTCATGCCATACGAAAGTGTCTGGTCTGAAAGAGCGTCTTATGCTGGCTCTCGGCGAAT	461		
QY	2780	CCTGACCATCGAGGCCCACTACCAACCCCTGGACTGAGCTTACATGTGGCACTGTCACAA	2839		
DB	462	TCTGACGCTGTGCTTTTACGGTCTTTGGAACGG-CTTGACATGTTTTCATTGGCCAC-A	519		
QY	2840	CCTCATTCAGGAGGATACGACATGATGG-CTGATATTCAGCTCACCGCCATGGAGGAGA	2898		
DB	520	CCTTGTACACGAAGATACACCATGATGGCCCGCTTCAACACGACACCCCTTGAACGCTG	579		
QY	2899	AGGGATATCTTCAGGAGGAC 2918			
DB	580	GGCTACGACTTCAACAGCAC 599			
RESULT 2					
LOCUS	BE187716	700 bp		mRNA	linear
DEFINITION	BILOX In vitro expressed cDNAs Cladosporium fulvum cDNA similar to				
ACCESSION	BE187716	Bilirubin oxidase precursor, mRNA sequence.			
KEYWORDS	EST	GI:8666955			
SOURCE	Cladosporium fulvum.				
ORGANISM	Cladosporium fulvum				
REFERENCE	1 (bases 1 to 700)				
AUTHORS	Clark,A.J., Rasmussen,S.W. and Oliver,R.P.				
TITLE	In vitro expressed genes of Cladosporium fulvum				
JOURNAL	Unpublished (2000)				

BEI88099
 BEI88099.1 GI:8667338
 EST.
 Cladosporium fulvum.
 Cladosporium fulvum
 Cladosporium fulvum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
 Chaetothyriomycetes incertae sedis; Mycosphaerellaceae; mitosporic
 Mycosphaerellaceae; Cladosporium.
 1 (bases 1 to 664)
 Clark,A.J., Rasmussen,S.W. and Oliver,R.P.
 In vitro expressed genes of Cladosporium fulvum
 Unpublished (2000)
 Contact: R.P.Oliver
 Necrotrophic Phytopathology Research Centre
 Murdoch University
 Murdoch University
 SABC, Perth 6150, Western Australia
 Tel: +61-8-9360-7404
 Fax: +61-8-9360-6303
 Email: roliver@central.murdoch.edu.au
 High quality sequence stop: 664
 POLYA=No.

[illegible]

RESULT 4	EST 24-JAN-2002
LOCUS	linear
DEFINITION	580 bp mRNA
	BJ159802 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone
	pBb17c15 5', mRNA sequence.
ACCSSION	BJ159802
VERSION	BJ159802.1
KEYWORDS	GI:18327798
SOURCE	EST.
ORGANISM	Physcomitrella patens subsp. patens.
	Physcomitrella patens subsp. patens
	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Bryophyta:
	Bryopsida: Funariidae, Funariales; Funariaceae; Physcomitrella.
REFERENCE	1 (bases 1 to 580)
AUTHORS	Fujita, T., Shin-i.T., Seki, M., Kamiya, A., Uchiyama, I., Nishiyama, T., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.

TITLE Comparison of the moss *Physcomitrella patens* genome with flowering plants genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified lPS phage vector (Mo bi Tec, Germany). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. *Protonemata* were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light.

```

FEATURES
  source
    Location/Qualifiers
      1..580
        /organism="Physcomitrella patens subsp. patens"
        /db_xref="taxon:145481"
        /clone="oph17c15"
        /clone_lib="full length cDNA library, chloronemata and
        young gametophores"
        /tissue_types="mixture of chloronemata and young
        gametophores with 2 to 5 leaves"
      BASE COUNT      124 a 138 c 170 g 148 t
      ORIGIN

Query Match      1.4%; Score 51.8; DB 13; Length 580;
Best Local Similarity 56.9%; Pred. No. 0.0095;
Matches 95; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 2003 CCAGGACCTGGGGAGATGTCATCCATGTCACGGACAGCCATGGCTTTCCTTACGT 2062
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 475 CCGGGAGTATTTCGGCGACGTGATTCCTCGTGAACGGCAAGACATGGCTTACCTTCGTCGT 416
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 2063 CCAGCCCGGAAGTACCGTTTCCGATTTCCTCAACGCCTCCGCTGTCTCGTGCTTGGCTCCCT 2122
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 415 CAAGCCTCGCAAGTACCGCTTCCTCGTCTCGTGAATGGTGGAATCCGAGAGTTTTCGAGCT 356
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 2123 CTACTCTCGTCAGGACCAAGCTCTCCCAACGTCAGAAATTCCTTTTCCAAG 2169
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 TTCCTCGAGCACCCACCAAAACCGGCTTCATTTCAAATTTGGTACCGAAG 309
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 5	
AW339201	
LOCUS	557 bp mRNA linear EST 31-JAN-2000
DEFINITION	ha74a03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879404 3', similar to TR:Q63928 Q63928 BRAHMA RELATED PROTEIN 1 ;, mRNA sequence.
ACCESSION	AW339201
VERSION	AW339201.1 GI:6835827
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1. (bases 1 to 557)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapsb-femail.nih.gov Life Technologies catalog #: 11548-013 DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

www-bio.1lnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand
Seq primer: -40up from Gibco
High quality sequence stop: 344.

FEATURES

source
1. .557
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2879404"
/clone_lib="NCI CGAP Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="organ: pancreas; Vector: pCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

BASE COUNT 162 a 152 c 161 g 78 t 4 others

Query Match 1.4%; Score 50.2; DB 10; Length 557;
Best Local Similarity 45.7%; Pred. No. 0.026;
Matches 166; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 2765 GGGCAGGGGTGAGACCTGACATCGAGCCGACCTACCAACCTGGACTGGAGCTTACAT 2824

Db 80 GGACAGCAGTGGACGTGACGTGAGGAGGTCTTCATCCAGCTGCCCTCGCGAAGGAGCT 139

QY 2825 GTGGCACTGTACACCTCATTCACGAGGATACACATGATGGCTGATTCACACGTGAC 2884

Db 140 GCCCGAGTACTACGAGCTATCCGACGCCCTGGAGCTTCAGAGATAAAGGAGCGCAT 199

QY 2885 CGCCATGGAGGAGGAGGATATCTTCAGAGGACTTTCAGAGGCCCATGAACCCCAAGTG 2944

Db 200 TCGCAACACAGTACCGGAGCTCAACGACCTAGAGAGGAGCGTCATGCTCTGTGCCA 259

QY 2945 GCGCGCGTTCCTTCAACCGCAAGACTTCCATGCTGCGCTGGAAATCTTCCGCCGA 3004

Db 260 GAACGCACAGACTTCAACCTGGAGGGTCCCTGATATGAAGACTCCATCGTCTTGCA 319

QY 3005 GTCCATCACTGCGGAGTGCAGGAGTGGCCGAGGAGCGGTACAAACCGCTCGATCA 3064

Db 320 GTCGGTCTTCACCGCTGCGGCAAAATCGAGAGGAGGATGACATGAAGGCGAGA 379

QY 3065 GATCTCGAGGAGTCTGGAATCGAGAGTAAACCCGAGCCACAGCTCTACAATCGTTT 3124

Db 380 GAGTGAGGANGAGAGAGCGGAGGAGAAAGCCGATCCATCTCGGTCGTCAAN 439

QY 3125 TGA 3127

Db 440 TGA 442

RESULT 6
BF258534
LOCUS
DEFINITION
599 bp mRNA linear EST 22-OCT-2001
HVSMEF0015P21f Hordeum vulgare seedling root EST library HVCDNA0007
(Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEF0015P21f, mRNA sequence.

ACCESSION
BF258534
VERSION
BF258534.2 GI:13119477

FEATURES

source
Hordeum vulgare.
Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 599)
Wing, R., Close, T.J., Klein, H., A., Wise, R., Begum, D., Frisch, D., Yu
, R.D., Oates, R. and Main, D.,
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling root cDNA library

JOURNAL
COMMENT

Unpublished (2001)
On Nov 16, 2000 this sequence version replaced gi:11187647.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 451
Seq primer: AATTACCCCTCACTAAAGG
High quality sequence stop: 552.

FEATURES

source
1. .599
Location/Qualifiers
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEF0015P21f"
/clone_lib="Hordeum vulgare seedling root EST library
HVCDNA0007 (Etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJCL21"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedling roots were
then harvested, total RNA was prepared, poly(A) RNA was
purified, one primary unamplified cDNA library was made,
and 1 million pfu were in vivo excised to give pBluescript
SK(-) cDNA phagemids. These steps were performed in the TJ
Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Klein H, A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT
ORIGIN

96 a 215 c 206 g 82 t
Query Match 1.3%; Score 48.6; DB 12; Length 599;
Best Local Similarity 63.0%; Pred. No. 0.074;
Matches 75; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 2016 GGAGATGTCATCATGTCACAGGACAGCATGGCTTTCTTAACGTCAGCCCCGCAAG 2075

Db 59 GCGCGTGTGCTGCTGCCCAACGCGCAAGGCTTCTCGCGTGGCGGCCGCCGC 118

QY 2076 TACCGTTTCCGATTCCTCAACGCTGCCGTCTCTGCTTGGCTCTCTACCTCGTCAG 2134

Db 119 TACCGCTTCCGATCTCTCAACGCTGCCGACAGCGCGGCTTCTTCGCCCTCTCGCTCTCGG 177

RESULT 7

LOCUS

DEFINITION
BG053739
RH122_9_B08.b1_A003 Rhizome2 (RH122) Sorghum propinquum cDNA, mRNA
sequence.

ACCESSION
BG053739

VERSION
BG053739.1 GI:12509741

KEYWORDS
EST.

SOURCE
Sorghum propinquum.

ORGANISM

Sorghum propinquum.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 465)
Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt, L.H.

An EST database from Sorghum: Sorghum propinquum rhizomes
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Seq primer: JEN REV
High quality sequence stop: 421
POLYA-No. Location/Qualifiers
1. .465

FEATURES
source

/organism="Sorghum propinquum"
/db_xref="taxon:132711"

/clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

72 a 128 c 193 g 72 t

Query Match 1.3%; Score 48.4; DB 12; Length 465;
Best Local Similarity 59.4%; Pred. No. 0.073;
Matches 82; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 2016 GGAGATGTCATCCATGTCAACGGACAGCATGGCTTTCCTTAAGTCCAGCCCGCAAG 2075

Db 185 GGTGAGGCGGTACCGTCAACGGCAAGCGTGGCGTTCCTTCGCGGTCCACCGCGCGGC 126

Qy 2076 TACCGTTTCCGATTCCTCAACGGCTGCCGTGCTGCTGGCTCTTACCTCGTCAGG 2135

Db 125 TACCGTTTCCGATTCCTCAACGGCAGCAACGGCGCTACTTCAAGTCTCGCTCCAC 66

Qy 2136 ACCAGCTTCCCAAGCTC 2153

Db 65 GGCATGCCCTCCAGCTC 48

RESULT 8
AI623533
LOCUS
DEFINITION
ts36a05.x1 NCI-CGAP Ut4 Homo sapiens cDNA clone IMAGE:2230640 3', similar to TR:Q63928 Q63928 BRAHMA RELATED PROTEIN 1 ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AI623533
AI623533.1 GI:4648464
human.
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 461)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 944 Std Error: 0.00
Seq primer: -40Up from Gibco
High quality sequence stop: 438
POLYA-No. Location/Qualifiers
1. .461

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2230640"
/clone_lib="NCI-CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
/lab_host="DH10B"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"

BASE COUNT 131 a 126 c 130 g 74 t

Query Match 1.3%; Score 47.8; DB 9; Length 461;
Best Local Similarity 46.1%; Pred. No. 0.11; 187; Indels 0; Gaps 0;

Matches 160; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

Qy 2767 GCAGGGGTGAGACCCCTGACCATCCAGGCCACCTACCAACCCCTGGACTGGAGCTTACATGT 2826

Db 85 GCAGCAGTGGACGTCAAGTCCAGGAGGTCTTCATCCAGCTGCCCTCGGAAGAGCTGC 144

Qy 2827 GGCATGTGCACAACCTATTCCAGGAGGATACGACATGATGGCTGTATTCAACGTACCG 2886

Db 145 CCGAGTACTAGAGTCTATCCGCAAGCCCGTGGACTTCAAGAAGATAAAGGAGCGCATTC 204

Qy 2887 CCATGGAGGAGAAGGATATCTTCAGGAGGACTTCAGAGACCCCATGAACCCCAAGTCGC 2945

Db 205 GCAACCAAGATACCGCAGCCTCAACGACCTAGAGAAGGAGCTCATGCTCTGTGCCAGA 264

Qy 2947 GCGCGCTTCTTACAAACCGCAACGACTTCCATGCTCGCGCTGGAACTTCTCCGCCGAGT 3006

Db 265 ACGCACAGACCTTCAACCTGGAGGGCTCCCTGATCTATGAAGACTCCATCGCTTTGCAGT 324

Qy 3007 CCATCACTGCCCGAGTGCAGGAGCTGCGCGAGCAGAGCCGCTACAAACGCTTCGATGAGA 3066

Db 325 CGGTCTTCACCAGCGTGGCGCAGAAAATCGAAGAGGAGGTACACAGTGAAGCGGAGGAGA 384

Qy 3067 TCCTGGAGGATCTTGGATCGAGGAGTAACCCCGAGCCCAAGCTC 3113

Db 385 GTGAGGAGGAGGAAGAGGGCGGAGAGAAGGCTCCGAATCCGAATCTC 431

RESULT 9

BE216983

LOCUS

DEFINITION

EST0376 Triticum aestivum Lambda zap Triticum aestivum cDNA clone

JAL-SA-A06_t3 5', mRNA sequence.

ACCESSION

BE216983

VERSION

BE216983.1 GI:8904523

KEYWORDS

SOURCE

ORGANISM

Triticum aestivum

bread wheat.

848 bp mRNA linear EST 03-JUL-2000

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Analysis of an EST database reveals a probable CF2 resistance gene homolog in wheat

Unpublished (2000)

Contact: Anderson, J.M.

Crop Production & Pest Control Research Unit

USDA-ARS

1150 Lilly Hall, West Lafayette, IN 47907, USA


```

Db      333  CGGTCCTCACCCAGCGTCCNCCACAGAAATCGAGAGAAGGAGGATGNCAGTGAAGCGGAGGAGA 392
Qy      3067  TCCTGGAGGATCTTGGAAATCGAGGAGGATAAACCCC 3100
Db      393  GTGAGGAGGAGGAAGAGGCGCGAGGAGGAAGGCTC 426

Search completed: February 13, 2003, 03:10:22
Job time : 4977.71 secs

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Search completed: February 13, 2003, 03:10:22
Job time : 4977.71 secs

Qy 3067 TCCTGGAGGATCTTGGAAATCGAGGACTAAACCCC 3100
 Db 393 GTGAGGAGGAGGAAGACGGCGCGAGGAGGAAGGCTC 426

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